



5'-most EST xpa700794387.hl Method BLASTX NCBI GI g2529685 BLAST score 644 E value 2.0e-67 Match length 150 % identity (AC002535) putative dimethyladenosine transferase NCBI Description [Arabidopsis thaliana] 26213 Seq. No. 136668 1.R1040 Contig ID $jC-gmf\overline{1}02220063f03d1$ 5'-most EST Method BLASTX g2880042 NCBI GI BLAST score 273 6.0e-24 E value Match length 79 % identity (AC002340) putative 3-hydroxyisobutyryl-coenzyme A NCBI Description hydrolase [Arabidopsis thaliana] Seq. No. 26214 136670 2.R1040 Contig ID rca700997758.h1 5'-most EST 26215 Seq. No. 136688_1.R1040 Contig ID 5'-most EST uC-gmropic087c03b1 BLASTX Method NCBI GI g2129955 199 BLAST score 1.0e-15 E value Match length 55 67 % identity photoassimilate-responsive protein PAR-1b precursor -NCBI Description common tobacco >gi 871487 emb CAA58731 (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum] 26216 Seq. No. 136690 1.R1040 Contig ID 5'-most EST $ncj700\overline{9}75715.h1$ Seq. No. 26217 136696 1.R1040 Contig ID $ncj700\overline{9}75723.h1$ 5'-most EST 26218 Seq. No. 136710 1.R1040 Contig ID kmv700741711.h15'-most EST 26219 Seq. No. Contig ID 136716 1.R1040

Seq. No. 26220

 $ncj700\overline{9}75761.h1$

5'-most EST

5'-most EST

```
Contig ID
                   136729 1.R1040
5'-most EST
                   zsg701123246.hl
Seq. No.
                   26221
Contig ID
                   136742 1.R1040
5'-most EST
                   ncj700975805.hl
Method
                   BLASTX
                   q2864614
NCBI GI
BLAST score
                   361
E value
                   2.0e-34
Match length
                   116
% identity
                   57
NCBI Description (ALO21811) putative protein [Arabidopsis thaliana]
Seq. No.
                   26222
Contig ID
                   136748 1.R1040
5'-most EST
                   q4302457
Method
                   BLASTX
NCBI GI
                   q3386609
BLAST score
                   271
E value
                   2.0e-23
Match length
                   172
% identity
NCBI Description
                   (AC004665) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   26223
Contig ID
                   136758 1.R1040
5'-most EST
                   uC-gmrominsoy071g11b1
Method
                   BLASTX
NCBI GI
                   g4567303
BLAST score
                   392
E value
                   9.0e-38
Match length
                   81
% identity
NCBI Description
                   (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                   26224
Contig ID
                   136777 1.R1040
5'-most EST
                   asn701\overline{1}41013.h1
Method
                   BLASTX
NCBI GI
                   g4580395
BLAST score
                   132
                   3.0e-13
E value
Match length
                   84
% identity
                   (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                   thaliana]
                   26225
Seq. No.
Contig ID
                   136790 1.R1040
5'-most EST
                   ncj700\overline{9}75914.h1
Seq. No.
                   26226
Contig ID
                   136793 1.R1040
```

ncj700978696.h1

```
Seq. No.
                  26227
                  136793 2.R1040
Contig ID
5'-most EST
                  ncj700979468.h1
Seq. No.
                  26228
Contig ID
                  136808 1.R1040
                  zhf700956972.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3135273
BLAST score
                  428
E value
                  3.0e-42
Match length
                  127
% identity
NCBI Description
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
                  >gi 4191773 (AC005917) putative WD-40 repeat protein
                  [Arabidopsis thaliana]
Seq. No.
                  26229
Contig ID
                  136815 1.R1040
5'-most EST
                  vzy700752479.hl
Method
                  BLASTX
NCBI GI
                  a320585
BLAST score
                  450
E value
                  1.0e-44
Match length
                  138
                  58
% identity
NCBI Description
                  polygalacturonase (EC 3.2.1.15) 1 beta chain precursor -
                  tomato >gi 170480 (M98466) polygalacturonase isoenzyme 1
                  beta subunit [Lycopersicon esculentum] >gi 1762586 (U63374)
                  polygalacturonase isoenzyme 1 beta subunit [Lycopersicon
                  esculentum]
Seq. No.
                  26230
Contig ID
                  136821 1.R1040
5'-most EST
                  ncj700976007.hl
                  26231
Seq. No.
Contig ID
                  136852 1.R1040
5'-most EST
                  leu701\overline{1}49191.h1
                  26232
Seq. No.
Contig ID
                  136856 1.R1040
5'-most EST
                  ncj700976137.hl
Method
                  BLASTX
NCBI GI
                  g3065835
BLAST score
                  492
E value
                  6.0e-50
Match length
                  108
% identity
NCBI Description
                  (AF058800) putative methyltransferase [Arabidopsis
                  thaliana]
                  26233
Seq. No.
Contig ID
                  136866 1.R1040
5'-most EST
                  uC-gmflminsoy040a02b1
```

Contig ID

26240

137019 1.R1040



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136879 1.R1040
Contig ID
5'-most EST
                   bth700846149.h1
Seq. No.
                   26235
                   136884 1.R1040
Contig ID
                   zzp700830287.h1
5'-most EST
Method
                   BLASTX
                   g3063471
NCBI GI
BLAST score
                   357
E value
                   6.0e-34
Match length
                   123
% identity
                   56
                   (AC003981) F22013.33 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26236
Contig ID
                   136903 1.R1040
                   ncj700976415.hl
5'-most EST
Seq. No.
                   26237
Contig ID
                   136947 1.R1040
5'-most EST
                   jex700907988.hl
Method
                   BLASTN
NCBI GI
                   g3894098
BLAST score
                   285
E value
                   1.0e-159
Match length
                   809
% identity
NCBI Description
                  Pisum sativum mRNA for protein encoded by MCM3 gene,
                  partial
Seq. No.
                   26238
Contig ID
                   137008 1.R1040
5'-most EST
                   ncj700976718.hl
Method
                   BLASTX
NCBI GI
                   g2252840
BLAST score
                   155
E value
                   1.0e-10
Match length
                   64
% identity
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                   26239
Contig ID
                   137009 1.R1040
5'-most EST
                   dpv701097153.h1
Method
                  BLASTX
NCBI GI
                   q3249066
BLAST score
                   387
E value
                   2.0e-37
Match length
                   130
% identity
NCBI Description
                   (AC004473) Similar to S. cerevisiae SIK1P protein
                  qb 984964. ESTs gb F15433 and gb AA395158 come from this
                  gene. [Arabidopsis thaliana]
```

BLAST score

E value

77

2.0e-35

```
5'-most EST
                  ncj700976735.h1
Seq. No.
                  26241
Contig ID
                  137024 1.R1040
5'-most EST
                  ncj700980607.h1
Method
                  BLASTX
NCBI GI
                  q464365
BLAST score
                   194
E value
                   4.0e-15
Match length
                   54
% identity
                  PEROXIDASE P7 >gi 66306 pir_OPNB7 peroxidase (EC 1.11.1.7)
NCBI Description
                  - turnip
                  26242
Seq. No.
Contig ID
                  137027 1.R1040
5'-most EST
                  ncj700\overline{9}76748.h1
Method
                  BLASTX
                  q4220445
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                  124
% identity
                   (AC006216) Similar to gi 3004555 F19F24.14 salt inducible
NCBI Description
                  protein homolog from Arabidopsis thaliana BAC gb AC003673.
                   [Arabidopsis thaliana]
                  26243
Seq. No.
                  137035 1.R1040
Contig ID
5'-most EST
                   fua701037758.hl
Method
                  BLASTX
NCBI GI
                  g3242721
BLAST score
                  288
                   7.0e-26
E value
Match length
                  84
% identity
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                  thaliana]
                  26244
Seq. No.
                  137082 1.R1040
Contig ID
5'-most EST
                  ncj700980969.h1
                  BLASTX
Method
NCBI GI
                  g3402684
                  237
BLAST score
                   6.0e-20
E value
Match length
                  127
% identity
                  (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  26245
Seq. No.
                  137088 1.R1040
Contig ID
                  ncj700976860.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1370143
```

Match length 179 % identity 91

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11B

Seq. No. 26246

Contig ID 137098_1.R1040 5'-most EST uC-gmropic033g02b1

Method BLASTX
NCBI GI g1669655
BLAST score 263
E value 1.0e-22
Match length 113
% identity 50

NCBI Description (X95962) CER3 [Arabidopsis thaliana]

Seq. No. 26247

Contig ID 137108_1.R1040 5'-most EST vzy700752796.h1

Seq. No. 26248

Contig ID 137125_1.R1040 5'-most EST ncj700976924.h1

Seq. No. 26249

Contig ID 137148_1.R1040 5'-most EST ncj700976970.h1

Method BLASTX
NCBI GI g4454033
BLAST score 284
E value 1.0e-25
Match length 97
% identity 48

NCBI Description (AL035394) putative potassium transport protein

[Arabidopsis thaliana]

Seq. No. 26250

Contig ID 137173_1.R1040 5'-most EST txt700735556.h1

Method BLASTX
NCBI GI g3157949
BLAST score 302
E value 3.0e-27
Match length 94
% identity 66

NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase

precursor gb_Z28697 from Nicotiana tabacum: ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No. 26251

Contig ID 137186_1.R1040 5'-most EST ncj700977123.h1

Seq. No. 26252

Contig ID 137188_1.R1040 5'-most EST fC-gmfl700903880a1

Method BLASTX NCBI GI g3688600

5'-most EST

```
BLAST score
                   2672
E value
                   0.0e+00
Match length
                   610
% identity
                   76
                   (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   26253
Seq. No.
                   137192 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400069g05a1
Method
                   BLASTX
                   q2499005
NCBI GI
BLAST score
                   202
E value
                   1.0e-15
Match length
                   109
% identity
                   42
NCBI Description
                   4-METHYL-5 (B-HYDROXYETHYL) -THIAZOLE MONOPHOSPHATE
                  BIOSYNTHESIS ENZYME >qi 1100872 (U34923) ThiJ [Escherichia
                  coli] >qi 1773108 (U82664)
                   4-\text{methyl}-\overline{5} (b-hydroxyethyl) -thiazole monophosphate
                  biosynthesis protein [Escherichia coli] >gi 1786626
                   (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole
                  monophosphate synthesis [Escherichia coli]
Seq. No.
                   26254
Contig ID
                   137221 1.R1040
5'-most EST
                  ncj700977219.hl
                   26255
Seq. No.
Contig ID
                   137222 1.R1040
5'-most EST
                  ncj700977222.hl
                   26256
Seq. No.
Contig ID
                   137246 1.R1040
5'-most EST
                  uC-gmrominsoy220d06b1
                  BLASTX
Method
NCBI GI
                   q3096947
BLAST score
                   186
E value
                   8.0e-30
Match length
                   117
                   54
% identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   26257
                  137248 1.R1040
Contig ID
5'-most EST
                   fde700874237.h1
                  BLASTX
Method
                  q4309731
NCBI GI
BLAST score
                   313
                   5.0e-29
E value
                  97
Match length
% identity
                   (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26258
                  137259 1.R1040
Contig ID
```

uC-qmrominsoy194b12b1

BLAST score

```
Method
                  BLASTX
NCBI GI
                   g4432863.
BLAST score
                   606
                   2.0e-73
E value
Match length
                   200
                   73
% identity
                   (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                   translocator protein [Arabidopsis thaliana]
                   26259
Seq. No.
                   137268 1.R1040
Contig ID
5'-most EST
                   ncj700977293.hl
                   26260
Seq. No.
Contig ID
                   137291 1.R1040
5'-most EST
                   jC-gmf102220073g03a1
                   BLASTX
Method
                   g2245039
NCBI GI
BLAST score
                   185
                   1.0e-13
E value
Match length
                   97
                   49
% identity
                   (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26261
Contig ID
                   137291 2.R1040
                   k11701\overline{2}08291.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245039
BLAST score
                   160
E value
                   9.0e-11
Match length
                   73
% identity
                   (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26262
Contig ID
                   137291 3.R1040
                   fde700873901.hl
5'-most EST
Seq. No.
                   26263
Contig ID
                   137314 1.R1040
                   ncj700977374.hl
5'-most EST
Seq. No.
                   26264
Contig ID
                   137325 1.R1040
5'-most EST
                   ncj700983016.hl
Seq. No.
                   26265
Contig ID
                   137365 1.R1040
5'-most EST
                   asn701138469.hl
Seq. No.
                   26266
Contig ID
                   137378 1.R1040
5'-most EST
                   kl1701211957.hl
Method
                   BLASTX
NCBI GI
                   q3582436
```

```
E value
                    5.0e-49
 Match length
                    145
 % identity
· NCBI Description
                    (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
 Seq. No.
                    26267
                    137378 2.R1040
 Contig ID
                    jC-qmle01810012d02a1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g3582436
                    295
 BLAST score
 E value
                    8.0e-45
 Match length
                    145
 % identity
 NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
 Seq. No.
                    26268
 Contig ID
                    137401 1.R1040
 5'-most EST
                    uC-gmflminsoy030c07b1
                   BLASTX
 Method
 NCBI GI
                    q3482920
 BLAST score
                    188
 E value
                    4.0e-14
 Match length
                    112
 % identity
 NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    137408 1.R1040
 Contig ID
 5'-most EST
                    ncj700977523.h1
                    26270
 Seq. No.
 Contig ID
                    137415 1.R1040
 5'-most EST
                    zzp700832246.h1
                    BLASTX
 Method
                    q3168840
 NCBI GI
 BLAST score
                    147
 E value
                    3.0e-09
                    63
 Match length
 % identity
 NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]
 Seq. No.
                    26271
 Contig ID
                    137418 1.R1040
                    fua701038626.h1
 5'-most EST
                    BLASTX
 Method
                    q4455300
 NCBI GI
 BLAST score
                    307
                    6.0e-53
 E value
 Match length
                    156
 % identity
 NCBI Description
                    (AL035528) putative pectate lyase All (fragment)
                    [Arabidopsis thaliana]
 Seq. No.
                    26272
                    137418 2.R1040
 Contig ID
```

 $jex700\overline{9}05217.h1$

5'-most EST

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26273
Seq. No.
Contig ID
                   137453 1.R1040
5'-most EST
                   ncj700977616.h1
                   26274
Seq. No.
                   137457 1.R1040
Contig ID
                   leu701146856.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g537317
BLAST score
                   1219
E value
                   1.0e-134
Match length
                   335
% identity
                   74
NCBI Description
                   (L36157) peroxidase [Medicago sativa]
                   26275
Seq. No.
Contig ID
                   137484 1.R1040
5'-most EST
                   ncj700977666.h1
Seq. No.
                   26276
Contig ID
                   137486 1.R1040
5'-most EST
                   ncj700977668.h1
Method
                   BLASTX
NCBI GI
                   g4240207
BLAST score
                   231
E value
                   5.0e-19
Match length
                   141
% identity
NCBI Description
                   (AB020666) KIAA0859 protein [Homo sapiens]
Seq. No.
Contig ID
                   137517 1.R1040
5'-most EST
                   jC-gmf102220078h08a1
                   26278
Seq. No.
Contig ID
                   137534 1.R1040
5'-most EST
                   ncj700\overline{9}77745.h1
Method
                   BLASTX
NCBI GI
                   q2827528
BLAST score
                   200
E value
                   8.0e-16
Match length
                   67
% identity
NCBI Description
                   (AL021633) predicted protein [Arabidopsis thaliana]
                   26279
Seq. No.
Contig ID
                   137549 1.R1040
5'-most EST
                   jC-gmf102220079b03d1
                   26280
Seq. No.
Contig ID
                   137574 1.R1040
5'-most EST
                   ncj700\overline{9}77809.h1
Seq. No.
                   26281
Contiq ID
                   137576 1.R1040
                   zzp700830316.h1
5'-most EST
```

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26282
Seq. No.
                   137581 1.R1040
Contig ID
5'-most EST
                   ncj700977821.h1
                   BLASTX
Method
                   g1184077
NCBI GI
BLAST score
                   215
                   2.0e-17
E value
                   109
Match length
% identity
                   2
                   (U42445) Cf-2.2 [Lycopersicon pimpinellifolium]
NCBI Description
Seq. No.
                   26283
                   137593 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}77844.h1
Seq. No.
                   26284
Contig ID
                   137610 1.R1040
5'-most EST
                   vzy700755310.h1
Method
                   BLASTX
NCBI GI
                   q4567095
BLAST score
                   290
E value
                   4.0e-26
Match length
                   80
% identity
NCBI Description
                   (AF129516) fertilization-independent endosperm protein
                   [Arabidopsis thaliana]
                   26285
Seq. No.
Contig ID
                   137621 1.R1040
5'-most EST
                   smc700746759.h1
Seq. No.
                   26286
Contig ID
                   137632 1.R1040
5'-most EST
                   kmv700738119.h1
                   BLASTX
Method
NCBI GI
                   g3451463
BLAST score
                   246
                   9.0e-21
E value
                   128
Match length
% identity
NCBI Description
                   (AL031349) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   137634 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy078b08b1
Seq. No.
Contig ID
                   137639 1.R1040
5'-most EST
                   ncj700\overline{9}77918.h1
                   26289
Seq. No.
Contig ID
                   137647 1.R1040
5'-most EST
                   ncj700\overline{9}77927.h1
Seq. No.
                   26290
```

137667 1.R1040

Contig ID

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5'-most EST
                   ncj700977960.h1
Seq. No.
                   26291
Contig ID
                   137676 1.R1040
5'-most EST
                   gsv701051166.hl
Method
                   BLASTX
NCBI GI
                   g2499931
BLAST score
                   724
E value
                   1.0e-76
Match length
                   183
% identity
                   77
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                   >gi 2129534 pir S71272 adenine phosphoribosyltransferase
                   (EC 2.4.2.7) - Arabidopsis thaliana
                   >gi_1321681_emb_CAA65609_ (X96866) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   137677 1.R1040
5'-most EST
                   ncj700\overline{9}86622.h1
Seq. No.
                   26293
                   137695 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05884.h1
Seq. No.
                   26294
Contig ID
                   137703 1.R1040
5'-most EST
                   ncj700978013.hl
Method
                   BLASTN
                   g2695860
NCBI GI
BLAST score
                   67
                   2.0e-29
E value
Match length
                   146
% identity
                   90
NCBI Description
                   Pisum sativum mRNA for
                   3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone
                   pPS40
                   26295
Seq. No.
                   137707 1.R1040
Contig ID
5'-most EST
                   ncj700978019.h1
Seq. No.
                   26296
Contig ID
                   137726 1.R1040
5'-most EST
                   pxt700942557.hl
                   26297
Seq. No.
                   137729 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}63755.h1
Seq. No.
                   26298
                   137797 1.R1040
Contig ID
                   pcp700992060.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2062171
BLAST score
                   166
```

8.0e-12

E value

```
Match length
                  87
% identity
                   45
                   (AC001645) DNA binding protein (CDC27SH) isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  26299
Contig ID
                  137846 1.R1040
5'-most EST
                  vzv700750680.hl
                  BLASTX
Method
NCBI GI
                  q3287683
BLAST score
                  243
                  9.0e-21
E value
                  110
Match length
% identity
                   (AC003979) Similar to apoptosis protein MA-3 gb D50465 from
NCBI Description
                  Mus musculus. [Arabidopsis thaliana]
                  26300
Seq. No.
                  137855 1.R1040
Contig ID
                  rlr700895922.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3080385
BLAST score
                  179
E value
                  7.0e-13
Match length
                  92
                  43
% identity
                   (AL022603) serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana] >gi 3402760 emb CAA20206.1 (AL031187)
                  serine/threonine kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  26301
                  137861 1.R1040
Contig ID
                  asn701142772.h1
5'-most EST
                  26302
Seq. No.
                  137874 1.R1040
Contig ID
5'-most EST
                  leu701146878.h1
                  26303
Seq. No.
                  137874 2.R1040
Contig ID
5'-most EST
                  leu701155970.hl
Seq. No.
                  26304
                  137916 1.R1040
Contig ID
                  ncj700\overline{9}78354.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q417570
BLAST score
                  388
E value
                  1.0e-58
                  141
Match length
                  87
% identity
                  DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE
NCBI Description
                  OXIDASE) (DHODEHASE) >gi_478676_pir__S23762 dihydroorotate
                  oxidase (EC 1.3.3.1) - Arabidopsis thaliana
                  >gi 16449 emb CAA44695 (X62909) dihydroorotate
```

dehydrogenase [Arabidopsis thaliana]

```
Seq. No.
                   26305
Contig ID
                   137917 1.R1040
5'-most EST
                   zhf700955804.hl
Seq. No.
                   26306
Contig ID
                   137924 1.R1040
5'-most EST
                   zhf700964637.h1
                   BLASTX
Method
NCBI GI
                   q1084334
BLAST score
                   348
                   7.0e-33
E value
                   81
Match length
% identity
NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) 1 -
                   Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                   26307
                   137933 1.R1040
Contig ID
                   ncj700\overline{9}78380.h1
5'-most EST
Seq. No.
                   26308
                   137950 1.R1040
Contig ID
5'-most EST
                   ncj700978404.h1
                   BLASTX
Method
NCBI GI
                   g2462825
BLAST score
                   234
E value
                   1.0e-26
                   73
Match length
% identity
NCBI Description
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
                   region [Arabidopsis thaliana]
                   26309
Seq. No.
Contig ID
                   137955 1.R1040
5'-most EST
                   fde700874521.h1
                   BLASTX
Method
NCBI GI
                   g4204793
BLAST score
                   588
E value
                   6.0e-84
                   273
Match length
% identity
                   31
NCBI Description
                  (U52079) P-glycoprotein [Solanum tuberosum]
Seq. No.
                   26310
                   137960 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy205f03b1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   34
                   2.0e-09
E value
                   34
Match length
                   59
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Match length

```
137966 1.R1040
Contig ID
                   zzp700833230.h1
5'-most EST
Seq. No.
                   26312
Contig ID
                   138009 1.R1040
5'-most EST
                   pxt700945573.h1
Method
                   BLASTX
NCBI GI
                   q3341694
BLAST score
                   342
E value
                   2.0e-32
Match length
                   86
% identity
                   79
NCBI Description
                   (AC003672) PREG-like protein [Arabidopsis thaliana]
                   26313
Seq. No.
Contig ID
                   138015 1.R1040
                   ncj700\overline{9}78509.h1
5'-most EST
                   26314
Seq. No.
Contig ID
                   138016 1.R1040
5'-most EST
                   ncj700978510.hl
Seq. No.
                   26315
Contig ID
                   138038 1.R1040
5'-most EST
                   jC-gmst02400006b07d1
Method
                   BLASTX
NCBI GI
                   g4539314
BLAST score
                   146
                   4.0e-09
E value
Match length
                   56
% identity
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26316
Contig ID
                   138053 1.R1040
5'-most EST
                   zhf700964503.h1
Method
                   BLASTX
NCBI GI
                   g4539010
BLAST score
                   310
E value
                   1.0e-28
Match length
                   104
% identity
NCBI Description
                   (AL049481) putative DNA-directed RNA polymerase
                   [Arabidopsis thaliana]
                   26317
Seq. No.
                   138065 1.R1040
Contig ID
                   epx701104375.h1
5'-most EST
Seq. No.
                   26318
                   138075_1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}78611.h1
Method
                   BLASTX
NCBI GI
                   q1086833
BLAST score
                   191
E value
                   2.0e-14
```

% identity

```
% identity
                   (U41264) coded for by C. elegans cDNA CEESN26F; coded for
NCBI Description
                   by C. elegans cDNA CEESI89F; similar to 60S acidic
                   ribosomal protein Po (L10) [Caenorhabditis elegans]
                   26319
Seq. No.
                   138105 1.R1040
Contig ID
                   pxt700941695.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4558556
BLAST score
                   155
E value
                   1.0e-22
Match length
                   101
% identity
                   60
NCBI Description
                   (AC007138) predicted protein of unknown function
                   [Arabidopsis thaliana]
Seq. No.
                   26320
Contig ID
                   138118 1.R1040
5'-most EST
                   ncj700978667.h1
Seq. No.
                   26321
Contig ID
                   138121 1.R1040
5'-most EST
                   ncj700978672.hl
Method
                   BLASTX
NCBI GI
                   q1685005
BLAST score
                   516
E value
                   4.0e-52
Match length
                   273
% identity
NCBI Description
                   (U32644) immediate-early salicylate-induced
                   glucosyltransferase [Nicotiana tabacum]
Seq. No.
Contig ID
                   138143 1.R1040
5'-most EST
                   uC-qmropic091e02b1
Seq. No.
                   26323
Contig ID
                   138149 1.R1040
5'-most EST
                   sat701010327.hl
Method
                   BLASTX
NCBI GI
                   q4063744
BLAST score
                   149
E value
                   9.0e-10
Match length
                   58
% identity
NCBI Description
                  (AC005851) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   26324
Contig ID
                   138180 1.R1040
5'-most EST
                   ncj700\overline{9}78777.h1
Method
                   BLASTX
NCBI GI
                   q2494905
BLAST score
                   210
E value
                   1.0e-16
Match length
                   157
```

```
NCBI Description MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi 2132107 pir S67174
                  hypothetical protein YOR272w - yeast (Saccharomyces
                  cerevisiae) >gi 1279699 emb CAA61778 (X89633) hypothetical
                  protein [Saccharomyces cerevisiae]
                  >gi 1420610 emb CAA99497 (Z75180) ORF YOR272w
                  [Saccharomyces cerevisiae] >qi 1928989 (U92821)
                  microtubule-associated protein [Saccharomyces cerevisiae]
                  26325
Seq. No.
Contig ID
                  138189 1.R1040
5'-most EST
                  zhf700963468.hl
                  BLASTX
Method
                  g3157941
NCBI GI
BLAST score
                  151
                  1.0e-09
E value
Match length
                  47
% identity
NCBI Description
                  (AC002131) Contains similarity to hypothetical protein
                  gb U95973 from A. thaliana. [Arabidopsis thaliana]
                  26326
Seq. No.
Contig ID
                  138197 1.R1040
5'-most EST
                  rry700808448.hl
                  26327
Seq. No.
                  138202 1.R1040
Contig ID
5'-most EST
                  uC-gmropic021a11b1
                  26328
Seq. No.
                  138204 1.R1040
Contig ID
5'-most EST
                  epx701108921.h1
                  26329
Seq. No.
                  138222 1.R1040
Contig ID
                  zhf700959203.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2285885
BLAST score
                  542
E value
                  2.0e-55
                  139
Match length
                  73
% identity
NCBI Description
                  (D89631) sulfate transporter [Arabidopsis thaliana]
                                                                . .
                  26330
Seq. No.
                  138224 1.R1040
Contig ID
5'-most EST
                  uC-gmropic025f07b1
Method
                  BLASTX
NCBI GI
                  g1362017
BLAST score
                  328
E value
                  1.0e-30
Match length
                  113
```

% identity

NCBI Description

Contig ID 138230 2.R1040

66

zinc finger protein 4 - Arabidopsis thaliana >gi_790679

(L39647) zinc finger protein [Arabidopsis thaliana]

Match length

410

```
5'-most EST
                  uC-gmropic012b05b1
Seq. No.
                   26332
Contig ID
                   138230 3.R1040
5'-most EST
                  pmv700892280.hl
Seq. No.
                   26333
Contig ID
                   138269 1.R1040
5'-most EST
                  uC-gmflminsoy042e10b1
Method
                  BLASTX
NCBI GI
                   g2462831
BLAST score
                   200
E value
                   2.0e-15
Match length
                   78
% identity
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   138276 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810062e01a1
Seq. No.
                  26335
                  138291 1.R1040
Contig ID
5'-most EST
                  ncj700\overline{9}78978.h1
Seq. No.
                  26336
                  138313 1.R1040
Contig ID
                  epx701107330.h1
5'-most EST
                  26337
Seq. No.
Contig ID
                  138314 1.R1040
                  rca701000761.hl
5'-most EST
Seq. No.
                  26338
Contig ID
                  138324 1.R1040
5'-most EST
                   jC-qmst02400053a11d1
Method
                  BLASTX
NCBI GI
                  g2145356
BLAST score
                   246
                   6.0e-21
E value
Match length
                  56
                   77
% identity
                   (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
NCBI Description
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                  26339
                  138333 1.R1040
Contig ID
5'-most EST
                  ncj700979044.hl
                  26340
Seq. No.
                  138341 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063h12a1
                  BLASTN
Method
NCBI GI
                  g2352083
BLAST score
                  134
E value
                   4.0e-69
```



% identity NCBI Description Arabidopsis thaliana serine/threonine kinase (SIK1) mRNA, complete cds 26341 Seq. No. 138373 1.R1040 Contig ID 5'-most EST gsv701044663.hl 26342 Seq. No. 138400 1.R1040 Contig ID `

k11701208735.h1 5'-most EST BLASTX Method

g4580397 NCBI GI BLAST score 177 E value 4.0e-13 Match length 98 % identity

(AC007171) putative RNA helicase [Arabidopsis thaliana] NCBI Description

Seq. No. 26343

Contig ID 138456 1.R1040 5'-most EST ncj700979345.hl

Method BLASTX NCBI GI g4544460 BLAST score 280 E value 1.0e-24 Match length 146 39 % identity

(AC006592) putative reverse transcriptase [Arabidopsis NCBI Description

thaliana]

26344 Seq. No.

Contig ID 138462 1.R1040 5'-most EST wrq700787528.hl

Method BLASTX NCBI GI q1076274 BLAST score 357 E value 9.0e-34 Match length 143 49 % identity

cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment) NCBI Description

Seq. No. 26345

Method

Contig ID 138471 1.R1040 5'-most EST ncj700987631.hl BLASTX

g4454043 NCBI GI BLAST score 167 E value 6.0e-12 Match length 54 % identity

(AL035394) putative receptor kinase [Arabidopsis thaliana] NCBI Description

26346 Seq. No.

Contig ID 138475 1.R1040

5'-most EST jC-qmro02910034f08a1

NCBI GI

```
26347
Seq. No.
                  138477 1.R1040
Contig ID
5'-most EST
                  eep700866060.hl
Seq. No.
                  26348
                  138510 1.R1040
Contig ID
5'-most EST
                   eep700864728.hl
                  BLASTX
Method
NCBI GI
                  g2191136
BLAST score
                  225
                  1.0e-18
E value
Match length
                   91
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                  26349
Contig ID
                  138513 1.R1040
5'-most EST
                  pcp700990402.h1
Seq. No.
                  26350
Contig ID
                  138514 1.R1040
5'-most EST
                  leu701149785.h1
Seq. No.
                  26351
Contig ID
                  138518 1.R1040
5'-most EST
                  jC-gmf102220138d02a1
                  26352
Seq. No.
Contig ID
                  138546 1.R1040
5'-most EST
                   zhf700964179.h1
                  BLASTX
Method
NCBI GI
                  q4056506
BLAST score
                  166
E value
                   7.0e-12
Match length
                   62
% identity
                   (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26353
Contig ID
                  138554 1.R1040
5'-most EST
                  ncj700982030.h1
                  BLASTN
Method
                  q2304954
NCBI GI
BLAST score
                  41
                  7.0e-14
E value
Match length
                  101
                  95
% identity
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
                  26354
Seq. No.
Contig ID
                  138558 1.R1040
5'-most EST
                  zpv700761529.hl
                  BLASTX
Method
```

q4160300

```
BLAST score
                   168
E value
                   8.0e-12
Match length
                   78
% identity
                   46
                   (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
NCBI Description
                   26355
Seq. No.
                   138573 1.R1040
Contig ID
5'-most EST
                   ncj700979537.h2
Method
                   BLASTX
                   g1617268
NCBI GI
BLAST score
                   294
                   5.0e-27
E value
Match length
                   88
% identity
                   (Z72153) acyl CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   26356
                   138587 1.R1040
Contig ID
5'-most EST
                   ncj700980527.hl
Method
                   BLASTX
                   q2244891
NCBI GI
BLAST score
                   168
E value
                   5.0e-12
Match length
                   73
% identity
                   (Z97338) strong similarity to cytochrome P450 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   26357
                   138607 1.R1040
Contig ID
5'-most EST
                   ncj700979629.h2
Seq. No.
                   26358
Contig ID
                   138607 2.R1040
5'-most EST
                   sat701\overline{0}02872.h1
Seq. No.
                   26359
Contig ID
                   138609 1.R1040
5'-most EST
                   awf700842139.h1
Seq. No.
                   26360
Contig ID
                   138609 2.R1040
5'-most EST
                   asn701138345.hl
                   26361
Seq. No.
Contig ID
                   138611 1.R1040
5'-most EST
                   pxt700944838.hl
Method
                   BLASTX
NCBI GI
                   g4539386
BLAST score
                   367
                   2.0e-35
E value
Match length
                   86
% identity
NCBI Description
                   (AL035526) extensin-like protein [Arabidopsis thaliana]
```

```
138616 1.R1040
Contig ID
5'-most EST
                   ncj700979642.h2
Seq. No.
                   26363
Contig ID
                   138629 1.R1040
5'-most EST
                   jC-gmf102220115d06a1
Seq. No.
                   26364
                   138652 1.R1040
Contig ID
5'-most EST
                   dpv701100659.hl
Seq. No.
                   26365
                   138675 1.R1040
Contig ID
                   hrw701\overline{0}56979.h1
5'-most EST
Seq. No.
                   26366
Contig ID
                   138675 2.R1040
5'-most EST
                   wrg700786026.h2
                   26367
Seq. No.
                   138692 1.R1040
Contig ID
5'-most EST
                   ncj700979777.h2
                   26368
Seq. No.
                   138721 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810064g11a1
Method
                   BLASTX
NCBI GI
                   q2529686
BLAST score
                   473
E value
                   2.0e-54
                   125
Match length
% identity
NCBI Description
                   (AC002535) putative G-beta-repeat containing protein, 5'
                   partial [Arabidopsis thaliana]
                   26369
Seq. No.
                   138724 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}79845.h2
Method
                   BLASTX
NCBI GI
                   g4539459
BLAST score
                   400
E value
                   4.0e-39
Match length
                   106
% identity
                   (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   26370
Seq. No.
                   138756 1.R1040
Contig ID
5'-most EST
                   pxt700943842.h1
Method
                   BLASTX
                   g1170409
NCBI GI
BLAST score
                   369
                   1.0e-35
E value
Match length
                   93
% identity
                   HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                   >qi 549887 (U09336) homeobox protein [Arabidopsis thaliana]
```

```
HAT22 [Arabidopsis thaliana]
Seq. No.
                  26371
Contig ID
                  138767 1.R1040
5'-most EST
                  q4396113
Method
                  BLASTX
NCBI GI
                  q3402704
BLAST score
                  547
E value
                  7.0e-56
Match length
                  187
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138794 1.R1040
Contig ID
5'-most EST
                  ncj700980025.hl
                  BLASTN
Method
                  g2264314
NCBI GI
BLAST score
                  33
                  7.0e-09
E value
                  105
Match length
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  26373
                  138812 1.R1040
Contig ID
5'-most EST
                  ncj700\overline{9}80082.h1
                  BLASTX
Method
NCBI GI
                  g3123130
BLAST score
                  208
E value
                  4.0e-29
Match length
                  108
                  45
% identity
                  HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN
NCBI Description
                  T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative
                  small nuclear ribonucleoprotein Prp4p [Arabidopsis
                  thaliana] >gi 3241948 (AC004625) putative small nuclear
                  ribonucleoprotein Prp4p [Arabidopsis thaliana]
                  26374
Seq. No.
Contig ID
                  138816 1.R1040
5'-most EST
                  epx701\overline{1}04215.h1
                  26375
Seq. No.
                  138821 1.R1040
Contig ID
                  ncj700980106.hl
5'-most EST
Method
                  BLASTX
                  g2501491
NCBI GI
BLAST score
                  169
                  2.0e-12
E value
                  81
Match length
% identity
                  43
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID
NCBI Description
                  3-O-GLUCOSYLTRANSFERASE 1) >gi 542014 pir S41950
```

>gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]
>qi_4490724 emb CAB38927.1 (AL035709) homeobox protein

Contig ID 5'-most EST

26383

138992 1.R1040

ncj700983574.hl

```
glucosyltransferase [Manihot esculenta]
Seq. No.
                  26376
                   138852 1.R1040
Contig ID
5'-most EST
                  ncj700980211.hl
Method
                  BLASTX
NCBI GI
                  g4185599
                   199
BLAST score
                   1.0e-15
E value
Match length
                   89
% identity
                   (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana
NCBI Description
                  triflora]
Seq. No.
                   26377
Contig ID
                   138853 1.R1040
5'-most EST
                   leu701153701.hl
Method
                  BLASTX
NCBI GI
                  q2580584
BLAST score
                   412
E value
                   2.0e-40
Match length
                   133
% identity
NCBI Description
                   (AF000976) 7-O-methyltransferase [Medicago sativa]
Seq. No.
                   138867 1.R1040
Contig ID
5'-most EST
                  ncj700980250.hl
                   26379
Seq. No.
Contig ID
                   138914 1.R1040
5'-most EST
                  ncj700980359.hl
                   26380
Seq. No.
                   138972 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy241g11b1
                  26381
Seq. No.
                  138975 1.R1040
Contig ID
5'-most EST
                   smc700748186.hl
Seq. No.
                  26382
                  138988 1.R1040
Contig ID
5'-most EST
                  ncj700980503.hl
                  BLASTX
Method
                  q4454043
NCBI GI
BLAST score
                  568
                  1.0e-58
E value
                  140
Match length
% identity
                  (AL035394) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
```

UTP-glucose glucosyltransferase - cassava >gi_453246_emb_CAA54609_ (X77459) UTP-glucose

```
Method
                  BLASTX
NCBI GI
                  q4455192
BLAST score
                  359
E value
                  9.0e-50
Match length
                  168
                  65
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26384
Contig ID
                  139000 1.R1040
                  pmv700889384.h1
5'-most EST
Method
                  BLASTX
                  g3522938
NCBI GI
BLAST score
                  345
E value
                  3.0e-32
Match length
                  187
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                  26385
Seq. No.
                  139001 1.R1040
Contig ID
5'-most EST
                  fC-amro7000746535d1
                  BLASTX
Method
                  q3860250
NCBI GI
BLAST score
                  576
                  3.0e-59
E value
Match length
                  213
% identity
                  (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  26386
Seq. No.
Contig ID
                  139009 1.R1040
                  bth700847360.h1
5'-most EST
                  BLASTX
Method
                  q2494736
NCBI GI
BLAST score
                  259
E value
                  3.0e-22
                  125
Match length
                  44
% identity
                  GLUCOSE INHIBITED DIVISION PROTEIN A
NCBI Description
                  >gi 1001595 dbj BAA10223 (D64000) glucose inhibited
                  division protein A [Synechocystis sp.]
                  26387
Seq. No.
                  139017 1.R1040
Contig ID
                  jC-gmro02910012d03d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3834323
BLAST score
                  283
                  3.0e-25
E value
Match length
                  87
% identity
NCBI Description
                  (AC005679) F9K20.25 [Arabidopsis thaliana]
Seq. No.
                  26388
```

139024 1.R1040

Contig ID

```
5'-most EST
                    pmv700890942.h1
 Method
                    BLASTX
 NCBI GI
                    q2244898
 BLAST score
                    256
 E value
                    3.0e-22
 Match length
                    111
 % identity
                    47
 NCBI Description
                    (Z97338) strong similarity to protein phosphatase 2A
                    regulatory chain, 74K [Arabidopsis thaliana]
 Seq. No.
                    26389
 Contig ID
                    139027 1.R1040
 5'-most EST
                    zsg701127504.h1
 Method
                    BLASTX
 NCBI GI
                    g1076821
 BLAST score
                    489
 E value
                    3.0e-49
Match length
                    135
 % identity
                    70
NCBI Description
                   probable 1-acyl-glycerol-3-phosphate acyltransferase -
                   maize >gi_575960_emb_CAA82638_ (Z29518)
                   1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea
                   mays]
Seq. No.
                   26390
Contig ID
                   139045 1.R1040
5'-most EST
                   ncj700\overline{9}80593.h1
Seq. No.
                   26391
Contig ID
                   139100 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220138c04a1
Seq. No.
                   26392
Contig ID
                   139100 2.R1040
5'-most EST
                   ncj700980690.h1
Seq. No.
                   26393
Contig ID
                   139104 1.R1040
5'-most EST
                   ncj700980695.hl
Method
                   BLASTX
NCBI GI
                   g2244839
BLAST score
                   304
E value
                   7.0e-32
Match length
                   131
% identity
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   26394
Contig ID
                   139106 1.R1040
5'-most EST
                   ncj700980706.h1
Seq. No.
                   26395
Contig ID
                   139114 1.R1040
5'-most EST
                   txt700736867.h1
Seq. No.
                   26396
Contig ID
                  139186_1.R1040
```

Match length

```
5'-most EST
                   ncj700980850.hl
                   26397
Seq. No.
                   139194 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}64920.h1
Seq. No.
                   26398
                   139195 1.R1040
Contig ID
                   epx701\overline{1}04057.h1
5'-most EST
                   26399
Seq. No.
                   139204 2.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}86459.h1
Method
                   BLASTX
NCBI GI
                   g3201554
BLAST score
                   202
                   5.0e-18
E value
Match length
                   103
% identity
                   (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
Seq. No.
                   26400
Contig ID
                   139207 1.R1040
5'-most EST
                   q43019\overline{2}5
Method
                   BLASTX
NCBI GI
                   q3063466
BLAST score
                   132
E value
                   2.0e-16
Match length
                   82
% identity
NCBI Description
                   (AC003981) F22013.28 [Arabidopsis thaliana]
Seq. No.
                   26401
Contig ID
                   139217 1.R1040
5'-most EST
                   uC-gmropic065c09b1
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   271
E value
                   1.0e-23
Match length
                   111
% identity
                   50
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
                   26402
Seq. No.
                   139232 2.R1040
Contig ID
5'-most EST
                   zhf700952549.h1
Seq. No.
                   26403
                   139267 1.R1040
Contig ID
5'-most EST
                   pxt700945232.h1
Method
                   BLASTX
NCBI GI
                   q3096919
BLAST score
                   576
                   2.0e-59
E value
```

```
77
% identity
NCBI Description
                   (AL023094) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   26404
                   139279 1.R1040
Contig ID
5'-most EST
                   ncj700980985.h1
Seq. No.
                   26405
Contig ID
                   139286 1.R1040
5'-most EST
                   ncj700980994.hl
Method
                   BLASTX
NCBI GI
                   q3355478
BLAST score
                   163
E value
                   3.0e-11
Match length
                   97
% identity
NCBI Description
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
                   26406
Seq. No.
                   139289 1.R1040
Contig ID
5'-most EST
                   leu701152205.hl
                   BLASTX
Method
                   g3603401
NCBI GI
BLAST score
                   351
                   4.0e-33
E value
Match length
                   111
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                   26407
                   139291 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy042c11b1
Method
                   BLASTX
NCBI GI
                   g2651302
BLAST score
                   486
E value
                   5.0e-49
Match length
                   141
% identity
                   (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26408
Seq. No.
Contig ID
                   139303 1.R1040
5'-most EST
                   ncj700981028.hl
                   26409
Seq. No.
                   139323 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}81065.h1
Method
                   BLASTX
NCBI GI
                   q4006854
BLAST score
                   238
E value
                   3.0e-20
Match length
                   96
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
```

26410

Seq. No.

NCBI GI

q116923

```
Contig ID
                  139338 1.R1040
5'-most EST
                  leu701152581.h1
                  26411
Seq. No.
Contig ID
                  139339 1.R1040
5'-most EST
                  gsv701055401.h1
Method
                  BLASTX
                  g3785989
NCBI GI
BLAST score
                  539
                  3.0e-55
E value
                  139
Match length
                  75
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  26412
                  139345_1.R1040
Contig ID
5'-most EST
                  wrg700788384.hl
Method
                  BLASTX
                  g629562
NCBI GI
BLAST score
                  812
E value
                  4.0e-87
Match length
                  172
% identity
                  87
                  sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis
NCBI Description
                  thaliana >gi 2129743 pir S68024 sulfate
                  adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) -
                  Arabidopsis thaliana >gi_487404_emb CAA55799 (X79210)
                  sulfate adenylyltransferase [Arabidopsis thaliana]
                  >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana]
                  >qi 1378028 (U40715) ATP sulfurylase precursor [Arabidopsis
                  thaliana] >qi 1575324 (U59737) ATP sulfurylase [Arabidopsis
                  thaliana]
                  26413
Seq. No.
Contig ID
                  139346 1.R1040
5'-most EST
                  uC-gmronoir008f03b1
Method
                  BLASTX
NCBI GI
                  g2828289
BLAST score
                  154
E value
                  5.0e-10
Match length
                  59
% identity
NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]
                  26414
Seq. No.
                  139346 2.R1040
Contig ID
5'-most EST
                  zzp700833537.h1
Seq. No.
                  26415
                  139400 1.R1040
Contig ID
5'-most EST
                  g5126598
                  26416
Seq. No.
Contig ID
                  139404 1.R1040
5'-most EST
                  ncj700981213.h1
                  BLASTX
Method
```

NCBI GI

```
BLAST score
                   325
E value
                   3.0e-30
Match length
                   118
% identity
                   57
NCBI Description
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
                   >gi 111414 pir S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
Seq. No.
                   26417
                   139409 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220146c08a1
Seq. No.
                   26418
Contig ID
                   139409 2.R1040
5'-most EST
                   bth700844803.hl
Seq. No.
                   26419
                   139431 1.R1040
Contig ID
5'-most EST
                   ncj700985758.h1
                   BLASTX
Method
NCBI GI
                   q4204295
BLAST score
                   205
                   3.0e-16
E value
Match length
                   98
% identity
                   41
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   26420
                   139482 1.R1040
Contig ID
                   ncj700981336.hl
5'-most EST
Seq. No.
                   26421
                   139525 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}02827.h1
Seq. No.
                   26422
                   139528 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810037f03a2
Seq. No.
                   26423
Contig ID
                   139535 1.R1040
5'-most EST
                   ncj700\overline{9}81420.h1
Method
                   BLASTX
NCBI GI
                   g3775993
                                                                       · / · .
BLAST score
                   359
E value
                   5.0e-34
Match length
                   71
% identity
                   96
NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   26424
Contig ID
                   139545 1.R1040
5'-most EST
                   pcp700989648.hl
Method
                   BLASTX
```

q4469012

1.5

```
BLAST score
                   172
E value
                   5.0e-12
Match length
                   62
                   55
% identity
NCBI Description
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  26425
                  139546 1.R1040
Contig ID
                  ncj700981436.hl
5'-most EST
Method
                  BLASTX
                  q3201554
NCBI GI
BLAST score
                  558
                  1.0e-83
E value
Match length
                  228
% identity
                   66
NCBI Description
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
                  26426
Seq. No.
                  139549 1.R1040
Contig ID
                  vzy700752472.hl
5'-most EST
                  26427
Seq. No.
                  139560 1.R1040
Contig ID
5'-most EST
                  zhf700958364.hl
                  BLASTN
Method
                  g2104674
NCBI GI
BLAST score
                  89
                  2.0e-42
E value
Match length
                  219
                  91
% identity
NCBI Description V.faba mRNA for transcription factor containing bZIP
                  26428
Seq. No.
                  139572 1.R1040
Contig ID
                  ncj700981485.hl
5'-most EST
                  26429
Seq. No.
                  139578 1.R1040
Contig ID
5'-most EST
                  ncj700\overline{9}81491.h1
                  26430
Seq. No.
                  139592 1.R1040
Contig ID
5'-most EST
                  uC-gmropic012b06b1
Seq. No.
                  26431
                  139596 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810010b04a1
                  26432
Seq. No.
                  139609 1.R1040
Contig ID
5'-most EST
                  ncj700\overline{9}81547.h1
                  26433
Seq. No.
                  139610 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810015a04d1
```

Match length

```
139613 1.R1040
Contig ID
                   jC-gmst02400060e10a1
5'-most EST
Seq. No.
                   26435
Contig ID
                   139635 1.R1040
                   jC-gmro02910013d12d1
5'-most EST
                   26436
Seq. No.
                   139664 1.R1040
Contig ID
5'-most EST
                   rlr700896745.hl
Method
                   BLASTX
                   g3193288
NCBI GI
BLAST score
                   177
E value
                   6.0e-13
Match length
                   112
% identity
                   (AF069298) similar to bacterial and fungi pectinesterases
NCBI Description
                   [Arabidopsis thaliana]
                   26437
Seq. No.
Contig ID
                   139665 1.R1040
5'-most EST
                   ncj700988637.hl
                   BLASTX
Method
NCBI GI
                   g3819099
BLAST score
                   521
                   3.0e-53
E value
Match length
                   138
% identity
                   (AJ009825) copper amine oxidase [Cicer arietinum]
NCBI Description
                   26438
Seq. No.
                   139672 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}55318.h1
Seq. No.
                   26439
                   139685 1.R1040
Contig ID
                   uC-gmrominsoy111h01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1817544
BLAST score
                   189
                   3.0e-14
E value
Match length
                   85
% identity
NCBI Description
                   (D83025) proline oxidase precursor [Arabidopsis thaliana]
Seq. No.
                   139690 1.R1040
Contig ID
                   qsv701\overline{0}51537.h1
5'-most EST
Seq. No.
                   26441
                   139700 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy167b10b1
Method
                   BLASTX
NCBI GI
                   g4490342
BLAST score
                   297
E value
                   9.0e-27
```

Contig ID

5'-most EST

```
% identity
NCBI Description
                   (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                   26442
Contig ID
                   139701 1.R1040
5'-most EST
                   leu701150580.hl
                   26443
Seq. No.
Contig ID
                   139717 1.R1040
5'-most EST
                   ncj700981712.h1
                   26444
Seq. No.
                   139790 1.R1040
Contig ID
                   ncj700\overline{9}81842.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2980806
BLAST score
                   145
E value
                   3.0e-09
Match length
                   36
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26445
                   139808 1.R1040
Contig ID
5'-most EST
                   zpv700759887.h1
                   26446
Seq. No.
                   139809 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}60688.h1
                   BLASTX
Method
                   g282964
NCBI GI
BLAST score
                   344
                   2.0e-32
E value
Match length
                   81
                   75
% identity
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                   petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
                   x hybrida]
Seq. No.
                   26447
                   139827_1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220114e07d1
                   26448
Seq. No.
                   139828 1.R1040
Contig ID
5'-most EST
                   xpa700792448.hl
Method
                   BLASTX
NCBI GI
                   g4454026
BLAST score
                   384
E value
                   1.0e-41
                   138
Match length
% identity
                   65
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                   26449
```

139836 1.R1040

ncj700981939.hl

Contig ID

```
Method
                   BLASTN
NCBI GI
                   g559505
BLAST score
                   128
E value
                   1.0e-65
Match length
                   368
% identity
                   84
                  P.hybrida mRNA for S-adenosylmethionine-synthetase
NCBI Description
                   26450
Seq. No.
Contig ID
                   139845 1.R1040
5'-most EST
                   ncj700981952.h1
                   BLASTX
Method
                   g3335353
NCBI GI
BLAST score
                   194
                   4.0e-15
E value
Match length
                   78
% identity
                   47
NCBI Description
                   (AC004512) Similar to cytochrome P450 gb X90458 from A.
                   thaliana. [Arabidopsis thaliana]
                   26451
Seq. No.
Contig ID
                   139861 1.R1040
                   k11701\overline{2}05476.h1
5'-most EST
                   BLASTX
Method
                   g3646336
NCBI GI
BLAST score
                   392
                   8.0e-38
E value
Match length
                   121
                   68
% identity
NCBI Description
                   (AJ001682) MdMADS9 [Malus domestica]
                   26452
Seq. No.
Contig ID
                   139874 1.R1040
5'-most EST
                   dpv701100857.h1
                   BLASTX
Method
NCBI GI
                   q1429226
BLAST score
                   315
                   6.0e-29
E value
Match length
                   96
% identity
NCBI Description (X98861) TFIIA [Arabidopsis thaliana]
                   26453
Seq. No.
Contig ID
                   139889 1.R1040
5'-most EST
                   uC-gmrominsoy108e12b1
Method
                   BLASTX
NCBI GI
                   g2497034
BLAST score
                   177
E value
                   8.0e-13
Match length
                   109
                   41
% identity
                   HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III
NCBI Description
                   >gi_3881502_emb_CAA87421_ (Z47357) ZK1128.2 [Caenorhabditis
                   elegans]
Seq. No.
                   26454
```

139937_1.R1040

```
5'-most EST
                  fua701040927.hl
                  26455
Seq. No.
                  139941 1.R1040
Contig ID
5'-most EST
                  gsf700698307.hl
                  26456
Seq. No.
                  139965 1.R1040
Contig ID
                  ncj700983310.hl
5'-most EST
Method
                  BLASTN
                  g1217993
NCBI GI
BLAST score
                  217
                  1.0e-119
E value
                  413
Match length
% identity
                  Glycine max dynamin-like protein SDL12A mRNA, complete cds
NCBI Description
                  26457
Seq. No.
                  139977 1.R1040
Contiq ID
                  gsv701046585.hl
5'-most EST
Seq. No.
                  26458
Contig ID
                  139989 1.R1040
5'-most EST
                  asn701141023.hl
Method
                  BLASTX
NCBI GI
                  g2880047
BLAST score
                  540
E value
                  3.0e-57
Match length
                  181
% identity
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26459
Contig ID
                  140018 1.R1040
5'-most EST
                  kl1701205510.hl
Method
                  BLASTX
NCBI GI
                  g3249098
BLAST score
                  245.
E value
                  2.0e-20
Match length
                  99
% identity
                   (AC003114) ESTs qb T04610, qb N38459, qb T45174, qb R30481
NCBI Description
                  and gb N64971 come from this gene. [Arabidopsis thaliana]
                  26460
Seq. No.
Contig ID
                  140025 1.R1040
5'-most EST
                  g5676821
Seq. No.
                  26461
Contig ID
                  140029 1.R1040
5'-most EST
                  gsv701053383.hl
                  26462
Seq. No.
Contig ID
                  140030 1.R1040
                  eep700863841.h1
5'-most EST
```

26463

Seq. No.

```
140030 3.R1040
Contig ID
5'-most EST
                   fde700876315.h1
Seq. No.
                   26464
                   140033 1.R1040
Contig ID
                   uC-gmrominsoy029h05b1
5'-most EST
                   BLASTX
Method
                   g231573
NCBI GI
BLAST score
                   266
E value
                   3.0e-26
Match length
                   94
                   70
% identity
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi 99970 pir S24757 asparaginase (EC 3.5.1.1) -
                   narrow-leaved blue lupine >gi 19135 emb CAA43099 (X60691)
                   developing seed L-asparaginase [Lupinus angustifolius]
Seq. No.
                   26465
Contig ID
                   140070 1.R1040
5'-most EST
                   jC-gmro02910019a06a1
Seq. No.
                   26466
Contig ID .
                   140070 2.R1040
5'-most EST
                   zsg701\overline{1}23769.h1
                   26467
Seq. No.
Contig ID
                   140072 1.R1040
5'-most EST
                   ncj700982317.hl
Seq. No.
                   26468
                   140079 1.R1040
Contig ID
5'-most EST
                   q56778\overline{4}9
                   26469
Seq. No.
                   140091 1.R1040
Contig ID
5'-most EST
                   ncj700982406.h1
                   BLASTX
Method
NCBI GI
                   g2244831
BLAST score
                   174
                   4.0e-13
E value
                   37
Match length
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   26470
Seq. No.
Contig ID
                   140097 1.R1040
5'-most EST
                   fC-qmro7000748540r1
                   BLASTN
Method
NCBI GI
                   g392822
BLAST score
                   456
                   0.0e + 00
E value
                   464
Match length
% identity
                   100
NCBI Description Glycine max Williams cellulase gene, partial cds
                   26471
Seq. No.
```

140101 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   g5752519
Seq. No.
                   26472
Contig ID
                   140108 1.R1040
5'-most EST
                   ncj700\overline{9}82429.h1
                   26473
Seq. No.
                   140109 1.R1040
Contig ID
5'-most EST
                   ncj700982430.hl
                   26474
Seq. No.
                   140122 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}82460.h1
Seq. No.
                   26475
Contig ID
                   140143 1.R1040
                   ncj700\overline{9}82503.h1
5'-most EST
Seq. No.
                   26476
Contig ID
                   140178 1.R1040
5'-most EST
                   zhf700961136.h1
Seq. No.
                   26477
Contig ID
                   140193 1.R1040
5'-most EST
                   fua701041857.hl
Seq. No.
                   26478
Contig ID
                   140251 1.R1040
5'-most EST
                   ncj700982660.hl
Method
                   BLASTN
NCBI GI
                   q294667
BLAST score
                   210
E value
                   1.0e-114
Match length
                   530
% identity
                   85
NCBI Description
                   Castor bean chloroplast beta-ketoacyl-ACP synthase (50 kDa
                   synthase) mRNA, complete cds
Seq. No.
                   26479
Contig ID
                   140262 1.R1040
5'-most EST
                   ncj700\overline{9}82674.h1
Method
                   BLASTX
NCBI GI
                   q4006878
BLAST score
                   401
E value
                   4.0e-39
Match length
                   134
% identity
NCBI Description
                   (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   140271 1.R1040
5'-most EST
                   ncj700982684.hl
Seq. No.
                   26481
Contig ID
                   140295 1.R1040
```

ncj700982722.h1

```
Seq. No.
                    26482
 Contig ID
                    140304 1.R1040
 5'-most EST
                    kmv700739574.h1
 Method
                    BLASTX
 NCBI GI
                    g2262157
 BLAST score
                    361
 E value
                    1.0e-34
 Match length
                    96
 % identity
                    69
 NCBI Description
                    (AC002329) putative ligand-gated ion channel protein
                    [Arabidopsis thaliana]
 Seq. No.
                    26483
 Contig ID
                    140329 1.R1040
 5'-most EST
                    ncj700\overline{9}82775.h1
Method
                    BLASTX
NCBI GI
                    g3785977
BLAST score
                    233
E value
                    1.0e-19
Match length
                    92
% identity
                    53
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   26484
Contig ID
                   140330 1.R1040
5'-most EST
                   leu701156303.h1
Method
                   BLASTX
NCBI GI
                   q629561
BLAST score
                   440
E value
                   2.0e-43
Match length
                   217
% identity
                   41
NCBI Description
                   SRG1 protein - Arabidopsis thaliana
                   >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana]
Seq. No.
                   26485
Contig ID
                   140382 1.R1040
5'-most EST
                   ncj700\overline{9}82879.h1
Method
                   BLASTX
NCBI GI
                   q3152572
BLAST score
                   322
E value
                   3.0e-30
Match length
                   78
% identity
                   90
NCBI Description
                   (AC002986) Contains homology to DNAJ heatshock protein
                   gb U32803 from Haemophilus influenzae. [Arabidopsis
                   thaliana]
Seq. No.
                   26486
Contig ID
                   140385 1.R1040
5'-most EST
                   jsh701\overline{0}64350.h1
Method
                   BLASTX
NCBI GI
                   q4006918
BLAST score
                   319
E value
```

2.0e-29

```
Match length
                   121
% identity
                   53
NCBI Description (Z99708) peroxidase like protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   140394 1.R1040
5'-most EST
                   kl1701212683.hl
                   26488
Seq. No.
                 140395 1.R1040
Contig ID
5'-most EST
                   ncj700982901.hl
                   26489
Seq. No.
                   140399 1.R1040
Contig ID
                   jex700907547.hl
5'-most EST
Seq. No.
                   26490
Contig ID
                   140416 1.R1040
                   ncj700\overline{9}82958.h1
5'-most EST
                   BLASTX ·
Method
NCBI GI
                   g2244833
BLAST score
                   263
E value
                   7.0e-23
Match length
                   137
% identity
                   44
                  (Z97337) centromere protein homolog [Arabidopsis thaliana]
NCBI Description
                   26491
Seq. No.
                   140421 1.R1040
Contig ID
5'-most EST
                   ncj700982975.hl
Seq. No.
                   26492
                   140470_1.R1040
Contig ID
5'-most EST
                   kwa701015680.h1
                   26493
Seq. No.
                   140493 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}83103.h1
Method
                   BLASTN
NCBI GI
                   g2104523
BLAST score
                   35
E value
                   3.0e-10
Match length
                   67
% identity
NCBI Description
                  Arabidopsis thaliana BAC T10M13 from chromosome IV, from
                   10.8 cM to 11.6 cM, complete sequence
Seq. No.
                   26494
                   140533 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}46889.h1
                   26495
Seq. No.
                   140543 1.R1040
Contig ID
5'-most EST
                   g5752614
Seq. No.
                   26496
Contig ID
```

140551 1.R1040

NCBI GI

```
5'-most EST
                   ncj700983211.h1
Seq. No.
                   26497
Contig ID
                   140556 1.R1040
5'-most EST
                   bth700849719.h1
Seq. No.
                   26498
Contig ID
                   140559 1.R1040
5'-most EST
                   ncj700983222.hl
Seq. No.
                   26499
Contig ID
                   140564 1.R1040
5'-most EST
                   ncj700\overline{9}83234.h1
                   26500
Seq. No.
Contig ID
                   140597 1.R1040
5'-most EST
                   jC-qmro02800025q08d1
                   26501
Seq. No.
Contig ID
                   140610 1.R1040
5'-most EST
                   ncj700983319.h1
Method
                   BLASTX
                   g1723738
NCBI GI
BLAST score
                   213
                   3.0e-17
E value
Match length
                   104
% identity
                   20
                   HYPOTHETICAL 55.1 KD PROTEIN IN TRX1-RTA1 INTERGENIC REGION
NCBI Description
                   >gi 2131699 pir S64534 hypothetical protein YGR211w -
                   yeast (Saccharomyces cerevisiae) >gi_1323379_emb_CAA97238
                   (Z72996) ORF YGR211w [Saccharomyces cerevisiae] >gi 3510466
                   (AF019769) zinc finger protein [Saccharomyces cerevisiae]
Seq. No.
                   26502
                   140638 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}47757.h1
Seq. No.
                   26503
                   140665 1.R1040
Contig ID
5'-most EST
                   ncj700983409.h1
Seq. No.
                   26504
Contig ID
                   140670 1.R1040
5'-most EST
                   jC-gmst02400063c02a1
Method
                   BLASTX
                   q728483
NCBI GI
BLAST score
                   915
                   5.0e-99
E value
Match length
                   208
% identity
                   82
                   (L41046) endo-1,4-beta-glucanase [Pisum sativum]
NCBI Description
                   26505
Seq. No.
Contig ID
                   140682 1.R1040
5'-most EST
                   xpa700793272.h1
                   BLASTX
Method
```

g2316016

5'-most EST

```
BLAST score
                   425
E value
                   4.0e-42
Match length
                  112
                  73
% identity
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
                  26506
Seq. No.
                  140695 1.R1040
Contig ID
                  pmv700891626.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2244987
BLAST score
                  346
                  1.0e-32
E value
Match length
                  156
                   45
% identity
NCBI Description
                   (Z97340) similarity to protein kinase - slime mold
                   (Dictyostelium) [Arabidopsis thaliana]
Seq. No.
                  26507
Contig ID
                  140696 1.R1040
5'-most EST
                  jC-gmro02910012b11a1
Seq. No.
                  26508
                  140697 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910019b04d1
                  26509
Seq. No.
                  140706 1.R1040
Contig ID
5'-most EST
                  ncj700983470.hl
Seq. No.
                  26510
Contig ID
                  140729 1.R1040
5'-most EST
                  zzp700831407.hl
Method
                  BLASTX
NCBI GI
                  g2154997
BLAST score
                  421
                   4.0e-41
E value
                  196
Match length
                   46
% identity
NCBI Description (Y12503) Man9-mannosidase [Sus scrofa]
                  26511
Seq. No.
                  140748 1.R1040
Contig ID
                  cf1700863544.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4490937
BLAST score
                  245
                  8.0e-21
E value
Match length
                  126
% identity
                  37
                  (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
NCBI Description
                  sapiens]
                  26512
Seq. No.
Contig ID
                  140752 1.R1040
```

jC-gmle01810060e10a1

```
Seq. No.
                   26513
                   140767 1.R1040
Contig ID
5'-most EST
                  ncj700983583.hl
Method
                  BLASTX
NCBI GI
                   g224797
BLAST score
                   165
E value
                   5.0e-17
Match length
                   64
% identity
                   70
NCBI Description
                  urease [Canavalia ensiformis]
                   26514
Seq. No.
                   140777 1.R1040
Contig ID
5'-most EST
                  uC-gmropic009a07b1
                  BLASTX
Method
NCBI GI
                   g3953470
BLAST score
                   403
E value
                   2.0e-39
                   85
Match length
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                   26515
Seq. No.
                   140781 1.R1040
Contig ID
                   fua701040863.h1
5'-most EST
Seq. No.
                   26516
                   140801 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir073c03b1
Seq. No.
                   26517
Contig ID
                   140809 1.R1040
5'-most EST
                  ncj700983651.hl
                   26518
Seq. No.
Contig ID
                   140813 1.R1040
5'-most EST
                  ncj700983655.hl
Method
                  BLASTX
NCBI GI
                  g3128173
BLAST score
                   407
                   2.0e-57
E value
Match length
                   121
% identity
NCBI Description
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   26519
                   140828_1.R1040
Contig ID
                   k11701\overline{2}12139.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3695062
BLAST score
                  194
                  1.0e-105
E value
Match length
                   402
                   87
% identity
                  Lotus japonicus rac GTPase activating protein 3 mRNA,
NCBI Description
```

partial cds

NCBI GI

```
26520
Seq. No.
                  140837 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400053a10d1
Seq. No.
                  26521
                  140844 1.R1040
Contig ID
                  zhf700964855.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4218120
BLAST score
                  277
E value
                  1.0e-24
Match length
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  26522
Seq. No.
Contig ID
                  140880 1.R1040
5'-most EST
                  asn701136306.hl
                  BLASTX
Method
                  g4455326
NCBI GI
BLAST score
                  675
                  4.0e-71
E value
Match length
                  171
                  71
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  26523
                  140888 1.R1040
Contig ID
5'-most EST
                  ncj700986805.hl
Seq. No.
                  26524
                  140902 1.R1040
Contig ID
                  pcp700995354.h1
5'-most EST
                  26525
Seq. No.
                  140916 1.R1040
Contig ID
5'-most EST
                  ncj700983850.hl
                  26526
Seq. No.
                  140937 1.R1040
Contig ID
5'-most EST
                  ncj700\overline{9}83884.h1
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  559
                  3.0e-66
E value
Match length
                  197
                  67
% identity
NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
                  26527
Seq. No.
Contig ID
                  140957 1.R1040
5'-most EST
                  leu701152930.hl
Method
                  BLASTX
```

q3785987

E value

5.0e-47

```
BLAST score
                  149
E value
                   2.0e-09
Match length
                   51
% identity
                   57
NCBI Description
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   140957 3.R1040
5'-most EST
                   kl1701206601.h1
Seq. No.
                   26529
                   140961 1.R1040
Contig ID
5'-most EST
                   ncj700983993.hl
                   26530
Seq. No.
Contig ID
                   140962 1.R1040
5'-most EST
                   bth700849269.h1
Seq. No.
                   26531
                   140985 1.R1040
Contig ID
                   ncj700984068.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2443886
BLAST score
                   148
E value
                   2.0e-09
Match length
                   89
% identity
NCBI Description
                   (AC002294) Unknown protein [Arabidopsis thaliana]
                   26532
Seq. No.
Contig ID
                   140986 1.R1040
5'-most EST
                   uC-gmropic025c08b1
Seq. No.
                   26533
                   141007 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}84122.h1
                   26534
Seq. No.
                   141042 1.R1040
Contig ID
5'-most EST
                   ncj700984174.hl
Method
                   BLASTX
NCBI GI
                   g1304227
BLAST score
                   362
E value
                   3.0e-37
Match length
                   146
% identity
                   47
                   (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
                   >gi 2764804 emb CAA55293 (X78547) epoxide hydrolase
                   [Glycine max]
                   26535
Seq. No.
                   141047 1.R1040
Contig ID
5'-most EST
                   ncj700984182.hl
Method
                   BLASTX
NCBI GI
                   g3367537
BLAST score
                   470
```

% identity

84

```
Match length
                   132
% identity
                   64
NCBI Description
                   (AC004392) Contains similarity to ANK repeat region of
                   Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi 485107
                   from Caenorhabditis elegans cosmid qb U00049. This gene is
                   continued from unannotated gene on BAC F19K23 gb AC000375.
                   [Arabid
                   26536
Seq. No.
Contig ID
                   141051 1.R1040
5'-most EST
                   ncj700984187.h1
                   BLASTX
Method
NCBI GI
                   g4539314
BLAST score
                   206
                   4.0e-16
E value
Match length
                   73
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   26537
Seq. No.
                   141055 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}84193.h1
Method
                   BLASTX
NCBI GI
                   g4218120
BLAST score
                   210
                   5.0e-17
E value
Match length
                   47
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   26538
                   141061 1.R1040
Contig ID
5'-most EST
                   eep700\overline{8}64079.h1
                   BLASTX
Method
NCBI GI
                   q2088651
BLAST score
                   173
                   2.0e-12
E value
Match length
                   105
% identity
                   43
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   26539
Seq. No.
Contig ID
                   141088 1.R1040
5'-most EST
                   ncj700984246.hl
                   26540
Seq. No.
                   141091 1.R1040
Contig ID
5'-most EST
                   ncj700984251.hl
Method
                   BLASTN
NCBI GI
                   g3869075
BLAST score
                   58
                   5.0e-24
E value
Match length
                   287
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

```
Seq. No.
                   26541
Contig ID
                   141094 1.R1040
5'-most EST
                   zhf700954649.hl
Seq. No.
                   26542
                   141097 1.R1040
Contig ID
                   ncj700\overline{9}84263.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g541913
BLAST score
                   363
                   5.0e-35
E value
                   84
Match length
                   79
% identity
                   oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
NCBI Description
                   rape >gi_435011_emb_CAA52069_ (X73849) oleoyl-[acyl-carrier
                  protein] hydrolase [Brassica napus]
                   26543
Seq. No.
                   141114 1.R1040
Contig ID
5'-most EST
                   uC-gmropic020c06b1
                   26544
Seq. No.
                   141136 1.R1040
Contig ID
                   uC-gmropic035b03b1
5'-most EST
Method
                   BLASTX
                   q4006876
NCBI GI
                   235
BLAST score
E value
                   2.0e-19
Match length
                   92
% identity
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]
                   26545
Seq. No.
Contig ID
                   141136 2.R1040
                   asn701\overline{1}40108.h1
5'-most EST
                   26546
Seq. No.
                   141146 1.R1040
Contig ID
                   ncj700\overline{9}84337.h1
5'-most EST
Seq. No.
                   26547
                   141161 1.R1040
Contig ID
                   fC-gmle700555881b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1170949
                   227
BLAST score
E value
                   1.0e-18
Match length
                   82
% identity
                  SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327
NCBI Description
                   protein kinase - Arabidopsis thaliana >gi_166811 (L07249)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                   26548
```

MXK3, complete sequence [Arabidopsis thaliana]

141178 1.R1040

Contig ID

```
5'-most EST
                   sat701003559.h1
                   26549
Seq. No.
Contig ID
                   141221 1.R1040
5'-most EST
                   ncj700\overline{9}84530.h1
                   26550
Seq. No.
Contig ID
                   141239 1.R1040
5'-most EST
                   ncj700984573.hl
                   BLASTX
Method
NCBI GI
                   q3212868
BLAST score
                   534
                   2.0e-54
E value
                   170
Match length
% identity
                   62
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   26551
Seq. No.
                   141260 1.R1040
Contig ID
                   sat701007938.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1350783
BLAST score
                   168
                   4.0e-12
E value
                   80
Match length
% identity
                   53
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                   >gi 282883 pir _S27756 receptor-like protein kinase
                   precursor - Arabidopsis thaliana >gi_166850 (M84660)
                   receptor-like protein kinase [Arabidopsis thaliana]
                   >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein
                   kinase 5 precursor (RLK5) [Arabidopsis thaliana]
                   26552
Seq. No.
                   141286 1.R1040
Contig ID
                   ncj700\overline{9}84706.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4490756
BLAST score
                   187
E value
                   2.0e-16
Match length
                   106
% identity
                   41
                   (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26553
                   141300 1.R1040
Contig ID
                   ncj700\overline{9}84726.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3080427
BLAST score
                   1541
                   1.0e-172
E value
Match length
                   338
% identity
                   (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26554
```

141303 1.R1040

Contig ID

Contig ID

5'-most EST

```
5'-most EST
                     jC-gmst02400055f01d1
  Method
                     BLASTX
  NCBI GI
                     g2288887
  BLAST score
                     164
  E value
                     3.0e-11
  Match length
                     44
  % identity
                     70
  NCBI Description
                     (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                     thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate
                     diphosphate decarboxylase [Arabidopsis thaliana]
                     >qi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                     [Arabidopsis thaliana]
                     26555
  Seq. No.
                     141332 1.R1040
  Contig ID
  5'-most EST
                     ncj700\overline{9}84770.h1
  Method
                     BLASTX
  NCBI GI
                     g3152559
  BLAST score
                     490
                     5.0e-49
  E value
                     197
  Match length
  % identity
                     49
                     (AC002986) Similarity to A. thaliana gene product
  NCBI Description
                     F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene.
                     [Arabidopsis thaliana]
                     26556
  Seq. No.
                     141335 1.R1040
  Contig ID
  5'-most EST
                     epx701\overline{1}10420.h1
  Seq. No.
                     26557
                     141345 1.R1040
  Contig ID
  5'-most EST
                     ncj700\overline{9}84788.h1
  Method
                     BLASTX
  NCBI GI
                     g2244852
  BLAST score
                     207
  E value
                     1.0e-16
  Match length
                     51
  % identity
  NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                     26558
  Seq. No.
                     141404 1.R1040
  Contig ID
  5'-most EST
                     ncj700\overline{9}84884.h1
  Method
                     BLASTX
  NCBI GI
                     g4204293
  BLAST score
                     183
  E value
                     6.0e-14
  Match length
                     83
  % identity
                     (AC003027) lcl_prt_seq No definition line found
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     26559
```

141442_1.R1040 leu701154394.h1

5'-most EST

```
26560
Seq. No.
Contig ID
                   141448 1.R1040
5'-most EST
                   k11701\overline{2}11248.h1
Seq. No.
                   26561
                   141466 1.R1040
Contig ID
5'-most EST
                   ncj700984989.hl
Seq. No.
                   26562
Contig ID
                   141510 1.R1040
5'-most EST
                   jex700907689.hl
Seq. No.
                   26563
Contig ID
                   141530 2.R1040
5'-most EST
                   jex700903484.h1
Method
                   BLASTX
                   g4006900
NCBI GI
BLAST score
                   227
E value
                   6.0e-19
Match length
                   76
% identity
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   141566 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy195d07b1
Method
                   BLASTX
NCBI GI
                   g3702323 ·
BLAST score
                   464
                   2.0e-46
E value
                   131
Match length
% identity
                   73
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                   26565
Seq. No.
                   141571 1.R1040
Contig ID
5'-most EST
                   asn701135056.h1
                   26566
Seq. No.
                   141584 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}14302.h1
Seq. No.
                   26567
Contig ID
                   141588 1.R1040
5'-most EST
                   k11701\overline{2}15142.h1
Method
                   BLASTX
                   q1777312
NCBI GI
BLAST score
                   145
E value
                   1.0e-08
Match length
                   35
% identity
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   26568
                   141605 1.R1040
Contig ID
```

 $jsh701\overline{0}64332.h1$

Method BLASTX NCBI GI g1532165 BLAST score 222 E value 3.0e-18 Match length 85 53 % identity (U63815) similar to dehydrogenase encoded by GenBank NCBI Description Accession Number S39508; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop 26569 Seq. No. 141636 1.R1040 Contig ID 5'-most EST $k11701\overline{2}03753.h2$ Seq. No. 26570 Contig ID 141650 1.R1040 5'-most EST uC-gmropic108g04b1 Seq. No. 26571 Contig ID 141650 2.R1040 5'-most EST uC-qmrominsoy256e09b1 26572 Seq. No. Contig ID 141663 1.R1040 5'-most EST $zhf700\overline{9}62075.h1$ 26573 Seq. No. Contig ID 141666 1.R1040 5'-most EST kl1701214514.h1 Seq. No. 26574 Contig ID 141691 1.R1040 5'-most EST ncj700985352.h1BLASTX Method NCBI GI g4314358 BLAST score 380 1.0e-36 E value 128 Match length

% identity 56
NCBI Description (AC006340) putative kinesin heavy chain protein

[Arabidopsis thaliana]

Seq. No. 26575

Contig ID 141733 1.R1040

5'-most EST jC-gmf102220052a02a1

Seq. No. 26576

Contig ID 141739_1.R1040

5'-most EST uC-gmflminsoy044g10b1

Method BLASTX
NCBI GI g4538987
BLAST score 279
E value 3.0e-24

Match length 228 % identity 25

Contig ID

```
NCBI Description (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
 Seq. No.
                    26577
 Contig ID
                    141771 1.R1040
 5'-most EST
                    zzp700834386.h1
 Seq. No.
                    26578
                    141773 1.R1040
 Contig ID
 5'-most EST
                   pcp700992358.h1
Method
                    BLASTX
                    g2244815
 NCBI GI
 BLAST score
                    143
 E value
                    5.0e-09
 Match length
                    51
 % identity
 NCBI Description
                    (Z97336) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    26579
 Contig ID
                    141782 1.R1040
 5'-most EST
                   uC-gmrominsoy060f03b1
 Method
                    BLASTX
 NCBI GI
                    q2632103
 BLAST score
                    207
 E value
                    2.0e-16
 Match length
                    70
 % identity
 NCBI Description (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]
                    26580
 Seq. No.
 Contig ID
                    141782 2.R1040
 5'-most EST
                    smc700748696.h1
 Seq. No.
                    26581
 Contig ID
                    141784 1.R1040
 5'-most EST
                    jC-qmst02400052d09a1
 Method
                   BLASTX
 NCBI GI
                    q3618320
 BLAST score
                    192
 E value
                    2.0e-14
 Match length
                    111
 % identity
 NCBI Description
                   (AB001888) zinc finger protein [Oryza sativa]
 Seq. No.
 Contig ID
                    141849 1.R1040
 5'-most EST
                   wrg700790875.h1
 Seq. No.
                   26583
 Contig ID
                   141863 1.R1040
 5'-most EST
                   jC-gmst02400071f06a1
 Seq. No.
                   26584
 Contig ID
                   141867 1.R1040
 5'-most EST
                   ncj700\overline{9}85591.h1
 Seq. No.
                   26585
```

141877 1.R1040

```
5'-most EST
                  ncj700985611.hl
Method
                  BLASTX
                  g2702268
NCBI GI
BLAST score
                   396
                   2.0e-38
E value
                   114
Match length
                   66
% identity
                   (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26586
                  141877_2.R1040
Contig ID
                  epx701109545.h1
5'-most EST
Method
                  BLASTX
                  g2702268
NCBI GI
BLAST score
                  223
E value
                  2.0e-18
Match length
                  81
% identity
                   57
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26587
                  141881 1.R1040
Contig ID
5'-most EST
                  ncj700985615.hl
Method
                  BLASTX
NCBI GI
                  g4210449
BLAST score
                   362
E value
                   5.0e-34
Match length
                  273
% identity
                   (AB016471) ARR1 protein [Arabidopsis thaliana]
NCBI Description
                  26588
Seq. No.
Contig ID
                  141903 1.R1040
5'-most EST
                  pcp700995658.hl
Method
                  BLASTX
NCBI GI
                  g3805851
BLAST score
                   400
E value
                   6.0e-39
Match length
                  102
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26589
Contig ID
                  141943 1.R1040
5'-most EST
                  pmv700890950.h1
Seq. No.
                  26590
Contig ID
                  141956 1.R1040
5'-most EST
                  ncj700985737.hl
Seq. No.
                  26591
Contig ID
                  141997 1.R1040
5'-most EST
                  asn701132792.h1
Seq. No.
                  26592
Contig ID
                  142003 1.R1040
5'-most EST
                  ncj700985810.hl
```

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   g807698
BLAST score
                   361
E value
                   2.0e-34
Match length
                   129
                   57
% identity
                   (D32206) prepro-cucumisin [Cucumis melo]
NCBI Description
Seq. No.
                   26593
Contig ID
                   142010 1.R1040
                   leu701152243.h1
5'-most EST
Seq. No.
                   26594
Contig ID
                   142017 1.R1040
5'-most EST
                   zhf700952286.h1
                   26595
Seq. No.
Contig ID
                   142022 1.R1040
5'-most EST
                   ncj700987179.h1
Seq. No.
                   26596
Contig ID
                   142024 1.R1040
5'-most EST
                   pcp700989817.hl
                   BLASTX
Method
NCBI GI
                   g2651316
BLAST score
                   225
E value
                   1.0e-18
                   62
Match length
% identity
NCBI Description
                   (AC002336) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   142025 1.R1040
5'-most EST
                   wrg700790609.h2
                   26598
Seq. No.
                   142044 1.R1040
Contig ID
5'-most EST
                   ncj700985869.h1
                   26599
Seq. No.
                   142046 1.R1040
Contig ID
5'-most EST
                   ncj700985871.h1
Seq. No.
                   26600
                   142103 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}85949.h1
Seq. No.
                   26601
Contig ID
                   142104 1.R1040
5'-most EST
                   jC-gmst02400029d04a1
Method
                   BLASTX
NCBI GI
                   q1553133
BLAST score
                   159
E value
                   1.0e-10
Match length
                   119
% identity
```

(U64722) actin-fragmin kinase [Physarum polycephalum]

Method

NCBI GI

BLASTX

q2443887

```
Seq. No.
                   26602
                   142117 1.R1040
Contig ID
5'-most EST
                   ncj700987991.h1
                   BLASTN
Method
                   q4140025
NCBI GI
BLAST score
                   186
                   1.0e-100
E value
Match length
                   428
%-identity
                   86
                   Vigna mungo UF3GaT mRNA for flavonoid 3-O-galactosyl
NCBI Description
                   transferase, complete cds
                   26603
Seq. No.
Contig ID
                   142123 1.R1040
5'-most EST
                   epx701105074.h1
Seq. No.
                   26604
Contig ID
                   142133 1.R1040
                   smc700747118.hl
5'-most EST
Seq. No.
                   26605
Contig ID
                   142139 1.R1040
5'-most EST
                   gsv701\overline{0}56689.h1
Seq. No.
                   26606
Contig ID
                   142148 1.R1040
5'-most EST
                   ncj700986016.hl
Seq. No.
                   26607
Contig ID
                   142193 1.R1040
5'-most EST
                   zhf700959032.h1
                   26608
Seq. No.
Contig ID
                   142193 2.R1040
5'-most EST
                   jex700\overline{9}06403.h1
Seq. No.
                   26609
Contig ID
                   142206 1.R1040
5'-most EST
                   uC-gmflminsoy075a05b1
Seq. No.
                   26610
Contig ID
                   142232 1.R1040
5'-most EST
                   jC-qmle01810022c01a1
Method
                   BLASTX
NCBI GI
                   a4490325
BLAST score
                   398
E value
                   7.0e-39
Match length
                   113
% identity
NCBI Description
                   (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   26611
Contig ID
                   142237 1.R1040
5'-most EST
                   ncj700986140.h1
```

% identity

73

```
BLAST score
                        520
     E value
                        4.0e-53
                        130
     Match length
     % identity
                        73
                        (AC002294) Similar to transcription factor
     NCBI Description
                        gb Z46606 1658307 and others [Arabidopsis thaliana]
                        26612
     Seq. No.
                        142239 1.R1040
     Contig ID
                        zhf700952977.h1
     5'-most EST
                        26613
     Seq. No.
                        142253 1.R1040
     Contig ID
                        zhf700965103.h1
     5'-most EST
     Seq. No.
                        26614
                        142267 1.R1040
     Contig ID
                        ncj700986195.hl
     5'-most EST
     Seq. No.
                        26615
     Contig ID
                        142272 1.R1040
     5'-most EST
                        ncj700986207.hl
     Seq. No.
                        26616
     Contig ID
                        142314 1.R1040
     5'-most EST
                        uC-gmropic112h07b1
     Method
                        BLASTX
     NCBI GI
                        g2501356
     BLAST score
                        666
     E value
                        4.0e-70
     Match length
                        138
     % identity
     NCBI Description
                        TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
                        >qi 1658322 emb CAA90427 (Z50099) transketolase precursor
                        [Solanum tuberosum]
                        26617
     Seq. No.
     Contig ID
                        142317 1.R1040
     5'-most EST
                       ncj700986301.hl
                        26618
     Seq. No.
     Contig ID
                        142325 1.R1040
     5'-most EST
                        uC-gmflminsoy036d01b1
                        26619
     Seq. No.
                        142355 1.R1040
     Contig ID
     5'-most EST
                       asn701142632.h1
     Seq. No.
                        26620
     Contig ID
                        142361 1.R1040
     5'-most EST
                        k11701\overline{2}08980.h1
    Method
                       BLASTX
     NCBI GI
                       g4104056
     BLAST score
                        456
     E value
                        9.0e-46
    Match length
                        107
```

Contig ID

5'-most EST

```
NCBI Description (AF031194) S276 [Triticum aestivum]
                  26621
Seq. No.
Contig ID
                  142375 1.R1040
5'-most EST
                  crh700\overline{8}54918.h1
Seq. No.
                  26622
Contig ID
                   142379 1.R1040
5'-most EST
                  uC-gmflminsoy067b12b1
                  26623
Seq. No.
Contig ID
                   142385 1.R1040
5'-most EST
                  ncj700986408.hl
Method
                  BLASTX
NCBI GI
                  g4185499
BLAST score
                   335
                   4.0e-31
E value
Match length
                   150
% identity
                   (AF096095) fertilization-independent seed 2 protein
NCBI Description
                   [Arabidopsis thaliana] >qi 4185501 (AF096096)
                   fertilization-independent seed 2 protein [Arabidopsis
                   thaliana]
Seq. No.
                   26624
Contig ID
                   142400 1.R1040
5'-most EST
                   zhf700964744.h1
Seq. No.
                  26625
Contig ID
                   142416 1.R1040
5'-most EST
                  jC-qmro02800033e10a1
Method
                  BLASTX
NCBI GI
                  q2262173
BLAST score
                   441
E value
                   6.0e-44
Match length
                   112
% identity
NCBI Description
                   (AC002329) NADPH thioredoxin reductase [Arabidopsis
                  thaliana]
                   26626
Seq. No.
Contig ID
                  142419 1.R1040
5'-most EST
                   jex700906483.hl
Method
                  BLASTX
NCBI GI
                  q1345132
BLAST score
                  376
E value
                  8.0e-44
Match length
                  117
% identity
NCBI Description
                   (U47029) ERECTA [Arabidopsis thaliana]
                  >gi 1389566 dbj BAA11869 (D83257) receptor protein kinase
                   [Arabidopsis thaliana] >gi 3075386 (AC004484) receptor
                  protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.
                  26627
```

142424 1.R1040

kmv700740451.h1

Method

NCBI GI

E value

BLAST score

Match length

26628 Seq. No. 142425 1.R1040 Contig ID 5'-most EST ncj700986457.hl 26629 Seq. No. 142452 1.R1040 Contiq ID ncj700986494.h15'-most EST Seq. No. 26630 142472 1.R1040 Contig ID ncj700986527.h1 5'-most EST Seq. No. 26631 Contig ID 142473 1.R1040 5'-most EST uC-gmflminsoy064c11b1 Method BLASTX NCBI GI q4539452 BLAST score 348 E value 4.0e-33 Match length 98 % identity NCBI Description (AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana] 26632 Seq. No. Contig ID 142478 1.R1040 5'-most EST uC-gmrominsoy157f04b1 Seq. No. 26633 142488 1.R1040 Contig ID 5'-most EST ncj700986543.h126634 Seq. No. Contig ID 142498 1.R1040 5'-most EST $hrw701\overline{0}60354.h1$ Seq. No. 26635 Contig ID 142501 1.R1040 5'-most EST ncj700987295.hl Seq. No. 26636 Contig ID 142504 1.R1040 5'-most EST smc700746405.h126637 Seq. No. Contig ID 142505 1.R1040 5'-most EST $jex700\overline{9}07810.h1$ 26638 Seq. No. Contig ID 142511 1.R1040 5'-most EST $epx701\overline{1}07806.h1$

BLASTX

292

105

g2618684

7.0e-42

```
% identity
 NCBI Description
                   (AC002510) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana] >gi 3241947 (AC004625) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana]
                   26639
 Seq. No.
                   142526 1.R1040
 Contig ID
                   wrg700791886.hl
 5'-most EST
                   26640
 Seq. No.
                   142531 1.R1040
 Contig ID
 5'-most EST
                   ncj700986608.hl
 Method
                   BLASTX
 NCBI GI
                   g509810
 BLAST score
                   160
 E value
                   6.0e-11
 Match length
                   76
 % identity
 NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
 Seq. No.
                   26641
 Contig ID
                   142533 1.R1040
 5'-most EST
                   ncj700986612.h1
                   BLASTX
 Method
                   q4544403
 NCBI GI
 BLAST score
                   259
                   6.0e-22
 E value
 Match length
                   81
 % identity
 NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                   precursor [Arabidopsis thaliana]
 Seq. No.
                   26642
 Contig ID .
                   142533 2.R1040
                   k11701\overline{2}12260.h1
 5'-most EST
                   BLASTX
 Method
                   g4544403
 NCBI GI
 BLAST score
                   152
E value
                   8.0e-10
 Match length
                   48
 % identity
 NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                   precursor [Arabidopsis thaliana]
 Seq. No.
                   26643
 Contig ID
                   142533 3.R1040
 5'-most EST
                   fC-qmf1700901194a1
                   BLASTX
 Method
 NCBI GI
                   q4544403
 BLAST score
                   141
 E value
                   6.0e-09
 Match length
                   96
```

. .

35

% identity

5'-most EST

```
NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                   precursor [Arabidopsis thaliana] *
                   26644
Seq. No.
                   142558 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}86645.h1
                   26645
Seq. No.
                   142562 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}86652.h1
                   26646
Seq. No.
                   142592 1.R1040
Contig ID
5'-most EST
                   bth700849607.h1
Seq. No.
                   26647
                   142595 1.R1040
Contig ID
5'-most EST
                   zsg701125958.hl
Seq. No.
                   26648
Contig ID
                   142596 1.R1040
5'-most EST
                   ncj700986706.h1
Method ·
                   BLASTX
NCBI GI
                   g3738297
BLAST score
                   312
E value
                   2.0e-28
Match length
                   130
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   26649
Contig ID
                   142610 1.R1040
5'-most EST
                   ncj700986731.hl
Seq. No.
                   26650
Contig ID
                   142615 1.R1040
5'-most EST
                   ncj700\overline{9}86737.h1
Seq. No.
                   26651
Contig ID
                   142628 1.R1040
5'-most EST
                   sat701010007.h2
Method
                   BLASTX
NCBI GI
                   g477430
BLAST score
                   418
E value
                   3.0e-41
Match length
                   122
% identity
NCBI Description nucleolar protein p120 - mouse (fragment)
Seq. No.
Contig ID
                   142642 1.R1040
5'-most EST
                   vzy700750782.h1
Seq. No.
                   26653
Contig ID
                   142681 1.R1040
```

ncj700986835.hl

Method

BLASTX

```
26654
Seq. No. .
                  142716 1.R1040
Contig ID
5'-most EST
                  vzy700753607.h1
Seq. No.
                  26655
                  142721 1.R1040
Contig ID
                   kl1701212835.h1
5'-most EST
                  26656
Seq. No.
                  142733_2.R1040
Contig ID.
5'-most EST
                  leu701151255.h1
                  BLASTX
Method
                  g4103757
NCBI GI
BLAST score
                  256
                   3.0e-22
E value
Match length
                  55
                   91
% identity
NCBI Description (AF027376) MADS1 [Corylus avellana]
Seq. No.
                  26657
                  142759 1.R1040
Contig ID
5'-most EST
                  pcp700990417.hl
                  26658
Seq. No.
                  142792_1.R1040
Contig ID
                  ncj700987043.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3201554
BLAST score
                   396
E value
                   1.0e-66
Match length
                   169
                   76
% identity
NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]
Seq. No.
                  26659
                   142801 1.R1040
Contig ID
5'-most EST
                  ncj700987054.hl
Seq. No.
                  26660
                   142832 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy111h09b1
Method
                  BLASTX
NCBI GI
                  g2459437
BLAST score
                  197
E value
                   3.0e-15
Match length
                  77
% identity
                   62
                   (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  26661
Seq. No.
                  142837 1.R1040
Contig ID
                  ncj700\overline{9}87110.h1
5'-most EST
                  26662
Seq. No.
                  142861 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy007a10b1
```

Method

BLASTX

```
NCBI GI
                   g4544436
BLAST score
                   295
E value
                   5.0e-28
Match length
                   139
% identity
NCBI Description
                   (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
                   3' partial [Arabidopsis thaliana]
                   26663
Seq. No.
Contig ID
                   142866 1.R1040
5'-most EST
                   leu701156129.h1
                   BLASTX
Method
                   g3242728
NCBI GI
BLAST score
                   221
                   9.0e-18
E value
Match length
                   204
% identity
NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]
Seq. No.
                   142871 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}87156.h1
                   26665
Seq. No.
Contig ID
                   142883 1.R1040
5'-most EST
                   jC-gmst02400065e08a2
                   BLASTX
Method
NCBI GI
                   g2760839
                   228
BLAST score
                   1.0e-18
E value
Match length
                   101
% identity
                   49
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   26666
Seq. No.
                   142885_1.R1040
Contig ID
                   dpv701\overline{1}00860.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4193320
BLAST score
                   465
E value
                   7.0e-47
Match length
                   99
% identity
NCBI Description (AF045473) histone deacetylase [Zea mays]
                   26667
Seq. No.
                   142907 1.R1040
Contig ID
5'-most EST
                   jC-gmfl02220137a09a1
                   26668
Seq. No.
                   142913 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220080b07a1
                   26669
Seq. No.
                   142915 1.R1040
Contig ID
                  ncj700\overline{9}87212.h1
5'-most EST
```

Contig ID

```
NCBI GI
                   g3122595
 BLAST score
                   118
 E value
                   1.0e-10
 Match length
                   57
 % identity
                   55
                   PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX PROTEIN P72)
 NCBI Description
                   >qi 1592565 (U59321) DEAD-box protein p72 [Homo sapiens]
                   >gi 2832596 emb CAB09792 (Z97056) dJ434P1.3 [Homo sapiens]
 Seq. No.
                   26670
 Contig ID
                   142920 1.R1040
 5'-most EST
                   uC-gmropic037d11b1
 Seq. No.
 Contig ID
                   142923 1.R1040
 5'-most EST
                   kmv700741889.h1
 Seq. No.
                   26672
                   142945 1.R1040
 Contig ID
5'-most EST
                   eep700864944.h1
 Seq. No.
                   26673
                   142957 1.R1040
 Contig ID
 5'-most EST
                   uC-gmrominsoy169a02b1
Method
                   BLASTX
                   g2494034
 NCBI GI
 BLAST score
                   602
E value
                   2.0e-62
Match length
                   188
                   62
 % identity
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
 NCBI Description
                   KINASE 1) >gi 2129573 pir S71467 diacylglycerol kinase -
                   Arabidopsis thaliana >gi 1374772_dbj_BAA09856_ (D63787)
                   diacylglycerol kinase [Arabidopsis thaliana]
                   26674
 Seq. No.
                   142960 1.R1040
Contig ID
 5'-most EST
                   jC-gmf102220136b04a1
Method
                   BLASTX
 NCBI GI
                   g2245004
                   495
 BLAST score
 E value
                   5.0e-50
Match length
                   160
 % identity
                   57
NCBI Description
                   (Z97341) similarity to membrane transport protein
                   [Arabidopsis thaliana]
                   26675
 Seq. No.
 Contig ID
                   142966 1.R1040
                   asn701\overline{1}39805.h1
 5'-most EST
 Seq. No.
                   26676
                   142994 1.R1040
 Contig ID
 5'-most EST
                   jC-gmro02910075e08a1
 Seq. No.
                   26677
```

142995 1.R1040

5'-most EST

```
5'-most EST
                  zhf700953284.h1
Method
                  BLASTX
                  g3004565
NCBI GI
BLAST score
                  280
E value
                  8.0e-25
Match length
                  86
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26678
                  143010 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy042d06b1
Method
                  BLASTX
NCBI GI
                  g2995370
BLAST score
                  156
E value
                  1.0e-10
Match length
                  66
% identity
                  39
NCBI Description (AL022245) hypothetical protein [Schizosaccharomyces pombe]
                  26679
Seq. No.
Contig ID
                  143018 1.R1040
5'-most EST
                  pxt700944424.h1
                  26680
Seq. No.
Contig ID
                  143025 1.R1040
5'-most EST
                  ncj700987375.hl
                  BLASTX
Method
                  g2920706
NCBI GI
BLAST score
                  145
                  2.0e-09
E value
Match length
                  62
% identity
NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]
                  26681
Seq. No.
                  143055 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy245a02b1
Seq. No.
                  143057 1.R1040
Contig ID
5'-most EST
                  ncj700987429.hl
Seq. No.
                  26683
                  143118 1.R1040
Contig ID
5'-most EST
                  ncj700987533.h1
                  BLASTX
Method
                  q4151068
NCBI GI
BLAST score
                  488
                  2.0e-49
E value
                  97
Match length
% identity
NCBI Description (Y10862) ribonucleotide reductase [Nicotiana tabacum]
Seq. No.
                  26684
                  143126 1.R1040
Contig ID
```

ncj700987549.h1

Method

NCBI GI

BLASTN

q166411

```
Method
                  BLASTX
NCBI GI
                   q1491710
BLAST score
                   125
E value
                   3.0e-10
Match length
                   65
                   41
% identity
                   (X96506) alpha subunit; forms heterodimer with NC2
NCBI Description
                   alpha/Dr1 [Homo sapiens]
Seq. No.
                   26685
                   143179 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220073g11a1
Seq. No.
                   26686
Contig ID
                   143238 1.R1040
5'-most EST
                   ncj700987731.hl
Seq. No.
                   26687
Contig ID
                   143253 1.R1040
5'-most EST
                   uC-gmrominsoy111d06b1
Method
                   BLASTX
NCBI GI
                   q2501296
BLAST score
                   301
E value
                   4.0e-27
Match length
                   77
% identity
                   71
                  DNA GYRASE SUBUNIT B >qi 1652801 dbj BAA17720 (D90908) DNA
NCBI Description
                   gyrase B subunit [Synechocystis sp.]
Seq. No.
                   26688
Contig ID
                   143259 1.R1040
5'-most EST
                  ncj700987765.h1
                26689
Seq. No.
Contig ID
                   143278 1.R1040
5'-most EST
                  gsv701048101.hl
Seq. No.
                   26690
Contig ID
                   143278 3.R1040
5'-most EST
                   zzp700835694.h1
                   26691
Seq. No.
Contig ID
                   143286 1.R1040
5'-most EST
                  ncj700987804.hl
Method
                  BLASTX
NCBI GI
                   q4467111
BLAST score
                   333
E value
                   4.0e-31
Match length
                   99
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  26692
Contig ID
                   143291 1.R1040
5'-most EST
                  jC-qmst02400029q04a1
```

Match length

77

```
BLAST score
                  195
                  1.0e-105
E value
Match length
                  463
                  85
% identity
NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds
Seq. No.
                  26693
                  143326 1.R1040
Contig ID
5'-most EST
                  jsh701067464.h1
Method
                  BLASTX
                  g4204285
NCBI GI
BLAST score
                  408
                  9.0e-40
E value
Match length
                  167
% identity
                  49
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  26694
Seq. No.
                  143333 1.R1040
Contig ID
5'-most EST
                  ncj700987868.hl
                  26695
Seq. No.
                  143335 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910063d01a1
                  26696
Seq. No.
Contig ID
                  143342 1.R1040
5'-most EST
                  jC-gmro02800035f12d1
Method
                  BLASTX
NCBI GI
                  g3319341
BLAST score
                  224
                  3.0e-18
E value
Match length
                  44
% identity
                  82
                   (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                  protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
                  26697
Seq. No.
Contig ID
                  143375 1.R1040
5'-most EST
                  bth700845896.h1
Method
                  BLASTX
NCBI GI
                  q2983347
BLAST score
                  163
E value
                  5.0e-11
Match length
                  89
% identity
NCBI Description
                  (AE000707) hemolysin [Aquifex aeolicus]
                  26698
Seq. No.
Contig ID
                  143401 1.R1040
5'-most EST
                  zsq701126126.h1
Method
                  BLASTX
NCBI GI
                  q4455359
BLAST score
                  226
E value
                  7.0e-19
```

Method

BLASTX

```
% identity
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  143463 1.R1040
5'-most EST
                  ncj700988163.hl
Method
                  BLASTN
NCBI GI
                  q16508
BLAST score
                   75
E value
                   4.0e-34
Match length
                   147
                   88
% identity
                  A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                   sam-1 >gi 166871 gb_M55077_ATHSAM A.thaliana
                  S-adenosylmethionine synthetase gene, complete cds
                   26700
Seq. No.
Contig ID
                  143470 1.R1040
                   zhf700955313.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                   565
E value
                   2.0e-58
Match length
                  124
                   87
% identity
NCBI Description
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  26701
                  143472 1.R1040
Contig ID
5'-most EST
                   zhf700952045.hl
Method
                  BLASTX
NCBI GI
                  g1172441
BLAST score
                  163
E value
                   7.0e-11
Match length
                   48
% identity
                  POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi 99685 pir S21883
NCBI Description
                  DNA-binding protein POSF21 - Arabidopsis thaliana
                  >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis
                  thaliana]
                  26702
Seq. No.
                  143472 2.R1040
Contig ID
5'-most EST
                  smc700744982.hl
                  26703
Seq. No.
Contig ID
                  143477 1.R1040
                  sat701012012.h1
5'-most EST
Seq. No.
                  26704
                  143519 1.R1040
Contig ID
                  ncj700\overline{9}88274.h1
5'-most EST
                  26705
Seq. No.
Contig ID
                  143520 1.R1040
5'-most EST
                  ncj700\overline{9}88275.h1
```

```
NCBI GI
                   g2832664
BLAST score
                   214
                   1.0e-17
E value
Match length
                   73
% identity
                   58
                   (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                   thaliana]
                   26706
Seq. No.
                   143582 1.R1040 ...
Contig ID
5'-most EST
                   ncj700\overline{9}88393.h1
Method
                   BLASTX
                   g4455278
NCBI GI
BLAST score
                   128
E value
                   4.0e-10
Match length
                   90
% identity
                  (AL035527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26707
Seq. No.
Contig ID
                   143588 1.R1040
5'-most EST
                   uC-qmflminsoy075c09b1
Method
                   BLASTX
NCBI GI
                   q2660677
BLAST score
                   722
E value
                   2.0e-76
Match length
                   251
% identity
                   59
NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]
                   26708
Seq. No.
Contig ID
                   143607 1.R1040
5'-most EST
                   uC-qmflminsoy035b02b1
                   26709
Seq. No.
Contig ID
                   143621 1.R1040
5'-most EST
                   fC-gmle700871981f3
Method
                   BLASTX
NCBI GI
                   g2623300
BLAST score
                   1045
E value
                   1.0e-114
Match length
                   372
% identity
NCBI Description
                  (AC002409) putative protein phosphatase 2C [Arabidopsis
                   thaliana]
                   26710
Seq. No.
Contiq ID
                   143639 1.R1040
5'-most EST
                   leu701147859.hl
                  BLASTX
Method
NCBI GI
                   g3510254
BLAST score
                   227
E value
                  8.0e-19
Match length
                  81
% identity
```

NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

```
26711
Seq. No.
                   143649 1.R1040
Contig ID
5'-most EST
                   ncj700988522.hl
Seq. No.
                   26712
                   143656 1.R1040
Contiq ID
5'-most EST
                   ncj700988535.h1
Seq. No.
                   26713
Contig ID
                   143658 1.R1040 -
5'-most EST
                   ncj700988541.h1
                   26714
Seq. No.
Contig ID
                   143668 1.R1040
5'-most EST
                   ncj700988559.h1
Method
                   BLASTX
NCBI GI
                   g1169128
BLAST score
                   228
                   1.0e-18
E value
                   111
Match length
                   42
% identity
NCBI Description
                   SERINE/THREONINE-PROTEIN KINASE CTR1 >qi 166680 (L08789)
                   protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                   protein kinase [Arabidopsis thaliana]
Seq. No.
                   26715
Contig ID
                   143680 1.R1040
5'-most EST
                   jC-gmro02910016e12a1
Seq. No.
                   26716
                   143730 1.R1040
Contig ID
                   zhf700964905.h1
5'-most EST
Seq. No.
                   26717
                   143735 1.R1040
Contig ID
5'-most EST
                   ncj700\overline{9}88655.h1
Method
                   BLASTX
NCBI GI
                   q1245343
BLAST score
                   242
E value
                   2.0e-20
Match length
                   76
% identity
                   (U50194) tripeptidylpeptidase II [Rattus norvegicus]
NCBI Description
Seq. No.
                   26718
                   143755 1.R1040
Contig ID
                   qsv701\overline{0}44887.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2160182
BLAST score
                   345
E value
                   2.0e-32
Match length
                   104
                   66
% identity
                   (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
```

26719

Seq. No.

5'-most EST Method

BLASTX

```
Contig ID
                  143765 1.R1040
5'-most EST
                  pst700645716.h1
Method
                   BLASTX
                   g2245009
NCBI GI
BLAST score
                   201
                   7.0e-16
E value
                  54
Match length
% identity
                  70
NCBI Description
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
                  26720
Seq. No.
                  143912 1.R1040
Contig ID
5'-most EST
                  txt700731337.h1
Seq. No.
                   26721
                   143912 2.R1040
Contig ID
5'-most EST
                   zhf700958462.h1
                   26722
Seq. No.
                   143936 1.R1040
Contig ID
5'-most EST
                  k11701207242.h1
Seq. No.
                   26723
Contig ID
                  143962 1.R1040
5'-most EST
                   txt700731496.h1
Method
                  BLASTX
NCBI GI
                   q1174718
BLAST score
                  178
E value
                   2.0e-13
Match length
                   41
% identity
NCBI Description
                   PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
                  >qi 322579 pir JQ1674 receptor protein kinase TMK1 (EC
                   2.7.1.-) precursor - Arabidopsis thaliana >gi 166888
                   (L00670) protein kinase [Arabidopsis thaliana]
Seq. No.
                   26724
Contig ID
                   144083 1.R1040
5'-most EST
                  k11701202564.h1
Seq. No.
                  26725
Contig ID
                  144117 1.R1040
5'-most EST
                  q5342789
Method
                  BLASTX
NCBI GI
                  q1705678
BLAST score
                   364
E value
                   1.0e-34
Match length
                  108
% identity
                  72
NCBI Description
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
                  PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                  26726
Contig ID
                  144139 2.R1040
                  txt700731771.h1
```

```
NCBI GI
                  g1055161
BLAST score
                  221
                  7.0e-18
E value
Match length
                  122
% identity
                  24
                   (U40029) similar to human 100 kDa coactivator (U22055)
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                  26727
Contig ID
                  144141 1.R1040
                  rlr700900684.h1
5'-most EST
                  26728
Seq. No.
Contig ID
                  144156 1.R1040
5'-most EST
                  txt700731814.hl
Method
                  BLASTX
                  q3269285
NCBI GI
BLAST score
                  349
                  3.0e-33
E value
Match length
                  78
% identity
                  (AL030978) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  26729
Seq. No.
                  144164 1.R1040
Contig ID
5'-most EST
                  gsv701045873.hl
Method
                  BLASTX
NCBI GI
                  g2981439
BLAST score
                  205
E value
                  2.0e-16
Match length
                  63
% identity
                  (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
NCBI Description
                  26730
Seq. No.
                  144178 1.R1040
Contig ID
5'-most EST
                  txt700731848.hl
Method
                  BLASTX
NCBI GI
                  g4325324
BLAST score
                  470
                  5.0e-47
E value
Match length
                  98
% identity
NCBI Description
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                  thaliana]
                  26731
Seq. No.
                  144277 1.R1040
Contig ID
5'-most EST
                  txt700732015.h1
                  BLASTX
Method
                  g1841357
NCBI GI
BLAST score
                  364
                  1.0e-34
E value
Match length
                  122
% identity
                  58
                  (D85382) mitochondrial ribosomal protein S11 (nuclear
NCBI Description
```

encoded) [Oryza sativa]

Match length

77

```
26732
Seq. No.
Contig ID
                  -144293 1.R1040
5'-most EST
                   ujr700646608.hl
Seq. No.
                   26733
                   144297 1.R1040
Contig ID
                   k11701\overline{2}12153.h1
5'-most EST
Seq. No.
                   26734
Contig ID
                   144315 1.R1040
5'-most EST
                   txt700732787.h1
                   26735
Seq. No.
Contig ID
                   144329 1.R1040
5'-most EST
                   txt700732113.hl
Seq. No.
                   26736
                   144345 1.R1040
Contig ID
                   uC-gmrominsoy167c09b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3702738
BLAST score
                   34
E value
                   1.0e-09
Match length
                   50
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWJ3, complete sequence [Arabidopsis thaliana]
                   26737
Seq. No.
Contig ID
                   144348 1.R1040
                   fua701037950.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2507300
BLAST score
                   237
E value
                   3.0e-20
Match length
                   57
                   74
% identity
                  ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD
NCBI Description
                   SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40)
                   >gi_1590811 (M87338) replication factor C, 40-kDa subunit
                   [Homo sapiens] >gi_2914760 (AF045555) replication factor C
                   subunit 2 [Homo sapiens] >gi_4506487_ref_NP_002905.1_pRFC2_
                   replication factor C (activator 1) 2 (40kD)
                   26738
Seq. No.
                   144359 1.R1040
Contig ID
5'-most EST
                   gsv701045178.hl
Seq. No.
                   26739
                   144390 1.R1040
Contig ID
                   txt700732216.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2827552
BLAST score
                   214
E value
                   1.0e-17
```

5'-most EST

Method

```
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   26740
Seq. No.
Contig ID
                   144398 1.R1040
5'-most EST
                   txt700732226.h1
                   26741
Seq. No.
                   144403 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}98967.h1
Method
                   BLASTX
                   g2204236
NCBI GI
BLAST score
                   539
                   3.0e-55
E value
                   141
Match length
% identity
                   77
NCBI Description (Y13861) enoyl-ACP reductase [Nicotiana tabacum]
Seq. No.
                   26742
                   144473 1.R1040
Contig ID
                   txt700732364.h1
5'-most EST
Seq. No.
                   26743
                   144488 1.R1040
Contig ID
                   txt700732403.h1
5'-most EST
                   26744
Seq. No.
Contig ID
                   144489 1.R1040
5'-most EST
                   jC-gmst02400001g06a1
                   BLASTX
Method
                   g3335378
NCBI GI
BLAST score
                   364
                   2.0e-34
E value
Match length
                   90
% identity
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
                   26745
Seq. No.
                   144509 1.R1040
Contig ID
5'-most EST
                   uC-gmropic074a10b1
Method
                   BLASTX
NCBI GI
                   g3152940
BLAST score
                   196
E value
                   5.0e-15
                   92
Match length
                   45
% identity
                  (AF065483) sorting nexin 1 [Homo sapiens]
NCBI Description
                   26746
Seq. No.
                   144509 2.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97363.h1
                   26747
Seq. No.
                   144514 1.R1040
Contig ID
```

awf700841065.hl

BLASTX

5'-most EST

```
NCBI GI
                    g2262115
 BLAST score
                    332
 E value
                    1.0e-30
 Match length
                    233
 % identity
                    (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
 NCBI Description
                    26748
 Seq. No.
                    144529 1.R1040
 Contig ID
 5'-most EST
                   uC-gmrominsoy041d07b1
                    26749
 Seq. No.
                    144543 1.R1040
 Contig ID
 5'-most EST
                    txt700732511.h1
                    26750
 Seq. No.
                  144549_1.R1040
 Contig ID
 5'-most EST
                    kl1701205179.hl
Method
                    BLASTX
 NCBI GI
                    g3033384
 BLAST score
                    443
                    6.0e-44
 E value
 Match length
                    142
                    63
 % identity
 NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]
                    26751
 Seq. No.
                    144562 1.R1040
 Contig ID
                    leu701157138.h1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g3297824
 BLAST score
                    141
                    1.0e-08
 E value
 Match length
                    94
                    39
 % identity
                    (AL031032) bZIP transcription factor - like protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    26752
                    144570 1.R1040
 Contig ID
                    txt700732562.h1
 5'-most EST
                    BLASTN
 Method
                    g2605511
 NCBI GI
 BLAST score
                    121
 E value
                    2.0e-61
 Match length
                    356
                    83
 % identity
                   Glycine max mRNA for beta subunit of beta conglycinin,
 NCBI Description
                    complete cds
                    26753
 Seq. No.
                    144589 2.R1040
 Contig ID
 5'-most EST
                    fua701041692.hl
 Seq. No.
                    26754
 Contig ID
                    144608 1.R1040
```

txt700732661.h1

E value

8.0e-22

```
Method
                  BLASTN
NCBI GI
                  q2995454
BLAST score
                  317
E value
                  1.0e-178
Match length
                  521
% identity
                  90
NCBI Description L.luteus mRNA for tRNA-glutamine synthetase
                  26755
Seq. No.
                  144609 1.R1040
Contig ID
5'-most EST
                  pxt700943328.h1
                  BLASTX
Method
                  g3702338
NCBI GI
BLAST score
                  269
                  6.0e-24
E value
Match length
                  80
% identity
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  26756
Seq. No.
                  144639 1.R1040
Contig ID
5'-most EST
                  txt700732737.h1
                  26757
Seq. No.
                  144643 1.R1040
Contig ID
5'-most EST
                  hrw701061473.hl
                  BLASTX
Method
NCBI GI
                  g3341684
BLAST score
                  236
                  4.0e-20
E value
Match length
                  87
% identity
NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]
                  26758
Seq. No.
                  144648 1.R1040
Contig ID
5'-most EST
                  fC-gmse700837723c1
Method
                  BLASTX
NCBI GI
                  g3641252
BLAST score
                  516
E value
                  2.0e-52
Match length
                  169
                  65
% identity
NCBI Description
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
                  domestica]
                  26759
Seq. No.
                  144670 1.R1040
Contig ID
                  txt700732816.h1
5'-most EST
Seq. No.
                  26760
                  144688 1.R1040
Contig ID
5'-most EST
                  epx701109140.hl
                  BLASTX
Method
NCBI GI
                  g267442
BLAST score
                  257
```

Match length 154 % identity 40 NCBI Description HYPOTHETICAL 18.7 KD PROTEIN IN RHLE-DING INTERGENIC REGION (F160) >gi 147599 (L02123) YbiA [Escherichia coli] >gi 1787017 (AE000182) orf, hypothetical protein [Escherichia coli] >gi 4062356 dbj BAA35458 (D90716) Hypothetical 18.7 kd protein in rhlE-dinG/rarB intergenic region (F160). [Escherichia coli] >gi 4062360 dbj BAA35464 (D90717) Hypothetical 18.7 kd protein in rhlE-dinG/rarB intergenic region (F160). [Escherichia coli] 26761 Seq. No. 144708 1.R1040 Contig ID 5'-most EST zhf700954866.hl Seq. No. 26762 144802 1.R1040 Contig ID 5'-most EST uC-qmropic062a07b1 Seq. No. 26763 Contig ID 144809 1.R1040 txt700733086.hl 5'-most EST Seq. No. 26764 Contig ID 144810 1.R1040 5'-most EST zpv700759801.hl 26765 Seq. No. Contig ID 144819 1.R1040 5'-most EST pmv700889162.h1 Method BLASTX NCBI GI q120777 BLAST score 827 E value 2.0e-88 Match length 251 % identity SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH) NCBI Description >qi 147901 (M88334) succinic semialdehyde dehydrogenase [Escherichia coli] >gi_1789015 (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli] Seq. No. 26766 Contig ID 144819 2.R1040 5'-most EST iC-qmf102220071c03d1 BLASTX Method NCBI GI a120777 BLAST score 223 E value 3.0e-18 Match length 66 % identity SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH) NCBI Description

activity [Escherichia coli]

[Escherichia coli] >gi_1789015 (AE000351)

>gi 147901 (M88334) succinic semialdehyde dehydrogenase

succinate-semialdehyde dehydrogenase, NADP-dependent

E value

```
Seq. No.
                   26767
                   144874 1.R1040
 Contig ID
 5'-most EST
                   rca701\overline{0}02368.h1
                   26768
 Seq. No.
                   144909 1.R1040
Contig ID
 5'-most EST
                   txt700733296.h1
Seq. No.
                   26769
                   144952 1.R1040
Contig ID
 5'-most EST
                   txt700733379.h1
                   26770
 Seq. No.
 Contig ID
                   144964 1.R1040
 5'-most EST
                   txt700733408.h1
                   26771
 Seq. No.
                   145017 1.R1040
 Contig ID
 5'-most EST
                   zsq701119121.h1
Method
                   BLASTX
NCBI GI
                   q3219269
BLAST score
                   279
E value
                   1.0e-48
Match length
                   117
 % identity
NCBI Description
                   (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana]
Seq. No.
                   26772
Contig ID
                   145028 1.R1040
                   txt700733518.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2880046
BLAST score
                   147
E value
                   2.0e-09
Match length
                   65
 % identity
                    (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26773
 Contig ID
                   145043 1.R1040
 5'-most EST
                   jC-gmf\overline{1}02220078a05a1
Seq. No.
                   26774
 Contig ID
                   145056 1.R1040
 5'-most EST
                   txt700737183.h1
Seq. No.
                   26775
Contig ID
                   145106 1.R1040
 5'-most EST
                   gsv701043865.hl
Seq. No.
                   26776
Contig ID
                   145110 1.R1040
 5'-most EST
                   g5126515
Method
                   BLASTX
NCBI GI
                   g2323410
BLAST score
                   994
```

1.0e-108

```
Match length
                   376
% identity
                   54
                   (AF015913) Skb1Hs [Homo sapiens]
NCBI Description
Seq. No.
                   26777
                   145133 1.R1040
Contig ID
5'-most EST
                   txt700733710.hl
                   BLASTX
Method
                   g2213626
NCBI GI
BLAST score
                   144
                   7.0e-09
E value
Match length
                   153
% identity
                   (AC000103) F21J9.18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26778
Contig ID
                   145156 1.R1040
5'-most EST
                   uC-gmropic111c10b1
Method
                   BLASTX
NCBI GI
                   q3885334
BLAST score
                   193
E value
                   7.0e-15
Match length
                   50
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   26779
Seq. No.
Contig ID
                   145196 1.R1040
5'-most EST
                   txt700733827.h1
                   26780
Seq. No.
Contig ID
                   145197 3.R1040
5'-most EST
                   jex700\overline{9}08479.h1
                   26781
Seq. No.
Contig ID
                   145201 1.R1040
5'-most EST
                   txt700733833.h1
Method
                   BLASTN
NCBI GI
                   g2687440
BLAST score
                   118
E value
                   5.0e-60
Match length
                   138
% identity
                   96
                   Tellima grandiflora large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   26782
Seq. No.
Contig ID
                   145226 1.R1040
5'-most EST
                   kmv700737717.h1
                   26783
Seq. No.
                   145232 1.R1040
Contig ID
5'-most EST
                   txt700733885.hl
Method
                   BLASTX
                   q4263704
NCBI GI
BLAST score ^
                   362
```

```
2.0e-34
E value
Match length
                  136
                  50
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                  [Arabidopsis thaliana]
                  26784
Seq. No.
                  145236 1.R1040
Contig ID
5.'-most EST
                  txt700733890.h1
                  26785
Seq. No.
                  145300 1.R1040
Contig ID
                  txt700734006.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3184285
BLAST score
                  296
E value
                  5.0e-27
Match length
                  96
% identity
                  (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26786
Contig ID
                  145328 1.R1040
5'-most EST
                  zzp700832617.hl
                  26787
Seq. No.
Contig ID
                  145330 1.R1040
5'-most EST
                  pxt700945528.hl
Method
                  BLASTX
NCBI GI
                  q2894611
BLAST score
                  155
                  2.0e-10
E value
Match length
                  47
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                  26788
Seq. No.
Contig ID
                  145330 2.R1040
5'-most EST
                  k11701\overline{2}15222.h1
                  26789
Seq. No.
                  145340 1.R1040
Contig ID
5'-most EST
                  txt700734093.h1
                  26790
Seq. No.
Contig ID
                  145393 1.R1040
5'-most EST
                  txt700734230.h1
                  BLASTX
Method
NCBI GI
                  g3123161
BLAST score
                  94.
E value
                  8.0e-09
Match length
                  111
% identity
NCBI Description
                  HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
                  F35G12.4 IN CHROMOSOME III >gi 3876723 emb CAA86335
                  (Z46242) similar to beta-transducin; cDNA EST EMBL: Z14703
```

comes from this gene; cDNA EST EMBL: D67532 comes from this

```
145499 1.R1040
Contig ID
5'-most EST
                   txt700734406.h1
Seq. No.
                   26792
                   145502 1.R1040
Contig ID
                   txt700734410.h1
5'-most EST
                   26793
Seq. No.
                   145514 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy307f01b1
Method
                   BLASTX
NCBI GI
                   g3142291
BLAST score
                   487
                   6.0e-49
E value
Match length
                   167
% identity
                   54
NCBI Description
                   (AC002411) Contains similarity to adenylate cyclase
                   qb AF012921 from Magnaporthe grisae. EST gb Z24512 comes
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   26794
Contig ID
                   145544_1.R1040
                   zpv700761035.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4249416
BLAST score
                   291
E value
                   4.0e-26
Match length
                   89
% identity
NCBI Description
                   (AC006072) putative exoribonuclease (also contains
                   zinc-finger C2H2-type domain) [Arabidopsis thaliana]
Seq. No.
                   26795
Contig ID
                   145570 1.R1040
5'-most EST
                   dpv701101324.h1
Method
                   BLASTX
NCBI GI
                   q3377843
BLAST score
                   151
E value
                   6.0e-10
Match length
                   102
% identity
                   (AF076274) contains similarity to rat p47 protein
NCBI Description
                   (GB:AB002086) [Arabidopsis thaliana]
Seq. No.
                   26796
Contig ID
                   145635 1.R1040
5'-most EST
                   jC-gmro02910062d04a1
Method
                   BLASTX
NCBI GI
                   g2911042
BLAST score
                   682
E value
                   3.0e-89
Match length
                   226
% identity
                   79
```

26791

Seq. No.

gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

```
NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein
                                                [Arabidopsis thaliana]
Seq. No.
                                                26797
                                                145698 1.R1040
Contig ID
                                                qsv701\overline{0}55801.h1
5'-most EST
Method
                                                BLASTX
                                                q4218011
NCBI GI
BLAST score
                                                442
E value
                                                6.0e-44
Match length
                                                101
% identity
                                                (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                                                >gi 4309721 gb AAD15491 (AC006439) putative
                                                serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                                                26798
Contig ID
                                                145700 1.R1040
5'-most EST
                                               pmv700888891.hl
Method
                                               BLASTX
NCBI GI
                                                q3132478
BLAST score
                                                311
E value
                                                1.0e-28
Match length
                                                146
% identity
NCBI Description
                                              (AC003096) bZIP-like protein [Arabidopsis thaliana]
Seq. No.
                                                145704 1.R1040
Contig ID
5'-most EST
                                                jC-gmle01810066b02d1
Seq. No.
Contig ID
                                                145713 1.R1040
5'-most EST
                                               pmv700888646.h1
                                                26801
Seq. No.
                                                145743 1.R1040
Contig ID
5'-most EST
                                                crh700852487.h1
Method
                                                BLASTX
NCBI GI
                                                g2244996
BLAST score
                                                262
E value
                                                7.0e-37
Match length
                                               131
% identity
                                                59
NCBI Description (297341) similarity to a membrane-associated salt-inducible
                                               protein [Arabidopsis thaliana]
Seq. No.
                                                26802
Contig ID
                                                145763 1.R1040
5'-most EST
                                               smc700746937.h1
                                               26803
Seq. No.
                                                145785 1.R1040
Contig ID
5'-most EST
                                               jC-gms\overline{t}02400013e01a1
Seq. No.
                                               26804
                                               145786_1.R1040
Contig ID
                                                                                                                                                       Commence of the commence of th
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But a not be fore the

```
5'-most EST
                   smc700744318.hl
Method
                   BLASTX
NCBI GI
                   q3549667
BLAST score
                   587
                   6.0e-61
E value
Match length
                   136
% identity
NCBI Description
                   (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
                   26805
Seq. No.
                   145799 1.R1040
Contig ID
5'-most EST
                  dpv701100879.h1
Seq. No.
                   26806
Contig ID
                  145803 1.R1040
                  txt700734949.h1
5'-most EST
Seq. No.
                  26807
Contiq ID
                  145828 1.R1040
5'-most EST
                  pmv700893370.h1
Method
                  BLASTX
NCBI GI
                  g1169198
BLAST score
                  267
E value
                   2.0e-23
Match length
                  92
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR
                  >gi 479738 pir S35270 hypothetical protein - Arabidopsis
                  thaliana >gi_166926 (L11367) [Arabidopsis thaliana
                  unidentified mRNA sequence, complete cds.], gene product
                   [Arabidopsis thaliana]
Seq. No.
                  26808
Contig ID
                  145839 1.R1040
5'-most EST
                  awf700837802.h1
Method
                  BLASTX
NCBI GI
                  q3386597
BLAST score
                  169
E value
                  1.0e-11
Match length
                  48
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
                  >gi 3702347 (AC005397) putative permease [Arabidopsis
                  thaliana]
Seq. No.
                  26809
Contig ID
                  145844 1.R1040
5'-most EST
                  k11701\overline{2}02434.h1
Method
                  BLASTX
NCBI GI
                  g3452263
BLAST score
                  435
E value
                  4.0e-53
Match length
                  133
% identity
                  (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
```

thaliana]

```
26810
Seq. No.
Contig ID
                  145846 1.R1040
5'-most EST
                  txt700735025.h1
Method
                  BLASTX
                  q730934
NCBI GI
BLAST score
                  227
                  7.0e-19
E value
                  102
Match length
% identity
                   46
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
                  >qi 2137015 pir S68430 queuine tRNA-ribosyltransferase (EC
                  2.4.2.29), 60K chain - rabbit >gi 623547 (L37420) queuine
                  tRNA-ribosyltransferase [Oryctolagus cuniculus]
Seq. No.
                  26811
Contig ID
                  145866 1.R1040
5'-most EST
                  txt700735055.hl
Seq. No.
                  26812
Contig ID
                  145873 1.R1040
5'-most EST
                  leu701153435.h1
                  26813
Seq. No.
Contig ID
                  145884 1.R1040
5'-most EST
                  txt700735091.hl
                  26814
Seq. No.
Contig ID
                  145929 1.R1040
5'-most EST
                  txt700735202.hl
Method
                  BLASTX
NCBI GI
                  q2494174
BLAST score
                  444
E value
                  3.0e-60
Match length
                  180
                   67
% identity
NCBI Description
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
                  glutamate decarboxylase [Arabidopsis thaliana]
                  26815
Seq. No.
Contig ID
                  145967 1.R1040
5'-most EST
                  pxt700944894.h1
                  26816
Seq. No.
Contig ID
                  146045 1.R1040
5'-most EST
                  txt700735414.h1
Seq. No.
                  26817
Contig ID
                  146091 1.R1040
5'-most EST
                  txt700735488.h1
                  26818
Seq. No.
Contig ID
                  146129 1.R1040
5'-most EST
                  txt700735551.h1
Method
                  BLASTX
NCBI GI
                  q440965
```

NCBI GI

. . .

BLAST score

```
BLAST score
                   281
E value
                   4.0e-25
Match length
                   88
% identity
                   67
                   (S66876) orf in promoter of Lhca3.St.1 [Solanum
NCBI Description
                   tuberosum=potatoes, Peptide Chloroplast, 137 aa] [Solanum
                   tuberosuml
                   26819
Seq. No.
Contig ID
                   146149 1.R1040
                   kl1701202403.h1
5'-most EST
Seq. No.
                   26820
Contig ID
                   146156 1.R1040
5'-most EST
                   txt700735610.h1
Seq. No.
                   26821
Contig ID
                   146163 1.R1040
5'-most EST
                   txt700735623.h1
                   26822
Seq. No.
Contig ID
                   146168 1.R1040
5'-most EST
                   txt700735630.hl
                   26823
Seq. No.
Contig ID
                   146204 1.R1040
5'-most EST
                   xpa700793442.h1
Method
                   BLASTN
NCBI GI
                   q210811
BLAST score
                   124
E value
                   2.0e-63
Match length
                   296
% identity
                   92
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   26824
Seq. No.
Contig ID
                   146232 1.R1040
5'-most EST
                   txt700735759.h1
Method
                   BLASTX
NCBI GI
                   q3953463
BLAST score
                   188
E value
                   3.0e-14
Match length
                   65
% identity
NCBI Description
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   146237 1.R1040
5'-most EST
                   zhf700\overline{9}62523.h1
Seq. No.
                   26826
                   146240 1.R1040
Contig ID
5'-most EST
                   hrw701058854.hl
Method
                   BLASTX
```

a3021409

BLAST score

```
E value
                   8.0e-22
Match length
                   86
                   17
% identity
                   (Y12781) transducin (beta) like 1 protein [Homo sapiens]
NCBI Description
Seq. No.
                   146248 1.R1040
Contig ID
5'-most EST
                   uC-gmropic104f07b1
                   26828
Seq. No.
Contig ID
                   146258 1.R1040
                   txt700735801.hl
5'-most EST
                   26829
Seq. No.
Contig ID
                   146261 1.R1040
5'-most EST
                   uC-gmrominsoy086c07b1
                   26830
Seq. No.
                   146338 1.R1040
Contig ID
                   jsh701\overline{0}67558.h1
5'-most EST
                   26831
Seq. No.
                   146351 1.R1040
Contig ID
                   txt700735962.h1
5'-most EST
                   26832
Seq. No.
                   146360 1.R1040
Contig ID
                   txt700735975.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3386604
BLAST score
                   322
E value
                   3.0e-30
                   82
Match length
% identity
NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]
                   26833
Seq. No.
                   146411 1.R1040
Contig ID
                   fua701040350.h1
5'-most EST
Seq. No.
                   26834
                   146414 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}14317.h1
Method
                   BLASTX
NCBI GI
                   g3746064
BLAST score
                   145
                   6.0e-09
E value
Match length
                   45
% identity
NCBI Description
                  (AC005311) unknown protein [Arabidopsis thaliana]
                   26835
Seq. No.
                   146423_1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy010g10b1
Method
                   BLASTX
NCBI GI
                   g4091810
```

Seq. No.

```
E value
                   9.0e-16
Match length
                   112
% identity
NCBI Description
                   (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1
                   [Arabidopsis thaliana]
                   26836
Seq. No.
Contig ID
                   146450 1.R1040
5'-most EST
                   txt700736183.h1
                   BLASTX
Method
NCBI GI
                   q1707945
BLAST score
                   295
                   4.0e-27
E value
Match length
                   81
% identity
NCBI Description
                   GLYCOGEN OPERON PROTEIN GLGX HOMOLOG
                   >gi 1403478 emb CAA98327 (Z74020) glgX [Mycobacterium
                   tuberculosis]
                   26837
Seq. No.
Contig ID
                   146452 1.R1040
5'-most EST
                   epx701108278.h1
Seq. No.
                   26838
                   146456 1.R1040
Contig ID
                  txt700736189.hl
5'-most EST
Seq. No.
                   26839
Contig ID
                   146502 1.R1040
                  hrw701\overline{0}62412.h1
5'-most EST
Seq. No.
                   26840
                   146531 2.R1040
Contig ID
5'-most EST
                  uC-gmropic107e10b1
                   26841
Seq. No.
                  146538 1.R1040
Contig ID
5'-most EST
                  txt700736335.h1
                   26842
Seq. No.
                  146599 1.R1040
Contig ID
                   txt700736452.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3850587
BLAST score
                   212
E value
                   4.0e-17
Match length
                  86
% identity
                   (AC005278) Strong similarity to gi 2244780 hypothetical
NCBI Description
                  protein from Arabidopsis thaliana chromosome 4 contig
                  gb Z97335. [Arabidopsis thaliana]
                  26843
Seq. No.
Contig ID
                  146647 1.R1040
5'-most EST
                  jC-gmf102220132ab10d1
```

```
146706 1.R1040
Contig ID
5'-most EST
                   zhf700960906.hl
Method
                  BLASTX
NCBI GI
                   g3024898
BLAST score
                   304
E value
                   4.0e-45
Match length
                   153
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE KIAA0224 (HA4657) >gi 1504028 dbj BAA13213
                   (D86977) similar to putative ATP-dependent RNA helicase
                  KO3H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906
                   (AF038391) pre-mRNA splicing factor [Homo sapiens]
                  26845
Seq. No.
Contig ID
                  146707 1.R1040
5'-most EST
                  bth700847556.h1
Method
                  BLASTX
NCBI GI
                  g4115379
BLAST score
                  266
                  2.0e-27
E value
Match length
                  119
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                  thaliana]
                  26846
Seq. No.
                  146736 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910013f05a1
Seq. No.
                  26847
                  146745 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220061d11a1
Method
                  BLASTX
NCBI GI
                  g2826884
BLAST score
                  352
E value
                   6.0e-33
Match length
                  151
% identity
                   51
                   (AJ223635) transcription factor IIA large subunit
NCBI Description
                   [Arabidopsis thaliana]
                  26848
Seq. No.
Contig ID
                  146792 1.R1040
                  kmv700740644.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3510343
BLAST score
                  47
                  2.0e-17
E value
Match length
                  95
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  26849
```

146801 1.R1040

txt700736866.h1

Contig ID

5'-most EST

Match length

```
26850
Seq. No.
Contig ID
                   146811 1.R1040
5'-most EST
                   txt700736883.h1
Method
                   BLASTX
                   g1046278
NCBI GI
BLAST score
                   361
                   8.0e-35
E value
Match length
                   93
% identity
                   77
                   (U28645) PvAlf [Phaseolus vulgaris]
NCBI Description
                   26851
Seq. No.
Contig ID
                   146883 1.R1040
5'-most EST
                   txt700737027.hl
Seq. No.
                   26852
Contig ID
                   146911 1.R1040
5'-most EST
                   jsh701065542.hl
                   26853
Seq. No.
Contig ID
                   147007 1.R1040
5'-most EST
                   jC-gmle01810006g05a1
                   26854
Seq. No. 5
                   147027 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}10749.h1
                   BLASTX
Method
NCBI GI
                   g4263524
BLAST score
                   169
                   4.0e-12
E value
Match length
                   95
% identity
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   26855
Seq. No.
Contig ID
                   147058 1.R1040
5'-most EST
                   uC-gmrominsoy125f08b1
Method
                   BLASTX
NCBI GI
                   g116923
BLAST score
                   329
E value
                   1.0e-30
Match length
                   107
% identity
                   58
NCBI Description
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
Seq. No.
                   26856
                   147058 2.R1040
Contig ID
                   sat701\overline{0}05136.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g116923
BLAST score
                   211
E value
                   6.0e-17
```

Match length

265

. . .

```
% identity
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
                  >gi 111414 pir S13520 beta-COP protein - rat
                  >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                  norvegicus]
                  26857
Seq. No.
                  147062 1.R1040
Contig ID
5'-most EST
                  g5126378
Method
                  BLASTX
NCBI GI
                  g2462749
BLAST score
                  265
E value
                  4.0e-23
Match length
                  145
% identity
NCBI Description
                  (AC002292) Putative Serine/Threonine protein kinase
                  [Arabidopsis thaliana]
                  26858
Seq. No.
Contig ID
                  147070 1.R1040
5'-most EST
                  kl1701211321.h1
Method
                  BLASTX
NCBI GI
                  q3924599
BLAST score
                  153
E value
                  6.0e-10
                  126
Match length
% identity
                 (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147072 1.R1040
Contig ID
5'-most EST
                  txt700737512.h1
                  26860
Seq. No.
                  147114 1.R1040
Contig ID
5'-most EST
                  txt700737589.h1
Method
                  BLASTX
NCBI GI
                  q2160156
BLAST score
                  441
                  7.0e-44
E value
                  122
Match length
% identity
NCBI Description
                  (AC000132) Strong similarity to S. pombe leucyl-tRNA
                  synthetase (gb Z73100). [Arabidopsis thaliana]
Seq. No.
                  147125 1.R1040
Contig ID
5'-most EST
                  txt700737617.hl
Seq. No.
                  26862
                  147148 1.R1040
Contig ID
5'-most EST
                  zhf700963702.h1
                  BLASTN
Method
NCBI GI
                  g1370187
BLAST score
                  185
                  1.0e-99
E value
```

E value

5.0e-15

```
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB7D
Seq. No.
                  26863
                  147174 1.R1040
Contig ID
                  rrt700645903.h1
5'-most EST
                  26864
Seq. No.
                  147180 1.R1040
Contig ID
                  rrt700645913.hl
5'-most EST
                  26865
Seq. No.
                  147183 1.R1040
Contig ID
                  rrt700645918.hl
5'-most EST
Seq. No.
                  26866
Contig ID
                  147195 1.R1040
5'-most EST
                  jC-gmst02400004a11d1
                  26867
Seq. No.
Contig ID
                  147212 1.R1040
5'-most EST
                  fC-gmro700843925h2
                  26868
Seq. No.
Contig ID
                  147212 2.R1040
5'-most EST
                  jsh701\overline{0}68555.h1
                  26869
Seq. No.
Contig ID
                  147213 1.R1040
5'-most EST
                  zhf700952872.h1
                  BLASTX
Method
NCBI GI
                  q2829923
BLAST score
                  410
                  2.0e-40
E value
                  108
Match length
% identity
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                  thaliana]
                  26870
Seq. No.
                  147214 1.R1040
Contig ID
5'-most EST
                  rrt700645957.h1
Method
                  BLASTX
NCBI GI
                  g4559356
BLAST score
                  209
                  6.0e-17
E value
                  72
Match length
% identity
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  26871
Contig ID
                  147225 1.R1040
                  q4298675
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3176709
BLAST score
                  198
```

```
187
Match length
% identity
                   32
                   (AC002392) putative anthranilate
NCBI Description
                  N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  26872
Contig ID
                  147311 1.R1040
5'-most EST
                  rrt700646090.hl
Seq. No.
                  26873
Contig ID
                  147323 1.R1040
5'-most EST
                  wrg700785919.h2
Method
                  BLASTX
NCBI GI
                  g3024871
BLAST score
                  171
E value
                   2.0e-12
Match length
                  71
% identity
                   48
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                  >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                  sp.]
                  26874
Seq. No.
                  147349 1.R1040
Contig ID
                  wrg700785953.h2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1076315
BLAST score
                  381
E value
                   4.0e-37
Match length
                  83
% identity
                  cytochrome P450 - Arabidopsis thaliana
NCBI Description
                 ->gi_853719_emb_CAA60793_ (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi_871988 emb CAA60794 (X87368)
                  CYP90 protein [Arabidopsis thaliana]
                  26875
Seq. No.
                  147389 1.R1040
Contig ID
                  bth700846474.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3913425
BLAST .score
                  663
E value
                  7.0e-70
Match length
                  133
                  95
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >qi 2275203 (AC002337) RNA helicase isolog
                  [Arabidopsis thaliana]
                  26876
Seq. No.
                  147396 1.R1040
Contig ID
                  sat701\overline{0}07529.h1
5'-most EST
Seq. No.
                  26877
                  147396 2.R1040
Contig ID
                  wrg700786022.h2
5'-most EST
```

Match length

```
Seq. No.
                  26878
                  147407 1.R1040
Contig ID
                  asn701135857.hl
5'-most EST
                  26879
Seq. No.
                  147410 1.R1040
Contig ID
                  fC-qmle7000786045a1
5'-most EST
                  BLASTX
Method
                  g131754
NCBI GI
BLAST score
                  145
                  1.0e-08
E value
Match length
                  81
% identity
NCBI Description
                  PPLZ02 PROTEIN >gi 99973 pir S11881 hypothetical protein
                   (clone pPLZ2) - large-leaved lupine >gi 19507 emb CAA36069
                   (X51767) put. pPLZ2 product (AA 1-164) [Lupinus
                _ polyphyllus]
                  26880
Seq. No.
Contig ID
                  147412 1.R1040
5'-most EST
                  fde700873366.hl
Method
                  BLASTX
NCBI GI
                  g2829895
BLAST score
                  336
E value
                  6.0e-32
Match length
                  81
% identity
                   (AC002311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  26881
Seq. No.
Contig ID
                  147420 1.R1040
5'-most EST
                  wrq700786058.h2
Method
                  BLASTX
NCBI GI
                  q3776025
BLAST score
                   410
E value
                  2.0e-40
Match length
                  97
% identity
NCBI Description
                   (AJ010474) RNA helicase [Arabidopsis thaliana]
Seq. No.
Contig ID
                  147448 1.R1040
5'-most EST
                  fua701040174.h1
Seq. No.
                  26883
Contig ID
                  147468 1.R1040
5'-most EST
                  asn701136493.h1
                  26884
Seq. No.
Contig ID
                  147499 1.R1040
5'-most EST
                  zhf700958443.h1
Method
                  BLASTX
NCBI GI
                  q4455131
BLAST score
                  224
E value
                  3.0e-18
```

```
% identity
                   (AF129433) histone deacetylase HDA2 [Drosophila
NCBI Description
                  melanogaster]
Seq. No.
                  26885
Contig ID
                  147516 1.R1040
5'-most EST
                  pcp700993668.h1
                  BLASTX
Method
                  g3023070
NCBI GI
BLAST score
                  229
E value
                  2.0e-19
                  84
Match length
% identity
                   (AF053702) hypothetical protein [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  26886
Contig ID
                  147521 1.R1040
                  fC-gmle7000786228a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3411266
BLAST score
                  458
E value
                  2.0e-63
Match length
                  147
                  79
% identity
                   (AF080567) pullulanase-type starch debranching enzyme [Zea
NCBI Description
                  mays]
                  26887
Seq. No.
                  147568 1.R1040
Contig ID
                  sat701004052.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4263784
BLAST score
                  275
                  2.0e-47
E value
                  176
Match length
% identity
                   (AC006068) putative glycogenin-2 protein [Arabidopsis
NCBI Description
                  thaliana]
                  26888
Seq. No.
                  147604 1.R1040
Contig ID
5'-most EST
                  fua701037144.hl
Method
                  BLASTX
NCBI GI
                  g1703292
BLAST score
                  434
                  2.0e-53
E value
Match length
                  131
                  78
% identity
                  HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473
NCBI Description
                   (X75879) amt1 [Arabidopsis thaliana]
                  26889
Seq. No.
                  147626 1.R1040
Contig ID
5'-most EST
                  wrg700786484.h1
```

26890

Seq. No.

Match length

```
Contig ID
                  147653 1.R1040
5'-most EST
                  wrg700792050.h1
Method
                  BLASTX
                  g3193330
NCBI GI
BLAST score
                   315
E value
                   6.0e-29
Match length
                  131
% identity
                   50
                   (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                   (GB:L22305) [Arabidopsis thaliana]
                  26891
Seq. No.
Contig ID
                   147675 1.R1040
                   jC-gmro02910037e08d1
5'-most EST
                  BLASTX
Method
                  g2764806
NCBI GI
BLAST score
                   373
                   9.0e-36
E value
                   91
Match length
                  74
% identity
                   (X78548) epoxide hydrolase [Glycine max]
NCBI Description
                   26892
Seq. No.
                   147680 1.R1040
Contig ID
5'-most EST
                  g5753630
                  26893
Seq. No.
Contig ID
                  147719 1.R1040
5'-most EST
                  wrg700786807.h2
                  26894
Seq. No.
Contig ID
                  147726 1.R1040
5'-most EST
                  wrg700786703.h2
                  26895
Seq. No.
Contig ID
                  147731 1.R1040
5'-most EST
                  vzy700752415.hl
Method
                  BLASTX
                  g4220512
NCBI GI
BLAST score
                  200
E value
                   6.0e-16
Match length
                   53
% identity
                   (AL035356) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                  26896
Seq. No.
                  147732 2.R1040
Contig ID
5'-most EST
                  yuv700862822.h1
Seq. No.
                  26897
Contig ID
                  147737 1.R1040
5'-most EST
                  wrg700788813.h2
Method
                  BLASTN
NCBI GI
                  g168702
BLAST score
                  255
E value
                  1.0e-141
```

5'-most EST

```
% identity
                   98
NCBI Description Corn 22 kDa zein protein gene, complete cds
                   26898
Seq. No.
                   147740 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}54242.h1
                   26899
Seq. No.
                   147753 1.R1040
Contig ID
5'-most EST
                   wrg700788061.hl
                   26900
Seq. No.
                   147765 1.R1040
Contig ID
5'-most EST
                   wrg700786754.h2
                   26901
Seq. No.
                   147792 1.R1040
Contig ID
5'-most EST
                   wrq700786840.h2
Method
                   BLASTN
                   g168681
NCBI GI
BLAST score
                   243
                   1.0e-134
E value
                   259
Match length
% identity
                   98
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi_270686_gb`I03333_ Sequence 8 from Patent US
                   26902
Seq. No.
Contig ID
                   147793 1.R1040
                   wrg700786793.h2
5'-most EST
Seq. No.
                   26903
Contig ID
                   147803 1.R1040
5'-most EST
                   fC-qmro7000747078r1
Method
                   BLASTX
NCBI GI
                   g4432846
BLAST score
                   372
E value
                   2.0e-35
Match length
                   121
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   26904
                   147821 1.R1040
Contig ID
5'-most EST
                   wrq700786834.h2
Seq. No.
                   26905
Contig ID
                   147832 1.R1040
5'-most EST
                   jC-gmst02400039h12a1
Seq. No.
                   26906
Contig ID
                   147887 1.R1040
5'-most EST
                   wrg700786944.h2
                   26907
Seq. No.
                   147887 2.R1040
Contig ID
                   smc700744330.hl
```

```
Seq. No.
                   26908
                   147911 1.R1040 .-
Contig ID
5'-most EST
                   zhf700960751.h1
Method
                   BLASTX
                   g3033384
NCBI GI
BLAST score
                   221
                   8.0e-18
E value
Match length
                   55
                   75
% identity
                   (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26909
Contig ID
                   147930 1.R1040
5'-most EST
                   g42931\overline{6}3
                   26910
Seq. No.
                   147940 1.R1040
Contig ID
                   r1r700\overline{9}00634.h1
5'-most EST
Seq. No.
                   26911
                   147941 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}67675.h1
Method
                   BLASTX
NCBI GI
                   q129726
BLAST score
                   201
E value
                   1.0e-15
Match length
                   129
% identity
                   PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL
NCBI Description
                   4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE
                   BINDING PROTEIN) (P55) >gi_68464_pir__ISBOSS protein
                   disulfide-isomerase (EC 5.3.4.1) precursor - bovine
                   >gi 163497 (M17596) PDI (E.C.5.3.4.1) [Bos taurus]
                   26912
Seq. No.
Contig ID
                   147953 1.R1040
5'-most EST
                   gsv701054945.hl
                   26913
Seq. No.
Contig ID
                   147986 1.R1040
5'-most EST
                   g4396513
Method
                   BLASTX
NCBI GI
                   q3482913
BLAST score
                   169
E value
                   6.0e-12
Match length
                   127
% identity
                   (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
                   26914
Seq. No.
Contig ID
                   147995 1.R1040
5'-most EST
                   wrg700787103.h2
                   26915
Seq. No.
```

147999 1.R1040

Contig ID

Method

BLASTX

```
5'-most EST
                   uC-gmrominsoy298e04b1
Method
                   BLASTX
NCBI GI
                   g4455153
BLAST score
                   158
                   2.0e-10
E value
Match length
                   107
 % identity
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   26916
Seq. No.
                   148010 1.R1040
Contig ID
                   fua701037886.hl
 5'-most EST
                   BLASTN
Method
                   g170645
NCBI GI
BLAST score
                   334
E value
                   0.0e + 00
Match length
                   477
                   93
% identity
                   Vigna aconitifolia pyrroline-5-carboxylate synthetase
NCBI Description
                   associated mRNA sequence. >qi 2471746 gb I47781 I47781
                   Sequence 1 from patent US
Seq. No.
                   26917
                   148015 1.R1040
Contig ID
5'-most EST
                   wrg700787129.h2
Method
                   BLASTX.
NCBI GI
                   q4519671
BLAST score
                   228
E value
                   1.0e-18
Match length
                   70
% identity
NCBI Description
                   (AB017693) transfactor [Nicotiana tabacum]
Seq. No.
                   26918
Contig ID
                   148045 1.R1040
5'-most EST
                   wrg700787173.h2
Method
                   BLASTX
NCBI GI
                   g3152558
BLAST score
                   519
E value
                   9.0e-53
Match length
                   139
% identity
NCBI Description
                   (AC002986) Similar to M. tuberculosis gene qb Z96072 and M.
                   leprae gene gb 400019. [Arabidopsis thaliana]
                   26919
Seq. No.
Contig ID
                   148051 1.R1040
5'-most EST
                   wrg700787183.h2
                   26920
Seq. No.
Contig ID
                   148066 1.R1040
5'-most EST
                   wrg700787217.h2
Seq. No.
                   26921
Contig ID
                   148068 1.R1040
5'-most EST
                   fC-qmle700788247a4
```

BLAST score

```
NCBI GI
                   g4567279
BLAST score
                   432
E value
                   1.0e-42
                   105
Match length
                   74
% identity
                   (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   26922
Seq. No.
                   148088 1.R1040
Contig ID
                   jC-gmf102220148c07a1
5'-most EST
                   26923
Seq. No.
                   148091 1.R1040
Contig ID
5'-most EST
                   g5127006
Method
                   BLASTX
                   g2160161
NCBI GI
BLAST score
                   207
E value
                   5.0e-16
Match length
                   162
% identity
                   (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26924
                   148098 1.R1040
Contig ID
5'-most EST
                   xzm700763723.h1
Method
                   BLASTN
NCBI GI
                   q3493646
BLAST score
                   79
E value
                   3.0e-36
Match length
                   187
% identity
                   86
                   Pimpinella brachycarpa transcription activator (MADS1)
NCBI Description
                   mRNA, complete cds
                   26925
Seq. No.
                                                              1-2
Contig ID
                   148177 1.R1040
5'-most EST
                   zzp700829984.h1
Method
                   BLASTX
NCBI GI
                   g2194142
BLAST score
                   259
E value
                   4.0e-22
Match length
                   112
% identity
                   (AC002062) ESTs qb N38288,qb T43486,qb AA395242 come from
NCBI Description
                   this gene. [Arabidopsis thaliana]
                   26926
Seq. No.
Contig ID
                   148184 1.R1040
5'-most EST
                   wrg700787429.h2
                   26927
Seq. No.
Contig ID
                   148191 1.R1040
5'-most EST
                   q56063\overline{3}7
Method
                   BLASTX
NCBI GI
                   q4432846
```

```
E value
                  3.0e-56
Match length
                  268
% identity
                  47
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  26928
Seq. No.
                  148193 1.R1040
Contig ID
5'-most EST
                  q5607183
Method
                  BLASTX
NCBI GI
                  g1084301
BLAST score
                  684
E value
                  4.0e-72
Match length
                  172
                  81
% identity
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
NCBI Description
                  plant >gi 559471 emb CAA55143 (X78347)
                  pyruvate, orthophosphate dikinase [Mesembryanthemum
                  crystallinum]
                  26929
Seq. No.
                  148203 1.R1040
Contig ID
5'-most EST
                  wrq700787450.h2
                  BLASTX
Method
                  g4538911
NCBI GI
BLAST score
                  151
                  3.0e-22
E value
Match length
                  85
% identity
                  67
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  26930
                  148206 1.R1040
Contig ID
5'-most EST
                  wrg700787453.h2
Method
                  BLASTX
NCBI GI
                  g2499989
BLAST score
                  144
E value
                  3.0e-09
Match length
                  85
% identity
                  39
                  PEPTIDYL-TRNA HYDROLASE (PTH) >gi 1001232 dbj BAA10473
NCBI Description
                  (D64003) peptidyl-tRNA hydrolase [Synechocystis sp.]
                  26931
Seq. No.
                  148220 1.R1040
Contig ID
5'-most EST
                  g5509244
                  BLASTX
Method
NCBI GI
                  q1001253
BLAST score
                  241
E value
                  4.0e-20
Match length
                  140
% identity
                  41
                 (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
                  26932
Seq. No.
Contig ID
                  148254 1.R1040
```

zhf700956404.h1

5'-most EST

NCBI Description

```
26933
Seq. No.
                   148264 1.R1040
Contig ID
5'-most EST
                   wrg700787537.hl
Seq. No.
                   26934
                   148276 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400043f08a1
                   26935
Seq. No.
Contig ID
                   148282 1.R1040
                   zhf700964075.h1
5'-most EST
Seq. No.
                   26936
Contig ID
                   148288 1.R1040
5'-most EST
                   pxt700943466.hl
Method
                   BLASTX
                   q3414930
NCBI GI
BLAST score
                   164
E value
                   7.0e-11
Match length
                   113
% identity
                   (AF076599) FutA [Dictyostelium discoideum]
NCBI Description
Seq. No.
Contig ID
                   148302 1.R1040
5'-most EST
                   uC-gmflminsoy022d03b1
Seq. No.
                   148306 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220141e08a1
                   BLASTX
Method
NCBI GI
                   g2827701
BLAST score
                   149
                   3.0e-09
E value
Match length
                   101
% identity
NCBI Description
                  (AL021684) predicted protein [Arabidopsis thaliana]
                   26939
Seq. No.
Contig ID
                   148313 1.R1040
5'-most EST
                   zhf700957008.h1
Seq. No.
                   26940
Contig ID
                   148353 1.R1040
5'-most EST
                   wrg700787647.h2
                   26941
Seq. No.
                   148359 1.R1040
Contig ID
5'-most EST
                   wrg700787654.h2
                   BLASTX
Method
                   g2827631
NCBI GI
BLAST score
                   236
                   2.0e-19
E value
Match length
                   90
% identity
```

(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.

```
26942
Seq. No.
                  148363 1.R1040
Contig ID
5'-most EST
                  jex700906321.hl
Method
                  BLASTX
NCBI GI
                  g2731443
BLAST score
                  214
                  5.0e-17
E value
Match length
                  185
% identity
                   (U96923) [prot= cDNA of the glycoamidase gene [Aspergillus
NCBI Description
                  niger]
                  26943
Seq. No.
Contig ID
                  148385 1.R1040
5'-most EST
                  uC-gmflminsoy079h05b1
Seq. No.
                  26944
Contig ID
                  148391 1.R1040
5'-most EST
                  jC-gmro02800030g06a1
                  BLASTX
Method
NCBI GI
                  g2414593
BLAST score
                  385
                  4.0e-37
E value
                  155
Match length
% identity
                  (Z99258) molybdopterin biosynthesis [Schizosaccharomyces
NCBI Description
                  pombe]
                  26945
Seq. No.
Contig ID
                  148395 1.R1040
5'-most EST
                  fua701042184.h1
                  BLASTN
Method
NCBI GI
                  q4322474
BLAST score
                  40
                  3.0e-13
E value
                  100
Match length
% identity
                  Eucalyptus globulus subsp. globulus putative MADS box
NCBI Description
                  transcription factor ETL mRNA, complete cds
                  26946
Seq. No.
Contig ID
                  148397 1.R1040
5'-most EST
                  leu701154637.h1
                  26947
Seq. No.
                  148401 1.R1040
Contig ID
5'-most EST
                  wrg700789607.h2
                  26948
Seq. No.
                  148409 1.R1040
Contig ID
                  wrg700787720.h2
5'-most EST
                  26949
Seq. No.
Contig ID
                  148424 1.R1040
5'-most EST
                  uC-gmrominsoy307h06b1
```

BLAST score

```
148437 1.R1040
Contig ID
5'-most EST
                  wrg700787755.h2
Seq. No.
                  26951
Contig ID
                  148449 1.R1040
                  wrg700787770.h2
5'-most EST
Seq. No.
                  26952
Contig ID
                  148467 1.R1040
5'-most EST
                   zsg701121122.hl
Method
                  BLASTN
NCBI GI
                  g2477521
BLAST score
                   41
E value
                   1.0e-13
Match length
                  128
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  26953
Seq. No.
Contig ID
                  148467 2.R1040
5'-most EST
                  wrg700787790.h2
                  26954
Seq. No.
Contig ID
                  148481 1.R1040
5'-most EST
                  wrg700787814.h2
                  26955
Seq. No.
                  148520 1.R1040
Contig ID
5'-most EST
                  wrg700787858.h2
                  BLASTX
Method
NCBI GI
                  q3643604
BLAST score
                  212
                   3.0e-17
E value
                  98
Match length
% identity
                   (AC005395) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  26956
Seq. No.
                  148543 1.R1040
Contig ID
5'-most EST
                  zhf700955802.h1
Method
                  BLASTX
NCBI GI
                  q2252840
BLAST score
                  356
                  5.0e-34
E value
                  107
Match length
% identity
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                  26957
                  148551 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810033c09a2
Method
                  BLASTX
NCBI GI
                  q4455367
```

5'-most EST

```
E value
                   4.0e-45
Match length
                   164
% identity
                   57
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
                   26958
Seq. No.
                   148557 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014f08d1
Seq. No.
                   26959
                   148574 1.R1040
Contig ID
5'-most EST
                   pcp700994010.hl
                   26960
Seq. No.
Contig ID
                   148583 1.R1040
5'-most EST
                   wrg700787970.hl
Method
                   BLASTX
NCBI GI
                   g3540184
BLAST score
                   404
E value
                   1.0e-39
Match length
                   110
% identity
                   59
NCBI Description (AC004122) Similar to endoxylanases [Arabidopsis thaliana]
                   26961
Seq. No.
Contig ID
                   148590 1.R1040
5'-most EST
                   ujr700\overline{6}46607.h1
Method
                   BLASTX
NCBI GI
                   q1084301
BLAST score
                   986
E value
                   1.0e-107
Match length
                   214
% identity
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
NCBI Description
                  plant >gi 559471 emb CAA55143 (X78347)
                   pyruvate, orthophosphate dikinase [Mesembryanthemum
                   crystallinum]
                   26962
Seq. No.
Contig ID
                   148600 1.R1040
5'-most EST
                   pcp700992466.h1
Method
                   BLASTX
NCBI GI
                   q2760836
BLAST score
                   156
E value
                   1.0e-10
                   67
Match length
% identity
                   (AC003105) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   26963
Seq. No.
Contig ID
                   148625 1.R1040
5'-most EST
                   wrg700788049.hl
Seq. No.
                   26964
Contig ID
                   148627 1.R1040
```

wrg700788052.hl

Contig ID

5'-most EST

```
BLASTX
Method
NCBI GI
                   g3004655
BLAST score
                   327
E value
                   2.0e-30
Match length
                   140
% identity
                   52
                   (AF017777) waclaw [Drosophila melanogaster]
NCBI Description
                   26965
Seq. No.
Contig ID
                   148629 1.R1040
5'-most EST
                   wrg700788056.hl
Seq. No.
                   26966
Contig ID
                   148632 1.R1040
5'-most EST
                   all700863205.h1
Seq. No.
                   26967
Contig ID
                   148660 1.R1040
5'-most EST
                   g4291611
                   26968
Seq. No.
Contig ID
                   148697 1.R1040
5'-most EST
                   wrg700788214.h1
                   26969
Seq. No.
                   148720 1.R1040
Contig ID
5'-most EST
                   fua701038872.hl
                   26970
Seq. No.
                   148721 1.R1040
Contig ID
5'-most EST
                   gsv701051145.hl
Method
                   BLASTX
NCBI GI
                   q461729
BLAST score
                   251
E value
                   8.0e-22
Match length
                   63
                   75
% identity
NCBI Description
                   10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
                   >gi_2146744_pir__S65597 probable chaperonin, 10K -
                   Arabidopsis thaliana >gi 166662 (L02843) 10 kDa chaperonin
                   [Arabidopsis thaliana]
Seq. No.
                   26971
Contig ID
                   148780 1.R1040
5'-most EST
                   wrq700788389.hl
                   BLASTX
Method
                   q2264382
NCBI GI
BLAST score
                   257
E value
                   2.0e-22
                   79
Match length
                   58
% identity
                   (AC002354) putative tetracycline transporter-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   26972
```

148827 1.R1040

leu701152971.hl

```
Method
                   BLASTX
NCBI GI .
                   g3550661
BLAST score
                   276
E value
                   2.0e-24
Match length
                   66
% identity
                   40
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
Seq. No.
                   26973
Contig ID
                   148874 1.R1040
5'-most EST
                  dpv701096930.h1
Method
                  BLASTX
NCBI GI
                  q3298548
BLAST score
                  371
E value
                   7.0e-36
Match length
                  95
% identity
                   (AC004681) putative spliceosomal protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  26974
                  148877 1.R1040
Contig ID
5'-most EST
                  wrg700788603.h1
                  BLASTX
Method
NCBI GI
                  g3023930
BLAST score
                  135
                   4.0e-12
E value
                  49
Match length
% identity
                   67
                  HISTONE DEACETYLASE 1 (HD1) >gi 2654077_gb_AAB87685_
NCBI Description
                   (AF032919) histone deacetylase [Strongylocentrotus
                  purpuratus]
                  26975
Seq. No.
Contig ID
                  148879 1.R1040
5'-most EST
                   jsh701\overline{0}65770.h1
Method
                  BLASTX
NCBI GI
                  q3513747
BLAST score
                  251
E value
                  2.0e-21
Match length
                  98
% identity
NCBI Description
                   (AF080118) contains similarity to reverse transcriptases
                   (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
                  26976
Seq. No.
                  148904 1.R1040
Contig ID
5'-most EST
                  q4295808
Method
                  BLASTX
NCBI GI
                  g4218011
BLAST score
                  241
E value
                  4.0e-20
Match length
                  172
% identity
                  41
NCBI Description
                  (AC006135) putative protein kinase [Arabidopsis thaliana]
                  >gi 4309721 gb AAD15491 (AC006439) putative
```

serine/threonine protein kinase [Arabidopsis thaliana] Seq. No. 26977 Contig ID 148917_1.R1040 5'-most EST uC-gmflminsoy078h07b1

Seq. No. 26978

Contig ID 149002_1.R1040 5'-most EST euj700697968.h1

Seq. No. 26979

Contig ID 149009_1.R1040 5'-most EST xpa700797596.h1

Method BLASTX
NCBI GI g3128176
BLAST score 384
E value 1.0e-36
Match length 150
% identity 47

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 26980

Contig ID 149015_1.R1040 5'-most EST jsh701065581.h1

Method BLASTX
NCBI GI g3033398
BLAST score 467
E value 1.0e-46
Match length 113
% identity 76

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No. 26981

Contig ID 149062 1.R1040 5'-most EST wrg700789023.h2

Method BLASTX
NCBI GI g3643088
BLAST score 114
E value 4.0e-09
Match length 117
% identity 46

NCBI Description (AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 26982

Contig ID 149065_1.R1040 5'-most EST epx701107708.h1

Method BLASTX
NCBI GI g537313
BLAST score 1276
E value 1.0e-141
Match length 287

% identity 53

NCBI Description (L36159) unknown protein [Medicago sativa]

Seq. No. 26983

```
149082 1.R1040
Contig ID
5'-most EST
                   fC-gmse7000751091d1
Seq. No.
                   26984
Contiq ID
                   149095 1.R1040
5'-most EST
                   jex700\overline{9}05143.h1
Seq. No.
                   26985
Contig ID
                   149106 1.R1040
5'-most EST
                   wrq700789096.h2
Method
                   BLASTX
                   q3128228
NCBI GI
BLAST score
                   584
E value
                   1.0e-60
Match length
                   118
% identity
                   92
NCBI Description
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
                   thaliana] >qi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
Seq. No.
                   26986
Contig ID
                   149115 1.R1040
5'-most EST
                   wrq700789117.h1
                   26987
Seq. No.
Contig ID
                   149117 1.R1040
5'-most EST
                   jC-qmle01810060c09d1
                   26988
Seq. No.
Contig ID
                   149117 2.R1040
5'-most EST
                   q56775<del>2</del>7
Seq. No.
                   26989
Contig ID
                   149142 1.R1040
5'-most EST
                   smc700\overline{7}48115.h1
                   26990
Seq. No.
Contig ID
                   149143 1.R1040
5'-most EST
                   wrg700789212.h2
                   BLASTX
Method
NCBI GI
                   g3355308
BLAST score
                   766
E value
                   2.0e-81
Match length
                   256
% identity
NCBI Description
                   (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   149148 1.R1040
5'-most EST
                   pcp700993475.hl
                   26992
Seq. No.
Contig ID
                   149160 1.R1040
5'-most EST
                   943140\overline{6}9
Method
                   BLASTX
NCBI GI
                   q2493895
BLAST score
                   671
```

Aug.

```
1.0e-70
E value
Match length
                   191
% identity
                   67
NCBI Description
                  CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
                   (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi 1071911 pir S46438 cysteine synthase (EC 4.2.99.8) -
                   watermelon >gi 540497 dbj BAA05965 (D28777) cysteine
                   synthase [Citrullus lanatus]
                   26993
Seq. No.
                   149168 1:R1040
Contig ID
5'-most EST
                   wrg700789246.h2
Method
                   BLASTX
NCBI GI
                   g3953463
BLAST score
                   360
                   1.0e-34
E value
                   91
Match length
                   78
% identity
                  (AC002328) F20N2.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   26994
                   149176 1.R1040
Contig ID
5'-most EST
                  wrg700789255.h2
Seq. No.
                   26995
Contig ID
                   149188 1.R1040
5'-most EST
                   wrg700789268.h2
Method
                  BLASTX
NCBI GI
                   q3980410
BLAST score
                   209
E value
                   2.0e-16
Match length
                   141
% identity
NCBI Description
                   (AC004561) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   26996
Contig ID
                  149193 1.R1040
5'-most EST
                  wrq700789275.h2
Seq. No.
                  26997
Contig ID
                  149193 2.R1040
5'-most EST
                  uC-gmflminsoy080c11b1
Seq. No.
                  26998
Contig ID
                  149198 1.R1040
5'-most EST
                  wrq700789285.h2
Method
                  BLASTX
NCBI GI
                  g3402683
BLAST score
                  570
E value
                  9.0e-61
Match length
                  155
% identity
NCBI Description
                  (AC004697) patatin-like protein [Arabidopsis thaliana]
```

26999

149204 1.R1040

Seq. No. Contiq ID

Match length

3.91

```
hrw701061007.hl
5'-most EST
Seq. No.
                   27000
Contig ID
                   149204 2.R1040
5'-most EST
                   uC-gmronoir015d09b1
Seq. No.
                   27001
Contig ID
                   149219 1.R1040
5'-most EST
                   uC-gmropic092b12b1
Seq. No.
                   27002
Contig ID
                   149228 1.R1040
5'-most EST
                   zhf700956157.h1
Method
                   BLASTX
NCBI GI
                   g4314357
BLAST score
                   262
E value
                   9.0e-23
Match length
                   153
% identity
NCBI Description
                   (AC006340) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
                   27003
Seq. No.
Contig ID
                   149229 1.R1040
5'-most EST
                   uC-qmflminsoy046f04b1
Method
                   BLASTX
NCBI GI
                   q4567227
BLAST score
                   581
                   5.0e-60
E value
Match length
                   197
% identity
                   (AC007119) putative transport protein [Arabidopsis
NCBI Description
                   thaliana]
                   27004
Seq. No.
Contig ID
                   149246 1.R1040
5'-most EST
                   wrg700789354.h2
                   27005
Seq. No.
Contig ID
                   149248 1.R1040
5'-most EST
                   rca701\overline{0}01671.h1
Method
                   BLASTX
NCBI GI
                   g437327
BLAST score
                   689
E value
                   2.0e-72
Match length
                   130
% identity
NCBI Description
                   (L04497) MYB A; putative [Gossypium hirsutum]
Seq. No.
Contig ID
                   149250 1.R1040
5.'-most EST
                   uC-gmflminsoy012a03b1
Method
                   BLASTN
NCBI GI
                   q1218003
BLAST score .
                   184
E value
                   5.0e-99
```

```
% identity
                   Glycine max dynamin-like protein SDL5A mRNA, complete cds
NCBI Description
Seq. No.
                   27007
                   149281 1.R1040
Contig ID
5'-most EST
                   crh700854590.h1
Method
                   BLASTX
                   q2980777
NCBI GI
BLAST score
                   262
E value
                   7.0e-23
Match length
                   123
% identity
                   45
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27008
Contig ID
                   149293 1.R1040
5'-most EST
                   zzp700831677.h1
Seq. No.
                   27009
Contig ID
                   149296 1.R1040
5'-most EST
                   fde700875241.hl
Method
                   BLASTX
NCBI GI
                   g2435517
BLAST score
                   319
E value
                   7.0e-30
Match length
                   84
% identity
                   (AF024504) contains similarity to peptidase family A1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   27010
Contig ID
                   149333 1.R1040
5'-most EST
                   wrg700789476.h2
Seq. No.
                   27011
Contig ID
                   149339 1.R1040
5'-most EST
                   bth700843894.h1
Method
                   BLASTX
NCBI GI
                   g2129918
BLAST score
                   149
E value
                   5.0e-10
Match length
                   62
% identity
                   53
NCBI Description
                   BPF-1 protein - parsley >qi 396197 emb CAA48413 (X68337)
                   BPF-1 [Petroselinum crispum] >gi 441310 emb CAA44518
                   (X62653) BPF-1 [Petroselinum crispum]
                   27012
Seq. No.
Contig ID
                   149342 1.R1040
5'-most EST
                   k11701\overline{2}04637.h1
Method
                   BLASTX
NCBI GI
                   q2809246
BLAST score
                   260
E value
                   8.0e-23
Match length
                   70
% identity
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
```

5'-most EST

```
27013
Seq. No.
                   149363 1.R1040
Contig ID
5'-most EST
                  pmv700892134.h1
Method
                   BLASTX
                   q529707
NCBI GI
BLAST score
                   180
                   3.0e-16
E value
Match length
                   89
% identity
                   47
                   (U13070) No definition line found [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  27014
                   149364 1.R1040
Contig ID
5'-most EST
                  wrg700789519.h2
Method
                  BLASTX
                  g3600061
NCBI GI
BLAST score
                   181
E value
                   1.0e-13
Match length
                   44
% identity
                   70
                   (AF080120) contains similarity to DNA binding proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   27015
Contig ID
                   149371 1.R1040
5'-most EST
                   q4300575
Method
                  BLASTX
NCBI GI
                  q1765899
BLAST score
                   753
E value
                   3.0e-80
Match length
                   174
% identity
                   74
NCBI Description
                   (Y07917) Spot 3 protein [Arabidopsis thaliana] >qi 1839244
                   (U86700) EGF receptor like protein [Arabidopsis thaliana]
Seq. No.
                  27016
Contig ID
                  149380 1.R1040
5'-most EST
                  wrg700789542.h2
Method
                  BLASTX
NCBI GI
                  q3695408
BLAST score
                  149
E value
                  1.0e-09
Match length
                  73
% identity
NCBI Description
                   (AF096373) contains similarity to Solanum lycopersicum
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >qi 4538956 emb CAB39780.1 (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
                  27017
Seq. No.
Contig ID
                  149398 1.R1040
5'-most EST
                  k11701\overline{2}06935.h1
Seq. No.
                  27018
Contig ID
                  149398 2.R1040
```

zsg701121559.h1

```
27019
Seq. No.
                   149413 1.R1040
Contig ID
5'-most EST
                   wrg700789585.h2
                   27020
Seq. No.
Contig ID .
                   149425 1.R1040
5'-most EST
                   zhf700\overline{9}61927.h1
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   633
                   5.0e-66
E value
Match length
                   186
% identity
                   71
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   27021
                   149425 2.R1040
Contig ID
5'-most EST
                   leu701146156.hl
Method
                   BLASTX
NCBI GI
                   q2369714
BLAST score
                   138
E value
                   1.0e-10
Match length
                   50
% identity
NCBI Description (297178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   27022
Contig ID
                   149450 1.R1040
5'-most EST
                   wrg700789631.h2
Method
                   BLASTN
NCBI GI
                   q3985958
BLAST score
                   50
E value
                   3.0e-19
Match length
                   170
% identity
                   82
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   27023
Contig ID
                   149458 1.R1040
5'-most EST
                   wrg700789641.h2
Seq. No.
                   27024
Contig ID
                   149462 1.R1040
5'-most EST
                   jC-gmle01810087b04a1
Method
                   BLASTX
NCBI GI
                   g476961
BLAST score
                   586
E value
                   1.0e-60
Match length
                   167
% identity
                   71
NCBI Description
                  chromodomain-helicase-DNA-binding protein, CHD-1 - mouse
Seq. No.
                   27025
Contig ID
                   149470 1.R1040
5'-most EST
                   vzy700755452.h1
```

Contig ID

```
27026
 Seq. No.
 Contig ID
                    149493 1.R1040
 5'-most EST
                    jC-gmst02400004g01d1
                    27027
 Seq. No.
                    149535 1.R1040
 Contig ID
 5'-most EST
                    wrq700789744.hl
 Method
                    BLASTX
                    g1168654
 NCBI GI
 BLAST score
                    312
                    6.0e-29
 E value
 Match length
                    78
                    69
 % identity
 NCBI Description
                   BETA-GALACTOSIDASE PRECURSOR (LACTASE)
                    >gi 542198 pir S41889 beta-galactosidase (EC 3.2.1.23) -
                    garden asparagus >gi 452712 emb CAA54525 (X77319)
                    beta-galactosidase [Asparagus officinalis]
                    27028
 Seq. No.
                    149564 1.R1040
 Contig ID
 5'-most EST
                    cf1700863631.h1
 Method
                    BLASTX
                    g2583123
 NCBI GI
 BLAST score
                    243
 E value
                    1.0e-20
 Match length
                    77
 % identity
                    60
 NCBI Description
                    (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                    thaliana]
 Seq. No.
                    27029
                    149596 1.R1040
 Contig ID
 5'-most EST
                    wrg700789823.h2
                    27030
 Seq. No.
 Contig ID
                    149615_1.R1040
 5'-most EST
                   g4302093
                    27031
 Seq. No.
 Contig ID
                    149619 1.R1040
 5'-most EST
                    jC-gmle01810004e04a1
Method
                   BLASTX
                   g3328240
 NCBI GI
 BLAST score
                    425
                    6.0e-42
 E value
Match length
                    125
 % identity
                    (AF064775) early nodule-specific protein [Medicago
NCBI Description
                   truncatula]
                   27032
Seq. No.
 Contig ID
                   149635 1.R1040
5'-most EST
                   jC-gmst02400045f07a1
                   27033
 Seq. No.
```

149670 1.R1040

Seq. No.

```
5'-most EST
                   bth700847278.h1
Seq. No.
                   27034
Contig ID
                   149676 1.R1040
5'-most EST
                   wrg700789950.h2
Seq. No.
                   27035
Contig ID
                   149678 1.R1040
5'-most EST
                   jC-qmst02400031q08d1
Seq. No.
                   27036
Contig ID
                   149680 1.R1040
5'-most EST
                   jC-gmle01810012c09d1
Seq. No.
                   27037
Contig ID
                   149717 1.R1040
5'-most EST
                   wrg700790013.h2
                   27038
Seq. No.
Contig ID
                   149721 1.R1040
5'-most EST
                   awf700838213.h1
                   27039
Seq. No.
                   149733 1.R1040
Contig ID
5'-most EST
                   wrg700790036.h2
Seq. No.
                   27040
                   149737_1.R1040
Contig ID
5'-most EST
                   leu701147009.h1
                   27041
Seq. No.
Contig ID
                   149741 1.R1040
5'-most EST
                   wrg700790044.h2
                   27042
Seq. No.
Contig ID
                   149790 1.R1040
5'-most EST
                   wrg700790186.hl
Method
                   BLASTX
NCBI GI
                   g3643611
BLAST score
                   480
                   4.0e-48
E value
Match length
                   103
% identity
NCBI Description
                  (AC005395) putative casein kinase [Arabidopsis thaliana]
                   27043
Seq. No.
Contig ID
                   149814 1.R1040
5'-most EST
                   asn701\overline{1}38651.h1
Method
                   BLASTX
NCBI GI
                   g3603401
BLAST score
                   304
                   5.0e-28
E value
                   92
Match length
% identity
NCBI Description
                  (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
```

NCBI GI

```
149817 1.R1040
Contig ID
5'-most EST
                   g5752548
Method
                   BLASTX
NCBI GI
                   g3757520
BLAST score
                   174
E value
                   2.0e-12
Match length
                   142
% identity
                   40
                   (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27045
                   149844 1.R1040
Contig ID
5'-most EST
                   wrg700790274.h2
Method
                   BLASTN
NCBI GI
                   g2293111
BLAST score
                   165
E value
                   1.0e-87
Match length
                   456
                   84
% identity
NCBI Description
                  V.faba mRNA for potassium channel
Seq. No.
                   27046
Contig ID
                   149871 1.R1040
5'-most EST
                   wrg700790603.h2
Method
                   BLASTX
NCBI GI
                   g498038
BLAST score
                   303
                   5.0e-28
E value
Match length
                   82
% identity
                   (L33792) lipid transfer protein [Senecio odorus]
NCBI Description
Seq. No.
                   27047
Contig ID
                   149877 1.R1040
5'-most EST
                   wrg700790319.h2
                   27048
Seq. No.
Contig ID
                   149882 1.R1040
5'-most EST
                   wrg700790324.h2
                   27049
Seq. No.
Contig ID
                   149883 1.R1040
5'-most EST
                   wrg700790325.h2
                   27050
Seq. No.
Contig ID
                   149889 1.R1040
5'-most EST
                   wrg700790435.h2
Seq. No.
                   27051
Contig ID
                   149893 1.R1040
5'-most EST
                   gsv701049523.hl
                   27052
Seq. No.
Contig ID
                   149911 1.R1040
5'-most EST
                   rca701001536.hl
                  BLASTX
Method
```

g3738298

Contig ID

```
BLAST score
                  166
                  8.0e-12
E value
Match length
                  93
% identity
                  41
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  >qi 4249394 (AC006072) unknown protein [Arabidopsis
                  thaliana]
                  27053
Seq. No.
Contig ID
                  149912 1.R1040
5'-most EST
                  fC-qmst700790363y3
                  BLASTX
Method
                  g462147
NCBI GI
BLAST score
                  755
                  1.0e-80
E value
Match length
                  154
% identity
                  92
NCBI Description
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
                  (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                  (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase
                  (EC 5.3.1.9) - Arabidopsis thaliana
                  >gi 415923 emb CAA48940 (X69195) glucose-6-phosphate
                  isomerase [Arabidopsis thaliana]
                  27054
Seq. No.
                  149918 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400007h06a1
                  27055
Seq. No.
Contig ID
                  149923 1.R1040
                  leu701146762.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4140026
BLAST score
                  655
E value
                  1.0e-68
Match length
                  196
% identity
                  (AB009370) flavonoid 3-0-galactosyl transferase [Vigna
NCBI Description
                  mungo]
                  27056
Seq. No.
                  149924 1.R1040
Contig ID
5'-most EST
                  jC-gmf\overline{1}02220052g10a1
Method
                  BLASTX
NCBI GI
                  g3176725
BLAST score
                  375
E value
                  5.0e-36
Match length
                  151
% identity
                  (AC002392) unknown protein [Arabidopsis thaliana]
NCBI Description
                  27057
Seq. No.
                  149925 2.R1040
Contig ID
5'-most EST
                  epx701104301.h1
Seq. No.
                  27058
```

149926_1.R1040

41:

```
5'-most EST
                   wrg700790636.h2
Method
                   BLASTX
                   q2854049
NCBI GI
BLAST score
                   148
                   3.0e-09
E value
Match length
                   80
                   39
% identity
                   (AF044260) receptor serine/threonine kinase; protein kinase
NCBI Description
                   [Oryza sativa]
                   27059
Seq. No.
                   149933 1.R1040
Contig ID
                   zhf700953875.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4508077
BLAST score
                   213
E value
                   3.0e-17
Match length
                   73
% identity
                   (AC005882) 62114 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27060
Contig ID
                   149965 1.R1040
5'-most EST
                   epx701\overline{1}04103.h1
Method
                   BLASTX
NCBI GI
                   q2961384
BLAST score
                   169
E value
                   4.0e-12
Match length
                   83
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
                                                                             ٠,
                   27061
Seq. No.
                   149975 1.R1040
Contig ID
5'-most EST
                   zzp700829909.h1
Method
                   BLASTX
NCBI GI
                   g2947062
BLAST score
                   144
                   2.0e-09
E value
Match length
                   66
% identity
NCBI Description
                  (AC002521) unknown protein [Arabidopsis thaliana]
                   27062
Seq. No.
                   150015 1.R1040
Contig ID
                   fde700875304.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3005983
BLAST score
                   461
                   2.0e-46
E value
Match length
                   104
% identity
NCBI Description
                  (Y14387) lycopene epsilon-cyclase [Lycopersicon esculentum]
Seq. No.
                   27063
```

150033 1.R1040

Contig ID

```
wrg700790543.h2
5'-most EST
Seq. No.
                  27064
Contig ID
                  150050 1.R1040
5'-most EST
                  wrg700790567.h2
                  27065
Seq. No.
Contig ID
                  150086 1.R1040
5'-most EST
                  wrg700790621.h2
Method
                  BLASTX
NCBI GI
                  q4432848
BLAST score
                  158
E value
                  7.0e-19
Match length
                  80
% identity
NCBI Description
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  150098 1.R1040
Contig ID
5'-most EST
                  wrg700790641.h2
Seq. No.
                  27067
                  150118 1.R1040
Contig ID
                  rca700997004.hl
5'-most EST
Method
                  BLASTX
                                                           73.
NCBI GI
                  g3914239
BLAST score
                  209
E value
                  1.0e-16
Match length
                  73
% identity
                  53
NCBI Description
                  PROTEIN PHOSPHATASE 2C ABI2 (PP2C)
                  >gi_1945140 emb CAA70163 (Y08966) ABI2 protein phosphatase
                  2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162
                   (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]
                  >gi 2564213 emb CAA72538 (Y11840) ABI2 [Arabidopsis
                  thaliana]
Seq. No.
                  27068
                  150131 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400006b05a1
                  27069
Seq. No.
Contig ID
                  150138 1.R1040
5'-most EST
                  sat701\overline{0}14816.h1
Seq. No.
                  27070
                  150146 1.R1040
Contig ID
5'-most EST
                  wrg700790712.hl
Method
                  BLASTX
NCBI GI
                  g1167982
BLAST score
                  689
                  3.0e-76
E value
Match length
                  266
% identity
NCBI Description
                  (U43892) ABC transporter-7 [Mus musculus]
```

27071

Seq. No.

5'-most EST

```
150151 1.R1040
Contig ID
5'-most EST
                   jex700904456.hl
Method
                   BLASTN
NCBI GI
                   q534971
BLAST score
                   251
E value
                   1.0e-139
Match length
                   419
                   90
% identity
NCBI Description
                  V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase
                   L isoform
                   27072
Seq. No.
                   150178 1.R1040
Contig ID
                   jC-gmf102220080g02a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2773249
BLAST score
                   175
E value
                   2.0e-12
                   77
Match length
% identity
                   45
NCBI Description
                   (AF039707) glutamate carboxypeptidase II [Rattus
                  norvegicus]
                   27073
Seq. No.
Contig ID
                   150181 1.R1040
                  wrg700790777.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4262186
BLAST score
                   515
                   3.0e-52
E value
Match length
                  125
% identity
                   77
                   (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   27074
Seq. No.
                   150183 1.R1040
Contig ID
5'-most EST
                  bth700846128.h1
                  27075
Seq. No.
                  150245 1.R1040
Contig ID
5'-most EST
                  wrg700790893.hl
                  BLASTX
Method
NCBI GI
                  g2618689
BLAST score
                  362
                  2.0e-34
E value
Match length
                  106
                  74
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  27076
Seq. No.
                  150246_1.R1040
Contig ID
5'-most EST
                  wrg700790894.hl
Seq. No.
                  27077
Contig ID
                  150272 1.R1040
```

 $wrg700\overline{7}91278.h1$

Seq. No.

```
27078
Seq. No.
                   150285 1.R1040
Contig ID
5'-most EST
                   wrg700790970.hl
                   27079
Seq. No.
Contig ID
                   150293 1.R1040
5'-most EST
                   epx701107494.hl
Seq. No.
                   27080
                   150313 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir064g02b1
Seq. No.
                   27081
Contig ID
                   150335 1.R1040
                   zsg701118364.h1
5'-most EST
Seq. No.
                   27082
Contiq ID
                   150338 1.R1040
5'-most EST
                   wrg700791052.hl
Method
                   BLASTX
NCBI GI
                   q3420054
BLAST score
                   173
E value
                   1.0e-12
Match length
                   78
% identity
NCBI Description
                  (AC004680) unknown protein [Arabidopsis thaliana]
                   27083
Seq. No.
Contig ID
                   150352 1.R1040
5'-most EST
                   wrg700791071.hl
Method
                   BLASTX
NCBI GI
                   g2674203
BLAST score
                   444
E value
                   2.0e-44
Match length
                   96
% identity
NCBI Description
                   (AF036328) CLP protease regulatory subunit CLPX
                   [Arabidopsis thaliana]
Seq. No.
                   27084
Contig ID
                   150363 1.R1040
5'-most EST
                   eep700868248.hl
Seq. No.
                   27085
Contig ID
                   150365 1.R1040
5'-most EST
                  q5677813
Seq. No.
                   27086
Contig ID
                   150377 1.R1040
5'-most EST
                  g5342507
Seq. No.
                  27087
Contig ID
                  150380 1.R1040
5'-most EST
                  wrg700791131.h1
```

Method

BLASTX

```
150387 1.R1040
Contig ID
5'-most EST
                  vzy700756265.hl
                  BLASTX
Method
                  g1174470
NCBI GI
BLAST score
                  295
                  1.0e-26
E value
                  97
Match length
% identity
                  60
                  OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                  (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi 1588285 prf 2208301A
                  integral membrane protein [Mus musculus]
                  27089
Seq. No.
Contig ID
                  150387 2.R1040
5'-most EST
                  q57537\overline{1}6
Method
                  BLASTX
NCBI GI
                  q1174470
BLAST score
                  253
E value
                  7.0e-22
Match length
                  70
% identity
                  OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                  (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi 1588285 prf 2208301A
                  integral membrane protein [Mus musculus]
                  27090
Seq. No.
                  150407 1.R1040
Contig ID
5'-most EST
                  wrg700791493.hl
                  27091
Seq. No.
Contig ID
                  150409 1.R1040
5'-most EST
                  iC-gmro02910012h12d1
Method
                  BLASTX
NCBI GI
                  q123178
BLAST score
                  358
E value
                  5.0e-34
Match length
                  77
% identity
                  HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH)
NCBI Description
                  >gi 99844 pir A39358 histidinol dehydrogenase (EC
                  1.1.1.23) precursor, chloroplast - cabbage >gi_167142
                  (M60466) histidinol dehydrogenase [Brassica oleracea]
Seq. No.
Contig ID
                  150413 1.R1040
5'-most EST
                  asn701137565.h1
                  27093
Seq. No.
Contig ID
                  150413 2.R1040
5'-most EST
                  jC-gmst02400008e07a1
Seq. No.
                  27094
Contig ID
                  150425 1.R1040
5'-most EST
                  sat701004066.h1
```

Seq. No.

```
g3135611
NCBI GI
BLAST score
                  354
                  1.0e-33
E value
                  109
Match length
% identity
                  62
                   (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                  27095
Seq. No.
                  150477 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810091g09a1
                  BLASTX
Method
                  q2398831
NCBI GI
BLAST score
                  392
                  8.0e-38
E value
Match length
                  213
% identity
                  43
                  (X75542) 4-coumarate:CoA ligase [Vanilla planifolia]
NCBI Description
Seq. No.
                  27096
                  150525 1.R1040
Contig ID
5'-most EST
                  wrq700791515.hl
Seq. No.
                  27097
Contig ID
                  150529 1.R1040
5'-most EST
                  wrg700791520.hl
Seq. No.
                  27098
Contig ID
                  150562 1.R1040
5'-most EST
                  rca700999075.hl
Method
                  BLASTX
NCBI GI
                  q3096949
BLAST score
                  262
E value
                   4.0e-34
Match length
                  88
% identity
                  74
NCBI Description
                   (Y16328) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  27099
Seq. No.
Contig ID
                  150583 1.R1040
5'-most EST
                  jsh701068834.h1
Seq. No.
                  27100
Contig ID
                  150617 1.R1040
5'-most EST
                  wrg700791687.hl
Method
                  BLASTX
NCBI GI
                  g2864610
BLAST score
                  168
E value
                  6.0e-12
Match length
                  45
% identity
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
                  >gi 4049336 emb CAA22561 (AL034567) putative protein
                  [Arabidopsis thaliana]
```

```
150635 1.R1040
Contig ID
5'-most EST
                  pxt700944468.h1
Method
                  BLASTX
NCBI GI
                  q2117620
BLAST score
                   447
                  2.0e-44
E value
                  101
Match length
% identity
                  86
NCBI Description
                  peroxidase (EC 1.11.1.7) 1A - alfalfa
                  >gi. 971558 emb CAA62225 (X90692) peroxidase1A [Medicago
                  sativa]
Seq. No.
                  27102
Contig ID
                  150638 1.R1040
5'-most EST
                  leu701149501.h1
Seq. No.
                  27103
Contig ID
                  150641 1.R1040
5'-most EST
                  smc700745926.h1
                  27104
Seq. No.
Contig ID
                  150666 1.R1040
5'-most EST
                  vzy700755518.h1
                  BLASTX
Method
NCBI GI
                  q2129609
BLAST score
                  284
E value
                 -1.0e-25
                  82
Match length
                  70
% identity
NCBI Description
                  HD-ZIP protein - Arabidopsis thaliana
                  >gi 1212757 emb CAA91183 (Z54356) HD-ZIP [Arabidopsis
                  thaliana]
                  27105
Seq. No.
                  150677 1.R1040
Contig ID
                  wrq700791793.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4115338
BLAST score
                  104
E value
                  2.0e-51
Match length
                  207
% identity
                  26
NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds
Seq. No.
                  27106
                  150699 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810088h12a1
Method
                  BLASTX
NCBI GI
                  g1169586
BLAST score
                  184
E value
                  7.0e-14
Match length
                  39
% identity
                  90
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC
                  3.1.3.11) - potato >gi 440591 emb CAA54265 (X76946)
```

fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 27107 Contig ID 150712 1.R1040 5'-most EST jC-gmf102220050b08d1 Seq. No. 27108 Contig ID 150715 1.R1040 5'-most EST rca701002482.hl Method BLASTX NCBI GI g2673918 BLAST score 403 E value 4.0e-39 Match length 96 % identity NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana] Seq. No. 27109 Contig ID 150721 1.R1040 5'-most EST kmv700743705.h1 Method BLASTX NCBI GI q2443350 BLAST score 172 E value 3.0e-19 Match length 95 % identity NCBI Description (AB001380) cytochrome P450 [Glycyrrhiza echinata] 27110 Seq. No. Contig ID 150726 1.R1040 5'-most EST wrg700791890.hl BLASTX Method NCBI GI g3176714 BLAST score 464 E value 3.0e-46 Match length 117 % identity NCBI Description (AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana] 27111 Seq. No. Contig ID 150738 1.R1040 5'-most EST wrg700792261.hl Method BLASTX NCBI GI q3461813 BLAST score 279 3.0e-25 E value Match length 83 % identity (AC004138) putative sucrose/H+ symporter [Arabidopsis NCBI Description thaliana] 27112 Seq. No. Contig ID 150739 1.R1040

5'-most EST leu701153333.h1 BLASTX Method

NCBI GI q4567249

Seq. No.

```
BLAST score
                   514
                   4.0e-52
E value
Match length
                   133
% identity
                   68
                   (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   27113
Seq. No.
                   150757 1.R1040
Contig ID
5'-most EST
                   wrg700791938.hl
                   27114
Seq. No.
Contig ID
                   150761 1.R1040
5'-most EST
                   wrg700791948.hl
Seq. No.
                   27115
Contig ID
                   150784 1.R1040
                   rca701\overline{0}00693.h1
5'-most EST
Seq. No.
                   27116
                   150787 1.R1040
Contig ID
5'-most EST
                   q5753431
Method
                   BLASTX
NCBI GI
                   g3395435
BLAST score
                   216
E value
                   4.0e-17
Match length
                   139
% identity
NCBI Description
                   (AC004683) myosin heavy chain-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   27117
Contig ID
                   150801 1.R1040
5'-most EST
                   dpv701102331.h1
Method
                   BLASTX
NCBI GI
                   g1922248
BLAST score
                   260
E value
                   7.0e-23
Match length
                   68
% identity
NCBI Description
                   (Y10087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27118
Contig ID
                   150807 1.R1040
5'-most EST
                   wrg700792046.hl
Method
                   BLASTX
NCBI GI
                   g2245026
BLAST score
                   341
E value
                   3.0e - 32
Match length
                   91
% identity
                   76
NCBI Description
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27119
Contig ID
                   150809 1.R1040
5'-most EST
                   wrg700792048.hl
```

```
150828 1.R1040
Contig ID
5'-most EST
                   kl1701207943.h1
Seq. No.
                   27121
                   150830 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400051b01a1
                   BLASTX
Method
                   g2443887
NCBI GI
BLAST score
                   911
E value
                   2.0e-98
Match length
                   285
% identity
                   (AC002294) Similar to transcription factor
NCBI Description
                   gb Z46606 1658307 and others [Arabidopsis thaliana]
Seq. No.
                   27122
Contig ID
                   150851 1.R1040
5'-most EST
                   gsv701056442.hl
Seq. No.
                   27123
Contig ID
                   150868 1.R1040
5'-most EST
                  wrg700792214.h1
                   27124
Seq. No.
Contig ID
                   150869 1.R1040
5'-most EST
                  fde700875090.h1
Method
                   BLASTX
NCBI GI
                   q3600059
BLAST score
                   367
E value
                   3.0e-35
Match length
                   103
% identity
NCBI Description
                   (AF080120) contains similarity to WB domains, G-beta
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
                   27125
Seq. No.
Contig ID
                   150893 2.R1040
5'-most EST
                  hrw701059939.hl
                   27126
Seq. No.
Contig ID
                   150914 1.R1040
5'-most EST
                   kl1701214979.hl
Seq. No.
                   27127
Contig ID
                   150927 1.R1040
5'-most EST
                  pcp700988714.h1
Seq. No.
                  27128
Contig ID
                  150946 1.R1040
5'-most EST
                  pcp700988754.hl
Seq. No.
                  27129
Contig ID
                  150949 1.R1040
5'-most EST
                  pcp700990760.hl
Method
                  BLASTX
NCBI GI
                  g3135269
```

Contig ID

5'-most EST

```
BLAST score
                   167
E value
                   4.0e-12
Match length
                   81
% identity
NCBI Description
                   (AC003058) unknown protein [Arabidopsis thaliana]
Seq. No.
                   27130
Contig ID
                   150955 1.R1040
5'-most EST
                   pcp700988771.h1
Seq. No.
                   27131
Contig ID
                   150958 1.R1040
5'-most EST
                   pcp700990778.hl
                   27132
Seq. No.
Contig ID
                   150967 1.R1040
5'-most EST
                   zhf700961446.h1
                   27133
Seq. No.
Contig ID
                   150991 1.R1040
5'-most EST
                   pcp700988848.hl
Method
                   BLASTX
                   q4056420
NCBI GI
BLAST score
                   376
                   4.0e-36
E value
Match length
                   111
% identity
                   (AC005322) ESTs gb_T144077 and gb_T43352 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
Seq. No.
                   27134
Contig ID
                   150999 1.R1040
5'-most EST
                   pcp700988872.h1
                   BLASTX
Method
NCBI GI
                   q4097549
BLAST score
                   162
E value
                   8.0e-11
Match length
                   72
% identity
NCBI Description
                   (U64907) ATFP4 [Arabidopsis thaliana]
Seq. No.
                   27135
Contig ID
                   151005 1.R1040
5'-most EST
                   zhf700961259.h1
Method
                   BLASTX
NCBI GI
                   g2072626
BLAST score
                   309
E value
                   4.0e-28
Match length
                   108
% identity
NCBI Description
                   (Y12904) hypothetical protein [Arabidopsis thaliana]
                   >gi 3281856 emb CAA19751 (AL031004) Transcription factor
                   II homolog [Arabidopsis thaliana]
Seq. No.
                   27136
```

151022 1.R1040

awf700838786.h1

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   q4558556
BLAST score
                   461
E value
                   3.0e-46
Match length
                   125
                   70
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   27137
                   151031 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir014g07b1
Seq. No.
                   27138
Contig ID
                   151032 1.R1040
5'-most EST
                   zsq701118058.h2
Seq. No.
                   27139
Contig ID
                   151032 2.R1040
5'-most EST
                   jC-gmro02910063a07a1
Seq. No.
                   27140
Contig ID
                   151033 1.R1040 ·
5'-most EST
                   jC-gmf102220062b09a1
Method
                   BLASTX
NCBI GI
                   q3928084
BLAST score
                   342
E value
                   3.0e-32
Match length
                   132
% identity
NCBI Description
                   (AC005770) retrotransposon-like protein [Arabidopsis
                   thalianal
Seq. No.
                   27141
Contig ID
                   151050 1.R1040
5'-most EST
                  pcp700991001.hl
Seq. No.
                   27142
Contig ID
                   151060 1.R1040
5'-most EST
                   zsq701\overline{1}25820.h1
Method
                   BLASTX
NCBI GI
                   q1617219
BLAST score
                   741
E value
                   2.0e-78
Match length
                   218
% identity
NCBI Description
                   (X99301) CPD photolyase [Arabidopsis thaliana] >qi 2984707
                   (AF053365) type II CPD photolyase PHR1 [Arabidopsis
                  thaliana]
Seq. No.
                  27143
Contig ID
                  151061 1.R1040
5'-most EST
                  pmv700888961.hl
Seq. No.
                  27144
                  151061 2.R1040
Contig ID
```

pcp700991019.hl

```
Seq. No.
                   27145
                   151062 1.R1040
Contig ID
5'-most EST
                   pcp700991020.h1
                   27146
Seq. No.
                   151063 1.R1040
Contig ID
5'-most EST
                   sat701010434.h1
Seq. No.
                   27147
                   151064 1.R1040
Contig ID
                   pxt700944710.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3738302
BLAST score
                   396
E value
                   3.0e-38
Match length
                   202
% identity
NCBI Description
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
                   >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thalianal
Seq. No.
                   27148
Contig ID
                   151069 1.R1040
5'-most EST
                   pcp700989034.h1
Method
                   BLASTX
NCBI GI
                   q4539389
BLAST score
                   320
E value
                   5.0e-30
Match length
                   82
% identity
NCBI Description
                   (AL035526) putative protein kinase [Arabidopsis thaliana]
                   27149
Seq. No.
Contig ID
                   151075 1.R1040
5'-most EST
                   sat701\overline{0}14344.h1
Method
                   BLASTX
NCBI GÍ
                   q2673947
BLAST score
                   277
                   1.0e-24
E value
Match length
                   98
% identity
NCBI Description
                   (U62931) multidrug resistance protein 1 [Aspergillus
                   flavus] >gi 2673949 (U62932) multidrug resistance protein 1
                   [Aspergillus flavus]
                   27150
Seq. No.
Contig ID
                   151076 1.R1040
5'-most EST
                   g5688315
                   27151
Seq. No.
Contig ID
                   151083 1.R1040
5'-most EST
                   pcp700991064.hl
Method
                   BLASTX
NCBI GI
                   g3695019
BLAST score
                   225
E value
                   7.0e-19
```

E value

```
Match length
                   81
% identity
                   54
NCBI Description
                   (AF055848) subtilisin-like protease [Arabidopsis thaliana]
                   27152
Seq. No.
                   151087 1.R1040
Contig ID
5'-most EST
                   pcp700991071.hl
Seq. No.
                   27153
                   151095 1.R1040
Contig ID
5'-most EST
                   pcp700991080.hl
                   27154
Seq. No.
Contig ID
                   151127 1.R1040
5'-most EST
                   pcp700989157.h1
Method
                   BLASTX
NCBI GI
                   q2660670
BLAST score
                   469
                   7.0e-48
E value
Match length
                   117
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   27155
Seq. No.
Contig ID
                   151135 1.R1040
5'-most EST
                   fde700875359.hl
Method
                   BLASTX
NCBI GI
                   q4468804
BLAST score
                   178
E value
                   4.0e-13
Match length
                   108
% identity
                   (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   27156
Seq. No.
Contig ID
                   151152 1.R1040
5'-most EST
                   kl1701214981.h1
Method
                   BLASTX
NCBI GI
                   g283966
BLAST score
                   590
E value
                   6.0e-61
Match length
                   173
% identity
                   67
NCBI Description activator 1 37K chain - human
                   27157
Seq. No.
Contig ID
                   151161 1.R1040
5'-most EST
                   pcp700989236.hl
                   27158
Seq. No.
Contig ID
                   151183 1.R1040
5'-most EST
                   zsg701122867.hl
                   BLASTN
Method
                   g1396053
NCBI GI
BLAST score
                   272
```

1.0e-151

Match length 644 % identity 86

NCBI Description Pisum sativum mRNA for phosphoribosylanthranilate

transferase, partial cds

Seq. No. 27159

Contig ID 151188 1.R1040

5'-most EST jC-gmfl02220113a12d1

Method BLASTX
NCBI GI g3894193
BLAST score 155
E value 2.0e-10
Match length 56
% identity 52

NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis

thalianal

Seq. No. 27160

Contig ID 151203_1.R1040

5'-most EST jC-gmf102220089e02d1

Method BLASTX
NCBI GI g4512657
BLAST score 265
E value 4.0e-23
Match length 77
% identity 58

NCBI Description (AC006931) putative APG protein [Arabidopsis thaliana]

>gi_4544463_gb_AAD22370.1_AC006580_2 (AC006580) putative

APG isolog protein [Arabidopsis thaliana]

Seq. No. 27161

Contig ID 151218_1.R1040 5'-most EST sat701014153.h1

Seq. No. 27162

Contig ID 151244_1.R1040 5'-most EST uC-gmropic006a01b1

Seq. No. 27163

Contig ID 151248_1.R1040 5'-most EST pcp700989507.h1

Method BLASTX
NCBI GI g1168940
BLAST score 219
E value 9.0e-18
Match length 104
% identity 47

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958

chorismate mutase precursor - Arabidopsis thaliana >gi 429153 emb CAA81286 (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 27164

Contig ID 151249_1.R1040 5'-most EST pcp700989509.h1

Seq. No. 27165

Seq. No.

```
Contig ID
                   151252 1.R1040
5'-most EST
                   asn701\overline{1}36972.h1
Seq. No.
                   27166
                   151256 1.R1040
Contig ID
5'-most EST
                   bth700847247.h1
                   27167
Seq. No.
                   151307 1.R1040
Contig ID
                   jC-gmf\overline{1}02220137e07a1
5'-most EST
                   BLASTX
Method
                   g267421
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
Match length
                   106
% identity
                   49
                   DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS HOMOLOG
NCBI Description
                   (XERODERMA PIGMENTOSUM GROUP G COMPLEMENTING PROTEIN
                   HOMOLOG) >gi_422627_pir__S35994 DNA repair protein XPGC -
                   African clawed frog >gi_312433_emb_CAA49597_ (X69977) XP-G
                   related factor [Xenopus laevis]
Seq. No.
                   27168
Contig ID
                   151324 1.R1040
5'-most EST
                   asn701\overline{1}42612.h1
Method
                   BLASTX
NCBI GI
                   g3540195
BLAST score
                   681
E value
                   7.0e-72
Match length
                   158
% identity
NCBI Description
                   (AC004260) Unknown protein [Arabidopsis thaliana]
                   27169
Seq. No.
Contig ID
                   151334 1.R1040
5'-most EST
                   pcp700989637.hl
Method
                   BLASTX
NCBI GI
                   q4263818
BLAST score
                   251
E value
                   2.0e-21
Match length
                   134
% identity
NCBI Description
                   (AC006067) unknown protein [Arabidopsis thaliana]
                   27170
Seq. No.
Contig ID
                   151361 1.R1040
5'-most EST
                   pcp700989680.h1
Seq. No.
                   27171
Contig ID
                   151366 1.R1040
5'-most EST
                   pcp700989685.hl
                   27172
Seq. No.
Contig ID
                   151373 1.R1040
5'-most EST
                   pcp700989794.h1
```

```
151382 1.R1040
Contig ID
5'-most EST
                  pcp700989709.h1
Method
                  BLASTX
NCBI GI
                  g585053
BLAST score
                  335
                  7.0e-59
E value
Match length
                  205
                  57
% identity
                  MITOTIC CONTROL PROTEIN DIS3 >gi 283075 pir A41944 mitotic
NCBI Description
                  control protein dis3+ - fission yeast (Schizosaccharomyces
                  pombe) >gi 173381 (M74094) mitotic control protein
                  [Schizosaccharomyces pombe] >gi 3650393 emb CAA21102
                   (AL031743) mitotic control protein dis3.
                   [Schizosaccharomyces pombe]
Seq. No.
                  27174
                  151382 2.R1040
Contig ID
                  hrw701\overline{0}60145.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q585053
BLAST score
                  265
E value
                  2.0e-23
Match length
                  93
% identity
                  57
                  MITOTIC CONTROL PROTEIN DIS3 >qi 283075 pir A41944 mitotic
NCBI Description
                  control protein dis3+ - fission yeast (Schizosaccharomyces
                  pombe) >gi 173381 (M74094) mitotic control protein
                  [Schizosaccharomyces pombe] >gi 3650393 emb CAA21102
                   (AL031743) mitotic control protein dis3.
                  [Schizosaccharomyces pombe]
                  27175
Seq. No.
Contig ID
                  151391 1.R1040
5'-most EST
                  pcp700990227.h1
                  27176
Seq. No.
Contig ID
                  151402 1.R1040
                  pcp700989740.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4375829
BLAST score
                  449
E value
                  2.0e-59
Match length
                  143
% identity
                  (AJ011977) RNA-directed RNA polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  27177
Seq. No.
Contig ID
                  151408 1.R1040
5'-most EST
                  zhf700963853.h1
Method
                  BLASTX
NCBI GI
                  q3287695
BLAST score
                  403
E value
                  3.0e-44
Match length
                  119
% identity
```

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

```
thaliana]
                   27178
Seq. No.
                   151408 2.R1040
Contig ID
                   hrw701\overline{0}58042.h1
5'-most EST
Method
                   BLASTX
                   g3287695
NCBI GI
BLAST score
                   235
                   6.0e-20
E value
                   59
Match length
                   76
% identity
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
Seq. No.
                   27179
                   151424 1.R1040
Contig ID
5'-most EST
                   pxt700945659.h1
Method
                   BLASTX
NCBI GI
                   g3341679
BLAST score
                   565
                   2.0e-58
E value
Match length
                   139
% identity
                   75
NCBI Description
                   (AC003672) dynamin-like protein phragmoplastin 12
                   [Arabidopsis thaliana]
Seq. No.
                   27180
Contig ID
                   151453 1.R1040
5'-most EST
                   asn701134317.hl
Seq. No.
                   27181
Contig ID
                   151455 1.R1040
5'-most EST
                   rca700\overline{9}99308.h1
Method
                   BLASTX
NCBI GI
                   g2911058
BLAST score
                   178
E value
                   3.0e-22
Match length
                   95
% identity
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   27182
Contig ID
                   151499 1.R1040
5'-most EST
                  pcp700989895.hl
Method
                   BLASTX
NCBI GI
                   g2500981
BLAST score
                   813
E value
                   2.0e-87
Match length
                   159
% identity
NCBI Description
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
                  >gi 1084418 pir S51685 glutamate--tRNA ligase (EC
                   6.1.1.17) - common tobacco >gi 603867 emb CAA58506
```

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

(X83524) glutamate--tRNA ligase [Nicotiana tabacum]

```
Seq. No.
                    27183
                    151503 1.R1040
 Contig ID
 5'-most EST
                    jC-gmf\overline{1}02220090d01d1
                    BLASTN
 Method
                    g1707656
 NCBI GI
 BLAST score
                    340
                    0.0e+00
 E value
 Match length
                    528
 % identity
                    91
 NCBI Description P.sativum mRNA for DnaJ-like protein
                    27184
 Seq. No.
                    151521 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy272a07b1
 Method
                    BLASTX
 NCBI GI
                    g3548808
 BLAST score
                    307
                    4.0e-28
 E value
 Match length
                    118
 % identity
                    46
 NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                    27185
 Seq. No.
                    151547 1.R1040
 Contig ID
 5'-most EST
                    jC-gmf102220051h11a1
 Method
                    BLASTX
 NCBI GI
                    q4218014
 BLAST score
                    544
 E value
                    9.0e-56
 Match length
                    114
 % identity
 NCBI Description
                    (AC006135) putative spliceosomal protein (RNA binding
                    protein) [Arabidopsis thaliana]
 Seq. No.
                    27186
 Contig ID
                    151555 1.R1040
 5'-most EST
                    epx701\overline{1}06345.h1
 Seq. No.
                    27187
 Contig ID
                    151575 1.R1040
 5'-most EST
                    pcp700990059.h1
 Seq. No.
                    27188
 Contig ID
                    151593 1.R1040
 5'-most EST
                    leu701154615.hl
 Seq. No.
                    27189
 Contig ID
                    151599 1.R1040
 5'-most EST
                    jC-gmst02400037c02a1
 Method
                    BLASTX
 NCBI GI
                    q1213629
 BLAST score
                    334
 E value
                    6.0e-31
 Match length
                    88
 % identity
```

NCBI Description (X95991) pectinesterase [Prunus persica]

5'-most EST

```
27190
Seq. No.
                   151617 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}11922.h1
Method
                   BLASTX
NCBI GI
                   q4371285
BLAST score
                   554
                   5.0e-57
E value
Match length
                   137
                   73
% identity
NCBI Description
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
                   27191
Seq. No.
                   151624 1.R1040
Contig ID
5'-most EST
                   vzy700755958.h1
Seq. No.
                   27192
                   151640 1.R1040
Contig ID
5'-most EST
                   pcp700990163.h1
Seq. No.
                   27193
Contig ID
                   151652 1.R1040
5'-most EST
                   pcp700990187.hl
Method
                   BLASTX
NCBI GI
                   g2190557
BLAST score
                   272
E value
                   2.0e-24
Match length
                   71
% identity
NCBI Description
                   (AC001229) F5I14.11 [Arabidopsis thaliana]
Seq. No.
                   27194
Contig ID
                   151658 1.R1040
5'-most EST
                   pcp700990202.h1
Seq. No.
                   27195
Contig ID
                   151699 1.R1040
5'-most EST
                   pcp700990264.hl
Method
                   BLASTX
NCBI GI
                   q2465925
BLAST score
                   345
E value
                   1.0e-32
Match length
                   122
% identity
                   54
NCBI Description
                   (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
                   27196
Seq. No.
Contig ID
                   151711 1.R1040
5'-most EST
                   leu701\overline{1}53711.h1
Seq. No.
                   27197
Contig ID
                   151713 1.R1040
5'-most EST
                   dpv701\overline{0}98422.h1
Seq. No.
                   27198
Contig ID
                   151714 1.R1040
```

hrw701060337.h1

West of

BLAST score

```
27199
Seq. No.
                   151716 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810048c02a1...
Method
                   BLASTX
                   g1853970
NCBI GI
BLAST score
                   445
                   3.0e-44
E value
                   139
Match length
% identity
                   60
                   (D88122) CPRD46 protein [Vigna unguiculata]
NCBI Description
Seq. No.
                   27200
Contig ID
                   151721 1.R1040
5'-most EST
                   pcp700990308.h1
Seq. No.
                   27201
Contig ID
                   151750 1.R1040
5'-most EST
                   uC-gmrominsoy315a04b1
Seq. No.
                   27202
Contig ID
                   151785 1.R1040
5'-most EST
                   dpv701097505.h1
Method '
                   BLASTN
NCBI GI
                   g2852444
BLAST score
                   147
E value
                   9.0e-77
Match length
                   347
% identity
                   86
NCBI Description
                   Salix bakko mRNA for SUI1 homolog, complete cds
                   27203
Seq. No.
Contig ID
                   151813 1.R1040
5'-most EST
                   jC-gmro02910016h12d1
                   27204
Seq. No.
Contig ID
                   151863 1.R1040
5'-most EST
                   pcp700990506.hl
                   27205
Seq. No.
Contig ID
                   151877 1.R1040
5'-most EST
                   vzy700756003.h1
Method
                   BLASTX
NCBI GI
                   q4218120
BLAST score
                   362
E value
                   9.0e-35
Match length
                   102
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
                   27206
Seq. No.
Contig ID
                   151894 1.R1040
5'-most EST
                   gsv701051906.hl
Method
                  BLASTX
NCBI GI
                   g4001803
```

5'-most EST

```
E value
                   3.0e-09
Match length
                   44
% identity
                   57
                   (AF041474) BAF53a [Homo sapiens] >gi 4218064 dbj BAA74577
NCBI Description
                   (AB015907) actin-related protein [Homo sapiens]
                   27207
Seq. No.
Contig ID
                   151959 1.R1040
5'-most EST
                   epx701\overline{1}06226.h1
Method
                   BLASTX
NCBI GI
                   g3176709
BLAST score
                   143
                   4.0e-09
E value
Match length
                   72
% identity
                   42
NCBI Description
                   (AC002392) putative anthranilate
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
                   27208
Seq. No.
Contig ID
                   151960 1.R1040
                   pcp700\overline{9}90806.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827534
BLAST score
                   471
E value
                   2.0e-47
Match length
                   108
% identity
                   87
NCBI Description
                   (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                   27209
Contig ID
                   151980 1.R1040
5'-most EST
                   pcp700990828.hl
Seq. No.
                   27210
Contig ID
                   151983 1.R1040
5'-most EST
                   pcp700990835.h1
Seq. No.
                   27211
Contig ID
                   151984 1.R1040
5'-most EST
                   pcp700990837.hl
Seq. No.
                   27212
Contig ID
                   151985 1.R1040
5'-most EST
                   sat701011675.hl
Method
                   BLASTX
NCBI GI
                   q4218991
BLAST score
                   222
E value
                   8.0e-20
Match length
                   94
% identity
NCBI Description
                   (AF098632) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   27213
Contig ID
                   151989 1.R1040
```

pcp700990844.h1

Match length

```
27214
Seq. No.
Contig ID
                   152017 1.R1040
5'-most EST
                  pcp700990879.h1
Seq. No.
                   27215
                   152030_1.R1040
Contig ID
5'-most EST
                   gsv701049324.h1
                -., 27216
Seq. No.
Contig ID
                   152032 1.R1040
5'-most EST
                   pcp700990902.h1
Method
                   BLASTX
                   g1582580
NCBI GI
BLAST score
                   167
E value
                   5.0e-17
Match length
                   78
% identity
                  caffeic acid O-methyltransferase [Stylosanthes humilis]
NCBI Description
Seq. No.
Contig ID
                   152057 1.R1040
5'-most EST
                   pcp700990933.h1
                   27218
Seq. No.
Contig ID
                   152077 1.R1040
5'-most EST
                   uC-gmropic065f04b1
Method
                   BLASTX
NCBI GI
                   g4567197
BLAST score
                   433
E value
                   9.0e-43
Match length
                   132
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                   27219
Seq. No.
Contig ID
                   152080 1.R1040
5'-most EST
                   jex700\overline{9}07316.h1
                   27220
Seq. No.
Contig ID
                   152094 1.R1040
5'-most EST
                   jC-qmle01810092f08a1
Method
                   BLASTX
NCBI GI
                   g2781357
BLAST score
                   178
E value
                   6.0e-13
Match length
                   57
% identity
NCBI Description (AC003113) F2401.13 [Arabidopsis thaliana]
                   27221
Seq. No.
Contig ID
                   152171 1.R1040
5'-most EST
                   zsg701117338.hl
Method
                  BLASTX
NCBI GI
                   g4314365
BLAST score
                   204
E value
                   3.0e-16
```

BLAST score

```
43
% identity
                   (AC006340) putative copia-like retrotransposon Hopscotch
NCBI Description
                   [Arabidopsis thaliana]
                   27222
Seq. No.
                   152182 1.R1040
Contig ID
                   k11701\overline{2}04629.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3868723
BLAST score
                   73
                   1.0e-32
E value
Match length
                   412
% identity
                   84
                   Arabidopsis thaliana chromosome V map 60.5 cM, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   27223
Seq. No.
                   152226 1.R1040
Contig ID
5'-most EST
                   kl1701214119.hl
Seq. No.
                   27224
Contig ID
                   152229 1.R1040
5'-most EST
                   pcp700991187.h1
Seq. No.
                   27225
Contig ID
                   152236 1.R1040
5'-most EST
                   pcp700991196.h1
Method
                   BLASTX
NCBI GI
                   q4218062
BLAST score
                   250
E value
                   1.0e-21
Match length
                   115
% identity
NCBI Description
                   (AB015906) actin-related protein [Homo sapiens]
Seq. No.
                   27226
Contig ID
                   152238 1.R1040
5'-most EST
                   uC-gmropic036h09b1
Seq. No.
                   27227
Contig ID
                   152253 1.R1040
5'-most EST
                   jC-gmro02910029a02d1
Seq. No.
                   27228
Contig ID
                   152262 1.R1040
5'-most EST
                   g4397342
Seq. No.
                   27229
Contig ID
                   152289 1.R1040
5'-most EST
                   pcp700991276.hl
Seq. No.
                   27230
Contig ID
                   152306 1.R1040
5'-most EST
                   zhf700\overline{9}61049.h1
Method
                  BLASTX
NCBI GI
                   q3024426
```

Seq. No.

```
E value
                  5.0e-09
Match length
                  90
% identity
                  44
NCBI Description
                  PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
                   (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi 1084302 pir S55478
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
                  plant >qi 854265 emb CAA57872 (X82489)
                  pyruvate, orthophosphate dikinase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  27231
Contig ID
                  152323 1.R1040
5'-most EST
                  leu701149479.h1
Method
                  BLASTX
NCBI GI
                  q4455299
BLAST score
                  264
                  3.0e-23
E value
Match length
                  73
% identity
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  27232
                  152332 1.R1040
Contig ID
                  epx701108066.hl
5'-most EST
Seq. No.
                  27233
Contig ID
                  152345 1.R1040
5'-most EST
                  zhf700954390.h1
Seq. No.
                  27234
Contig ID
                  152397 1.R1040
                  pcp700991432.h1
5'-most EST
Method
                  BLASTX
                  g2865433
NCBI GI
BLAST score
                  142
                  7.0e-09
E value
Match length
                  81
                  37
% identity
NCBI Description (AF039374) chromomethylase [Arabidopsis suecica]
Seq. No.
                  27235
Contig ID
                  152399 1.R1040
5'-most EST
                  jC-gmle01810047e05a1
Method
                  BLASTX
NCBI GI
                  g541816
BLAST score
                  1689
E value
                  0.0e + 00
Match length
                  398
                  81
% identity
NCBI Description
                  protein kinase - common ice plant >gi 457689 emb CAA82990
                  (Z30329) protein kinase [Mesembryanthemum crystallinum]
Seq. No.
                  27236
                  152410 1.R1040
Contig ID
5'-most EST
                  smc700746390.h1
```

NCBI Description

vinifera]

```
152421 1.R1040
Contig ID
                   rlr700896803.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4309698
BLAST score
                   399
                   1.0e-38
E value
Match length
                   133
% identity
                   65
NCBI Description
                   (AC006266) putative glucosyltransferase [Arabidopsis
                   27238
Seq. No.
                   152428 1.R1040
Contig ID
5'-most EST
                   dpv701102248.hl
Seq. No.
                   27239
Contig ID
                   152430 1.R1040
5'-most EST
                   pcp700991510.hl
Seq. No.
                   27240
Contig ID
                   152435 1.R1040
5'-most EST
                   eep700866705.hl ,
Method
                   BLASTX
NCBI GI
                   g3702332
BLAST score
                   141
E value
                   1.0e-15
Match length
                   85
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   27241
Contig ID
                   152449 1.R1040
5'-most EST
                   pcp700991553.hl
Method
                   BLASTX
NCBI GI
                   g4220514
BLAST score
                   376
E value
                   4.0e-36
Match length
                   142
% identity
NCBI Description
                   (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   27242
Contig ID
                   152456 1.R1040
5'-most EST
                   pmv700892711.h1
Seq. No.
                   27243
Contig ID
                   152459 1.R1040
5'-most EST
                   pcp700991575.h1
Method
                   BLASTX
NCBI GI
                   g1854386
BLAST score
                   236
E value
                   5.0e-20
Match length
                   56
% identity
```

(AB001375) similar to soluble NSF attachment protein [Vitis

```
Seq. No.
                   27244
Contig ID
                   152480 1.R1040
5'-most EST
                   jC-gmro02910016d02a1 .
Method
                   BLASTX
                   g2262107
NCBI GI
BLAST score
                   820
                   5.0e-88
E value
Match length
                   196
% identity
                   (AC002343) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   27245
Seq. No.
Contig ID
                   152518 1.R1040
5'-most EST
                  pcp700991671.hl
                   27246
Seq. No.
                   152529 1.R1040
Contig ID
                   g4289922
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3033384
BLAST score
                   502
                   6.0e-51
E value
Match length
                   137
% identity
NCBI Description
                   (AC004238) putative CTP synthase [Arabidopsis thaliana]
Seq. No.
                   27247
Contig ID
                   152534 1.R1040
5'-most EST
                   pcp700991688.hl
Method
                   BLASTX
NCBI GI
                   q4512657
BLAST score
                   155
E value
                   2.0e-10
Match length
                   103
% identity
NCBI Description
                   (AC006931) putative APG protein [Arabidopsis thaliana]
                   >qi 4544463 qb AAD22370.1 AC006580 2 (AC006580) putative
                  APG isolog protein [Arabidopsis thaliana]
Seq. No.
                   27248
                   152537 1.R1040
Contig ID
5'-most EST
                   jsh701068142.h1
Method
                   BLASTX
NCBI GI
                   q3769472
BLAST score
                   272
E value
                   5.0e-24
Match length
                   79
% identity
                   (AF064732) putative phospholipase A2 [Dianthus
NCBI Description
                  caryophyllus]
Seq. No.
                   27249
Contig ID
                  152547 1.R1040
```

g4512705

BLASTX

pcp700991707.hl

5'-most EST

Method

NCBI GI

Contig ID

5'-most EST

```
BLAST score
                   353
 E value
                   3.0e-44
 Match length
                   136
 % identity
                   67
 NCBI Description
                   (AC006569) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
 Seq. No.
                   27250
 Contig ID
                   152601 1.R1040
 5'-most EST
                   pcp700991775.hl
 Seq. No.
                   27251
 Contig ID
                   152625 1.R1040
 5'-most EST
                   jC-gmst02400053f11d1
Seq. No.
                   27252
Contig ID
                   152638 1.R1040
5'-most EST
                   jC-gmf102220064f05a1
Method
                   BLASTX
NCBI GI
                   g4508083
BLAST score
                   225
E value
                   2.0e-18
Match length
                   67
% identity
                   73
NCBI Description
                  (AC005882) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27253
Contig ID
                   152645 1.R1040
5'-most EST
                   jC-gmro02910074g05d1
Seq. No.
                   27254
Contig ID
                  152659 1.R1040
5'-most EST
                  pcp700991863.h1
Method
                  BLASTX
NCBI GI
                  g1001263
BLAST score
                  497
E value
                  3.0e-51
Match length
                  177
% identity
NCBI Description
                  (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                  27255
Contig ID
                  152686 1.R1040
5'-most EST
                  zhf700957194.h1
Method
                  BLASTX
NCBI GI
                  g4415931
BLAST score
                  564
E value
                  3.0e-58
Match length
                  137
% identity
                  76
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
                  >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  27256
```

152695 1.R1040

 $pcp700\overline{9}91916.h1$

5'-most EST

Method

```
27257
Seq. No.
                   152698 1.R1040
Contig ID
5'-most EST
                   pmv700892414.h1
Method
                   BLASTX
                   q3879119
NCBI GI
BLAST score
                   162
                   2.0e-11
E value
Match length
                   65
% identity
                   48
                   (Z70310) similar to Glutathione S-transferases.
NCBI Description
                   [Caenorhabditis elegans]
                   27258
Seq. No.
Contig ID
                   152715 1.R1040
5'-most EST
                   fua701039413.h1
                   27259
Seq. No.
                   152717 1.R1040
Contig ID
5'-most EST
                   sat701004613.hl
Seq. No.
                   27260
                   152747 1.R1040
Contig ID
5'-most EST
                   gsv701056878.h1
Seq. No.
                   27261
Contig ID
                   152768 1.R1040
5'-most EST
                   pcp700992052.hl
Method
                   BLASTX
NCBI GI
                   q1076427
BLAST score
                   174
E value
                   3.0e-24
Match length
                   70
% identity
                   83
NCBI Description
                   ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
                   thaliana
Seq. No.
                   27262
Contig ID
                   152770 1.R1040
                   k11701\overline{2}04316.h2
5'-most EST
                   27263
Seq. No.
Contig ID
                   152790 1.R1040
5'-most EST
                   fde700870510.hl
Method
                   BLASTX
NCBI GI
                   q2398853
BLAST score
                   227
E value
                   4.0e-19
Match length
                   69
% identity
NCBI Description
                   (AB004822) plastid RNA polymerase sigma-subunit
                   [Arabidopsis thaliana]
Seq. No.
                   27264
Contig ID
                   152793 1.R1040
```

fC-qmle700559592q3

BLASTX

% identity

NCBI Description

```
g3169171
NCBI GI
                  887
BLAST score
E value
                  2.0e-95
Match length
                  340
                  51
% identity
                  (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana] >gi 3445213 (AC004786) putative serine
                  carboxypeptidase I [Arabidopsis thaliana]
                  27265
Seq. No.
                  152800 1.R1040
Contig ID
5'-most EST
                  pcp700992101.hl
Method
                  BLASTX
NCBI GI
                  q3080436
BLAST score
                  94
                  2.0e-09
E value
Match length
                  77
                  53
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27266
                  152833 1.R1040
Contig ID
5'-most EST
                  rca700997618.h1
Method
                  BLASTN
                  g3985955
NCBI GI
BLAST score
                  67
                  8.0e-29
E value
Match length
                  271
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  27267
                  .152879 1.R1040
Contig ID
5'-most EST
                  pcp700992237.hl
Method
                  BLASTX
NCBI GI
                  g3881189
BLAST score
                  185
                  6.0e-14
E value
Match length
                  76
% identity
                  49
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
NCBI Description
                  EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
Seq. No.
                  27268
Contig ID
                  152882 1.R1040
5'-most EST
                  jC-gmf102220073d01a1
Method
                  BLASTX
                  g3135269
NCBI GI
BLAST score
                  316
E value
                  4.0e-29
Match length
                  111
```

(AC003058) unknown protein [Arabidopsis thaliana]

5'-most EST

```
27269
Seq. No.
                   152908 1.R1040
Contig ID
5'-most EST
                   pcp700992291.h1
Seq. No.
                   27270
                   152910 1.R1040
Contig ID
                   pcp700992296.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2826900
BLAST score
                   446
E value
                   2.0e-44
Match length
                   135
% identity
NCBI Description
                   (AB004461) DNA polymerase alpha catalytic subunit [Oryza
                   sativa]
Seq. No.
                   27271
Contig ID
                   152911 1.R1040
5'-most EST
                   jC-gmle01810084g05a1
                   BLASTX
Method
NCBI GI
                   g2245095
BLAST score
                   209
                   1.0e-16
E value
Match length
                   66
% identity
                   (Z97343) formyltransferase purU homolog [Arabidopsis
NCBI Description
                   thaliana]
                   27272
Seq. No.
Contig ID
                   152930 1.R1040
                   pcp700992322.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4490316
BLAST score
                   595
E value
                   1.0e-61
Match length
                   156
% identity
NCBI Description
                   (AL035678) nucellin-like protein [Arabidopsis thaliana]
                   27273
Seq. No.
                   152979 1.R1040
Contig ID
5'-most EST
                  pcp700992394.h1
                   27274
Seq. No.
                  152982 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy077g08b1
                  BLASTX
Method
NCBI GI
                  g4567250
BLAST score
                  275
                   3.0e-24
E value
Match length
                  83
% identity
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27275
                  152987 1.R1040
Contig ID
```

gsv701046566.h1

E value

1.0e-19

```
Method
                     BLASTX
  NCBI GI
                     g3868800
  BLAST score
                     340
  E value
                     4.0e-32
  Match length
                     107
  % identity
                     60
                     (AB013603) topoisomerase III beta [Mus musculus]
  NCBI Description
  Seq. No.
                     27276
  Contig ID
                     153000 1.R1040
  5'-most EST
                     pxt700945348.h1
  Method
                     BLASTX
  NCBI GI
                     g2809246
  BLAST score
                     284
  E value
                     4.0e-25
  Match length
                     68
  % identity
  NCBI Description
                     (AC002560) F2401.15 [Arabidopsis thaliana]
  Seq. No.
                     27277
  Contig ID
                     153000 4.R1040
  5'-most EST
                     sat701007226.h2
                     27278
  Seq. No.
  Contig ID
                     153040 1.R1040
  5'-most EST
                     pcp700992508.h1
  Method
                     BLASTN
  NCBI GI
                     g2760172
  BLAST score
                     39
  E value
                     1.0e-12
  Match length
                     135
  % identity
                     82
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MUB3, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     27279
  Contig ID
                     153067 1.R1040
  5'-most EST
                    pcp700992566.hl
  Seq. No.
                     27280
  Contig ID
                     153084 1.R1040
  5'-most EST
                    pcp700992605.h1
  Method
                    BLASTX
  NCBI GI
                     q2244806
  BLAST score
                     144
  E value
                     2.0e-09
  Match length
                    76
  % identity
  NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     27281
  Contig ID
                     153103 1.R1040
  5'-most EST
                    pcp700992649.h1
  Method
                    BLASTX
  NCBI GI
                    q3135693
  BLAST score
                    232
```

Seq. No.

Contig ID

27289

153265_1.R1040

```
89 .
Match length
% identity
                   49
NCBI Description
                   (AF064201) glutathione S-transferase [Gossypium hirsutum]
Seq. No.
                   27282
Contig ID
                   153127 1.R1040
5'-most EST
                   jC-gmle01810020d10a1
                   27283
Seq. No.
Contig ID
                   153150 1.R1040
5'-most EST
                   xpa700798018.h1
                   27284
Seq. No.
                   153188 1.R1040
Contig ID
5'-most EST
                   pcp700992794.hl
                   27285
Seq. No.
Contig ID
                   153207 1.R1040
5'-most EST
                   pcp700992831.hl
Seq. No.
                   27286
Contig ID
                   153246 1.R1040
5'-most EST
                   uC-gmrominsoy154d12b1
Method
                   BLASTX
NCBI GI
                   g3695406
BLAST score
                   580
E value
                   4.0e-60
Match length
                   139
                   80
% identity
NCBI Description
                   (AF096373) similar to isoleucyl-tRNA synthetases
                   [Arabidopsis thaliana]
Seq. No.
                   27287
                   153249 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810051e08a1
Method
                   BLASTX
NCBI GI
                   g3269292
BLAST score
                   164
E value
                   4.0e-11
Match length
                   50
% identity
NCBI Description
                   (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                   27288
                   153250_1.R1040
Contig ID
5'-most EST
                   sat701015386.h1
Method
                   BLASTX
NCBI GI
                   g3548810
BLAST score
                   273
E value
                   4.0e-24
Match length
                   99
% identity
                   (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
```

5'-most EST

 $q56067\overline{3}3$

```
5'-most EST
                   q5058090
Method
                   BLASTX
NCBI GI
                   q3941289
BLAST score
                   354
E value
                   2.0e-33
Match length
                   82
% identity
NCBI Description
                  (AF018093) similarity to SCAMP37 [Pisum sativum]
                   27290
Seq. No.
Contig ID
                   153268 1.R1040
5'-most EST
                   gsv701\overline{0}46031.h1
                   BLASTX
Method
NCBI GI
                   q3861199
BLAST score
                   224
E value
                   6.0e-22
Match length
                   124
% identity
                   46
NCBI Description
                   (AJ235272) 50S RIBOSOMAL PROTEIN L3 (rplC) [Rickettsia
                   prowazekii]
                   27291
Seq. No.
                   153280 1.R1040
Contig ID
                   pcp700993176.h1
5'-most EST
Seq. No.
                   27292
Contig ID
                   153307 1.R1040
5'-most EST
                   sat701010787.h1
                   27293
Seq. No.
Contig ID
                   153307 2.R1040
5'-most EST
                   k11701206563.h1
Seq. No.
                   27294
                   153310 1.R1040
Contig ID
5'-most EST
                   pcp700993030.hl
Seq. No.
                   27295
                   153326 1.R1040
Contig ID
                   zhf700963321.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3023928
BLAST score
                   133
E value
                   4.0e-12
Match length
                   49
% identity
                   67
                   PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3 HOMOLOG)
NCBI Description
                   >gi 2444430 (AF020658) deacetylase [Xenopus laevis]
Seq. No.
                   27296
                   153333 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy033c05b1
Seq. No.
                   27297
                   153344 1.R1040
Contig ID
```

5'-most EST

```
27298
Seq. No.
Contig ID
                   153374 1.R1040
                   jex700\overline{9}08896.h1
5'-most EST
Seq. No.
                   27299
Contig ID
                   153384 1.R1040
5'-most EST
                   jC-qmle01810092b12a1
                   27300
Seq. No.
Contig ID
                   153402 1.R1040
5'-most EST
                   uC-gmflminsoy053c07b1
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   47
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   27301
Contig ID
                   153442 1.R1040
5'-most EST
                   ish701\overline{0}64316.h1
Method
                   BLASTX
NCBI GI
                   q3790587
BLAST score
                   222
E value
                   2.0e-18
Match length
                   92
% identity
                   57
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thalianal
Seq. No.
                   27302
Contig ID
                   153447 1.R1040
5'-most EST
                   pcp700993261.h1
Method
                   BLASTX
NCBI GI
                   q3834307
BLAST score
                   378
E value
                   3.0e-36
Match length
                   100
% identity
NCBI Description
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                   putative protein from Arabidopsis thaliana BAC qb AL021712.
                   ESTs gb N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   27303
Contig ID
                   153451 1.R1040
5'-most EST
                   jex700\overline{9}07782.h1
Seq. No.
                   27304
Contig ID
                   153473 1.R1040 .
5'-most EST
                   g4291688
Seq. No.
                   27305
Contig ID
                   153481 1.R1040
```

pcp700993321.hl

٠, .

```
27306
Seq. No.
                   153504 1.R1040
Contig ID
                   pmv700894323.hl
5'-most EST
Seq. No.
                   27307
                   153543 1.R1040
Contig ID
                   pcp700993431.h1
5'-most EST
                   27308
Seq. No.
Contig ID
                  153552 1.R1040
                   pcp700993446.h1
5'-most EST
Seq. No.
                   27309
Contig ID
                   153564 1.R1040
5'-most EST
                   uC-qmflminsoy098c05b1
Method
                   BLASTX
NCBI GI
                   q3746568
BLAST score
                   506
E value
                   4.0e-51
Match length
                   104
% identity
                   (AF061638) branched-chain alpha-keto acid decarboxylase E1
NCBI Description
                   beta subunit [Arabidopsis thaliana]
                   27310
Seq. No.
Contig ID
                   153574 1.R1040
5'-most EST
                   pcp700993477.h1
                   BLASTX
Method
                   q3075399
NCBI GI
BLAST score
                   173
                   1.0e-12
E value
Match length
                   47
% identity
NCBI Description
                   (AC004484) SF16-like protein [Arabidopsis thaliana]
Seq. No.
                   153575 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}47759.h1
                   27312
Seq. No.
                   153591 1.R1040
Contig ID
5'-most EST
                   zzp700831713.h1
Seq. No.
                   27313
                   153601 1.R1040
Contig ID
5'-most EST
                   bth700846617.h1
                   27314
Seq. No.
Contig ID
                   153621 1.R1040
5'-most EST
                   pcp700993572.h1
                   BLASTX
Method
NCBI GI
                   q2191175
BLAST score
                   223
E value
                   2.0e-18
Match length
                  103
% identity
```

NCBI Description (AF007270) A IG002P16.24 gene product [Arabidopsis

thaliana] 27315 Seq. No. Contig ID 153623 1.R1040 5'-most EST $jex700\overline{9}04779.h1$ Method BLASTX NCBI GI q3445209 BLAST score 266 E value 2.0e-23 Match length 65 % identity NCBI Description (ACO04786) putative serine carboxypeptidase I [Arabidopsis thaliana] Seq. No. 27316 Contig ID 153642 1.R1040 5'-most EST rca700996494.hl Seq. No. 27317 153649 1.R1040 Contig ID 5'-most EST pcp700993619.hl Method BLASTX NCBI GI g3851584 BLAST score 227 1.0e-18 E value Match length . 58 % identity 76 NCBI Description (AF092563) chromosome-associated protein-E [Homo sapiens] Seq. No. 27318 Contig ID 153653 1.R1040 5'-most EST uC-gmrominsoy122b10b1 Seq. No. 27319 Contig ID 153695 1.R1040 5'-most EST uC-qmropic031f04b1 Seq. No. 27320 Contig ID 153713 1.R1040 5'-most EST pcp700995761.h1 Method BLASTN NCBI GI q2564336 BLAST score 120 E value 6.0e-61 Match length 264 % identity NCBI Description Brassica campestris mRNA for Tat binding protein 1, complete cds Seq. No. 27321

Contig ID 153723_1.R1040
5'-most EST pcp700993740.h1
Method BLASTX
NCBI GI g3688209
BLAST score 568

E value 568

E value 2.0e-58

Match length 158

```
% identity
NCBI Description
                  (AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
Seq. No.
                  27322
Contig ID
                  153754 1.R1040
5'-most EST
                  pcp700993803.h1
Seq. No.
                  27323
Contig ID
                  153816 1.R1040
5'-most EST
                  asn701138734.h1
Method
                  BLASTX
NCBI GI
                  g4558462
BLAST score
                  797
E value
                 2.0e-85
Match length
                  194
% identity
                  (AF079404) cell cycle switch protein [Medicago sativa
NCBI Description
                  subsp. X varia]
Seq. No.
                  27324
Contig ID
                  153820 1.R1040
5'-most EST
                  jC-gmro02910040e02a1
                  27325
Seq. No.
                  153850 1.R1040
Contig ID
5'-most EST
                  pxt700942373.hl
Method
                  BLASTX
NCBI GI
                  q3860250
BLAST score
                  408
E value
                  6.0e-40
Match length
                  131
% identity
NCBI Description
                  (AC005824) putative chloroplast prephenate dehydratase
                  [Arabidopsis thaliana]
                  27326
Seq. No.
                  153852 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400040a05a1
Method
                  BLASTX
NCBI GI
                  q114276
BLAST score
                  204
                  6.0e-23
E value
Match length
                  106
% identity
                  55
                  N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
NCBI Description
                  (GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE)
                  (N4-(N-ACETYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE)
                  (AGA) >gi 67759 pir MUHUGD
                  N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26)
                  precursor - human >gi 28534 emb CAA39029 (X55330)
                  N4-(beta-N-acetylglucosaminyl)-L- asparaginase [Homo
                  sapiens] >gi 34760 emb CAA39288 (X55762)
                  glycosylasparaginase precursor (AA -23 to 323) [Homo
                  sapiens] >gi 4557273 ref NP 000018.1 pAGA_
                  aspartylglucosaminidase precursor
```

Seq. No. 27327

```
153861 1.R1040
 Contig ID
5'-most EST
                    pcp700993951.hl
 Seq. No.
                    27328
 Contig ID
                    153867 1.R1040
                    zhf700958665.h1
 5'-most EST
 Seq. No.
                    27329
 Contig ID
                    153873 1.R1040
 5'-most EST
                    pcp700\overline{9}93969.h1
 Seq. No.
                    27330
 Contig ID
                    153879 1.R1040
 5'-most EST
                    pcp700993978.h1
 Seq. No.
                    27331
 Contig ID
                    153895 1.R1040
 5'-most EST
                    pcp700994004.h1
                    27332
 Seq. No.
 Contig ID
                    153919 1.R1040
 5'-most EST
                    uC-qmrominsoy300g11b1
                    27333
 Seq. No.
                    153935 1.R1040
 Contig ID
 5'-most EST
                    rca700999021.hl
 Method
                    BLASTX
 NCBI GI
                    g3924613
 BLAST score
                    227
                    5.0e-27
 E value
 Match length
                    147
 % identity
                    54
 NCBI Description
                    (AF069442) hypothetical protein [Arabidopsis thaliana]
                    >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein
                    [Arabidopsis thaliana]
                    27334
 Seq. No.
 Contig ID
                    153935 2.R1040
 5'-most EST
                    fC-gmro700864959d3
                    27335
 Seq. No.
 Contig ID
                    153938 1.R1040
 5'-most EST
                    pmv700888824.h1
                    27336
 Seq. No.
 Contig ID
                    153941 1.R1040
 5'-most EST
                    uC-gmrominsoy304h12b1
 Seq. No.
                    27337
 Contig ID
                    153941 2.R1040
 5'-most EST
                    jC-gmfl02220113e06d1
 Seq. No.
                    27338
 Contig ID
                    153943 1.R1040
 5'-most EST
                    uC-qmflminsoy010d11b1
```

27339

Seq. No.

NCBI GI

```
153958 1.R1040
 Contiq ID
 5'-most EST
                    pcp700994093.h1
 Seq. No.
                    27340
 Contig ID
                    153988 1.R1040
 5'-most EST
                    jC-gmst02400041b03a1
 Method
                    BLASTX
 NCBI GI
                    g640021
 BLAST score
                    689
                    7.0e-73
 E value
Match length
                    144
 % identity
                    95
NCBI Description
                   (X83695) gamma-tubulin 1 [Zea mays]
Seq. No.
                   27341
Contig ID
                   154029 1.R1040
 5'-most EST
                   smw700\overline{6}46254.h1
Method
                   BLASTX
NCBI GI
                   g4455226
BLAST score
                   286
E value
                   4.0e-42
Match length
                   129
% identity
NCBI Description
                   (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   27342
Contig ID
                   154036 1.R1040
5'-most EST
                   bth700847334.h1
Method
                   BLASTX
NCBI GI
                   g4454006
BLAST score
                   263
E value
                   2.0e-22
Match length
                   181
% identity
NCBI Description
                   (AL035396) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27343
Contig ID
                   154045 1.R1040
5'-most EST
                   pcp700994234.h1
Seq. No.
                   27344
Contig ID
                   154060 1.R1040
5'-most EST
                   dpv701100937.h1
Method
                   BLASTX
NCBI GI
                   g3924603
BLAST score
                   247
E value
                   4.0e-27
Match length
                   99
% identity
NCBI Description
                   (AF069442) putative WD-repeat protein [Arabidopsis
                   thaliana]
Seq. No.
                   27345
Contig ID
                   154068 1.R1040
5'-most EST
                   pcp700994270.h1
Method
                   BLASTX
```

g. t

g1399828

Contig ID

```
BLAST score
                   157
                   1.0e-10
E value
Match length
                   111
% identity
                   39
NCBI Description
                   (U59235) unknown [Synechococcus PCC7942]
Seq. No.
                   27346
Contig ID
                   154071 1.R1040
5'-most EST
                   pcp700994273.h1
Seq. No.
                   27347
Contig ID
                   154073 1.R1040
5'-most EST
                   epx701\overline{1}07468.h1
Method
                   BLASTX
NCBI GI
                   g3329368
BLAST score
                   261
E value
                   7.0e-23
Match length
                   110
% identity
NCBI Description
                   (AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                   27348
                   154081 1.R1040
Contig ID
5'-most EST
                   pcp700994285.h1
                   BLASTN
Method
NCBI GI
                   g2262200
BLAST score
                   505
                   0.0e+00
E value
                   819
Match length
% identity
                   93
                   Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete
NCBI Description
                   27349
Seq. No.
                   154089 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}62711.h1
Method
                   BLASTX
NCBI GI
                   g3080414
BLAST score
                   476
                   1.0e-47
E value
                   120
Match length
% identity
NCBI Description
                   (AL022604) putative protein [Arabidopsis thaliana]
                   27350
Seq. No.
                   154097 1.R1040
Contiq ID
5'-most EST
                   sat701008351.hl
Method
                   BLASTX
NCBI GI
                   g3549626
BLAST score
                   228
                   6.0e-19
E value
Match length
                   106
% identity
                   45
NCBI Description
                   (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.
                   27351
```

154100 1.R1040

```
5'-most EST
                   pcp700994314.h1
Seq. No.
                   27352
Contig ID
                   154104 1.R1040
                   pcp700\overline{9}94319.h1
5'-most EST
Method
                   BLASTX
                   q3860251
NCBI GI
BLAST score
                   310
                   9.0e-29
E value
Match length
                   90
% identity
NCBI Description
                   (AC005824) putative permease [Arabidopsis thaliana]
Seq. No.
                   27353
Contig ID
                   154108 1.R1040
5'-most EST
                   fC-qmle7000741294a1
Method
                   BLASTX
NCBI GI
                   q3021270
BLAST score
                   687
E value
                   2.0e-72
Match length
                   191
% identity
                   69
NCBI Description
                   (AL022347) serine/threonine kinase -like protein
                   [Arabidopsis thaliana]
Seq. No.
                   27354
Contig ID
                   154128 1.R1040
5'-most EST
                   pcp700\overline{9}94357.h1
Seq. No.
                   27355
Contig ID
                   154143 1.R1040
5'-most EST
                   uC-qmrominsoy125f07b1
Method
                   BLASTX
NCBI GI
                   q2160694
BLAST score
                   927
E value
                   1.0e-100
Match length
                   231
% identity
NCBI Description
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
                   thaliana]
                   27356
Seq. No.
Contig ID
                   154158 1.R1040
5'-most EST
                   pcp700994392.h1
Seq. No.
                   27357
Contig ID
                   154165 1.R1040
5'-most EST
                   pcp700994404.h1
Method
                   BLASTX
NCBI GI
                   q3183077
BLAST score
                   227
E value
                   4.0e-28
Match length
                   156
% identity
                   48
NCBI Description
                   PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE
                   (DHNA-OCTAPRENYLTRANSFERASE) >gi 1653114 dbj BAA18030
```

(D90911) menaquinone biosynthesis protein [Synechocystis

```
sp.]
Seq. No.
                   27358
Contig ID
                   154211 1.R1040
5'-most EST
                  pcp700994466.hl
Method
                   BLASTX
NCBI GI
                   q4115938
BLAST score
                   830
E value
                   4.0e-89
Match length
                   225
% identity
                   74
NCBI Description
                   (AF118223) contains similarity several bacterial
                   glutathione-regulated potassium efflux system proteins
                   [Arabidopsis thaliana]
Seq. No.
                   27359
Contig ID
                   154239 1.R1040
5'-most EST
                   leu701152401.hl
Method
                  BLASTX
NCBI GI
                   q1076580
BLAST score
                   242
E value
                   1.0e-20
Match length
                   72
% identity
                  alcohol dehydrogenase homolog ADH3b - tomato
NCBI Description
                  >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH
                   {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
                  cherry, Peptide, 390 aa] [Lycopersicon esculentum]
Seq. No.
                   27360
                  154260 1.R1040
Contig ID
5'-most EST
                  pmv700893490.hl
Method
                  BLASTX
NCBI GI
                  a3947613
BLAST score
                   205
                   2.0e-16
E value
Match length
                  82
% identity
                   (AL023828) cDNA EST EMBL: M89008 comes from this gene; cDNA
NCBI Description
                  EST yk282d3.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  27361
Contig ID
                  154271 1.R1040
5'-most EST
                  pcp700994568.h2
Seq. No.
                  27362
                  154327 1.R1040
Contig ID
5'-most EST
                  fua701\overline{0}37573.h1
Method
                  BLASTX
                  g3688173
NCBI GI
BLAST score
                  461
                  4.0e-46
E value
Match length
                  121
% identity
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
```

27,3,63

Seq. No.

```
Contig ID
                   154332 1.R1040
5'-most EST
                   zhf700960473.h1
Method
                  BLASTN
NCBI GI
                   q4417264
BLAST score
                   39
                   1.0e-12
E value
Match length
                   87
                   86
% identity
NCBI Description 'Arabidopsis thaliana chromosome II BAC F7D8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                  27364
Seq. No.
                  154344 1.R1040
Contig ID
5'-most EST
                  pcp700994703.hl
Method
                  BLASTX
NCBI GI
                  g2109293
BLAST score
                   450
E value
                   4.0e-45
Match length
                  103
% identity
                  81
NCBI Description
                  (U97568) serine/threonine protein kinase [Arabidopsis
Seq. No.
                  27365
Contig ID
                  154349 1.R1040
5'-most EST
                  pcp700994708.hl
Seq. No.
                  27366
Contig ID
                  154358 1.R1040
5'-most EST
                  pcp700994724.h1
Seq. No.
                  27367
Contig ID
                  154376 1.R1040
5'-most EST
                  pcp700994752.h1
Seq. No.
                  27368
Contig ID
                  154382 1.R1040
5'-most EST
                  pcp700994763.hl
Method
                  BLASTX
NCBI GI
                  q3004564
BLAST score
                  377
E value
                  4.0e-36
Match length
                  150
% identity
NCBI Description
                   (AC003673) putative receptor Ser/Thr protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  27369
Contig ID
                  154389 1.R1040
5'-most EST
                  pcp700994778.h1
Method
                  BLASTX
NCBI GI
                  q1172633
BLAST score
                  420
E value
                  1.0e-41
Match length
                  101
% identity
```

NCBI Description PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5

family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

```
27370
 Seq. No.
                    154397 1.R1040
 Contig ID
 5'-most EST
                    zhf700951878.h1
 Seq. No.
                   27371
                   154398 1.R1040
 Contig ID
 5'-most EST
                   pxt700943565.hl
                   27372
 Seq. No.
 Contig ID
                   154403 1.R1040
 5'-most EST
                   rca700999409.h1
 Method
                   BLASTX
                   q4539343
 NCBI GI
 BLAST score
                    255
                    6.0e-22
 E value
Match length
                    94
                   57
 % identity
                    (AL035539) putative protein [Arabidopsis thaliana]
 NCBI Description
                   27373
 Seq. No.
                   154436 1.R1040
 Contig ID
 5'-most EST
                   xpa700796580.h1
Method
                   BLASTX
                   g3820614
 NCBI GI
 BLAST score
                   333
 E value
                    3.0e-31
Match length
                   110
 % identity
                   59
NCBI Description (AF094516) E1-like protein [Homo sapiens]
 Seq. No.
                   27374
                   154450 1.R1040
. Contig ID
 5'-most EST
                   dpv701\overline{0}97012.h1
 Seq. No.
                   27375
 Contig ID
                   154496 1.R1040
 5'-most EST
                   uC-gmronoir036c08b1
 Seq. No.
                   27376
Contig ID
                   154499 1.R1040
 5'-most EST
                   pcp700994952.hl
Method
                   BLASTX
NCBI GI
                   q1170619
BLAST score
                   149
E value
                   5.0e-20
Match length
                   138
 % identity
NCBI Description
                   KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
                   kinesin-related protein katA - Arabidopsis thaliana
                   >gi 303502 dbj BAA01972 (D11371) kinesin-like motor
                   protein heavy chain [Arabidopsis thaliana]
```

protein katA [Arabidopsis thaliana]

>gi 2911084 emb CAA17546 (AL021960) kinesin-related

.Contig ID

:· `

```
Seq. No.
                    27377
 Contig ID
                    154509 1.R1040
 5'-most EST
                    kmv700741667.h1
 Seq. No.
                    27378
 Contig ID
                    154517 1.R1040
 5'-most EST
                    jex700\overline{9}03173.h1
 Seq. No.
                    27379
 Contig ID
                   154524 1.R1040
 5'-most EST
                   uC-gmropic016c08b1
Method
                   BLASTX
NCBI GI
                   g733554
BLAST score
                    156
E value
                   1.0e-10
Match length
                   58
 % identity
                   48
NCBI Description
                   (U23450) similar to RNA-binding protein [Caenorhabditis
                   elegans]
Seq. No.
                   27380
Contig ID
                   154524 2.R1040
5'-most EST
                   vzy700755643.h1
Seq. No.
                   27381
Contig ID
                   154530 1.R1040
5'-most EST
                   uC-gmflminsoy100g09b1
Seq. No.
                   27382
Contig ID
                   154530 2.R1040
5'-most EST
                   jC-gmro02910056f04a1
Seq. No.
                   27383
Contig ID
                   154539 1.R1040
5'-most EST
                   sat701\overline{0}05972.h1
Method
                   BLASTX
NCBI GI
                   g1001135
BLAST score
                   273
E value
                   3.0e-24
Match length
                   104
% identity
                   52
NCBI Description (D64001) acetolactate synthase [Synechocystis sp.]
Seq. No.
                   27384
Contig ID
                   154545 1.R1040
5'-most EST
                   uC-gmflminsoy075c04b1
Method
                   BLASTX
NCBI GI
                   g4512704
BLAST score
                   146
E value
                   3.0e-09
Match length
                  117
% identity
                  29
NCBI Description
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  27385
```

154557 1.R1040

```
5'-most EST
                   jC-gmle01810055c05a1
Seq. No.
                   27386
                  154558 1.R1040
Contig ID
5'-most EST
                  kmv700737854.h1
Method
                  BLASTX
NCBI GI
                  q4239696
BLAST score
                  266
E value
                   3.0e-23
Match length
                   63
% identity
                  73
                   (AJ132767) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  27387
Seq. No.
Contig ID
                  154562 1.R1040
5'-most EST
                  epx701110279.h1
                  27388
Seq. No.
Contig ID
                  154564 1.R1040
5'-most EST
                  uC-gmronoir014g04b1
Method
                  BLASTX
NCBI GI
                  g4539009
BLAST score
                  525
                  3.0e-53
E value
Match length
                  169
% identity
                  58
                  (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27389
                  154569 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220148h03a1
Method
                  BLASTX
NCBI GI
                  q4454011
BLAST score
                  195
E value
                  8.0e-15
Match length
                  85
% identity
NCBI Description
                  (AL035396) putative protein [Arabidopsis thaliana]
                  27390
Seq. No.
Contig ID
                  154588 1.R1040
5'-most EST
                  zhf700963125.h1
                  27391
Seq. No.
Contig ID
                  154595 1.R1040
5'-most EST
                  pcp700995152.hl
Method
                  BLASTX
NCBI GI
                  g3025189
BLAST score
                  147
E value
                  5.0e-09
Match length
                  57
% identity
                  42
NCBI Description
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                  >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
```

27392

Seq. No.

Seq. No.

Contig ID

27400

154731 1.R1040

```
154597 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014d10d1
Seq. No.
                   27393
Contig ID
                   154610 1.R1040
                  pcp700995171.h1
5'-most EST
Seq. No.
                   27394
Contig ID
                   154619 1.R1040
5'-most EST
                  pmv700892329.h1
Seq. No.
                   27395
Contig ID
                   154634 1.R1040
5'-most EST
                   jC-gmle01810059f08a1
Method
                  BLASTX
NCBI GI
                  q1362781
BLAST score
                   154
E value
                   1.0e-09
Match length
                   121
                   20
% identity
                  cytokine inducible nuclear protein C193 - human
NCBI Description
                  >gi 793841 emb CAA58676 (X83703) nuclear protein [Homo
                  sapiens]
                  27396
Seq. No.
Contig ID
                  154635 1.R1040
5'-most EST
                  pcp700995205.hl
                  BLASTX
Method
NCBI GI
                  g3628757
BLAST score
                  181
E value
                   1.0e-13
                  75
Match length
% identity
NCBI Description (AF038007) FIC1 [Homo sapiens]
Seq. No.
Contig ID
                  154638 1.R1040
5'-most EST
                  asn701\overline{1}36321.h1
                  27398
Seq. No.
Contig ID
                  154708 1.R1040
5'-most EST
                  pcp700995314.h1
Method
                  BLASTX
NCBI GI
                  q3599489
BLAST score
                  1859
E value
                  0.0e + 00
Match length
                  491
% identity
NCBI Description
                  (AF085148) 3-oxoacyl-[acyl-carrier-protein] synthase
                   [Capsicum chinense]
                  27399
Seq. No.
Contig ID
                  154708 2.R1040
5'-most EST
                  leu701154660.h1
```

Match length

```
5'-most EST
                   gsv701045552.h1
                                           v, **
Method
                   BLASTX
                   g2245115
NCBI GI
BLAST score
                   208
                   2.0e-16
E value
Match length
                   126
% identity
                   39
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   27401
Seq. No.
                   154732 1.R1040
Contig ID
5'-most EST
                   pcp700995353.hl
                   27402
Seq. No.
                   154732 2.R1040
Contig ID
                   asn701\overline{1}35077.h1
5'-most EST
                   27403
Seq. No.
                   154736 1.R1040
Contig ID
                   pcp700995357.hl
5'-most EST
                   27404
Seq. No.
                   154754 1.R1040
Contig ID
                   epx701\overline{1}08951.h1
5'-most EST
                   BLASTX
Method
                   g3327389
                                                                 . ..
NCBI GI
BLAST score
                   665
                   5.0e-70
E value
Match length
                   145
                   81
% identity
                   (AC004483) putative DNA replication licensing factor, mcm5
NCBI Description
                   [Arabidopsis thaliana]
                   27405
Seq. No.
                   154770 1.R1040
Contig ID
                   uC-gmronoir019f07b1
5'-most EST
Method
                   BLASTX
                   q421980
NCBI GI
BLAST score
                   363
E value
                   1.0e-34
Match length
                   87
% identity
                   76
                  transforming protein (myb3) - barley
NCBI Description
                   >gi 19059 emb CAA50223 (X70878) MybHv33 [Hordeum vulgare]
                   27406
Seq. No.
Contig ID
                   154789 1.R1040
5'-most EST
                   pcp700995433.hl
                   27407
Seq. No.
                   154801 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118d08b1
Method
                   BLASTX
                   q4530126
NCBI GI
BLAST score
                   413
                   2.0e-43
E value
```

% identity

```
% identity
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                  27408
Seq. No.
                  154812 1.R1040
Contig ID
5'-most EST
                  gsf700698449.h1
                  27409
Seq. No.
Contig ID
                  154816 1.R1040
5'-most EST
                  pcp700995472.hl
Method
                  BLASTX
                  g3785977
NCBI GI
BLAST score
                  357
E value
                  5.0e - 34
Match length
                  120
% identity
                  53
                  (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  27410
                  154822 1.R1040
Contig ID
5'-most EST
                  sat701004175.hl
Method
                  BLASTX
NCBI GI
                  q3250675
BLAST score
                  754
E value
                  5.0e-80
Match length
                  342
% identity
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  154833 1.R1040
5'-most EST
                  jex700905056.h1
                  27412
Seq. No.
Contig ID
                  154836 1.R1040
5'-most EST
                  uC-gmropic063d08b1
Seq. No.
Contig ID
                  154848 1.R1040
5'-most EST
                  smw700646161.h1
Seq. No.
                  27414
                  154848 2.R1040
Contig ID
5'-most EST
                  pcp700995515.h1
                  27415
Seq. No.
Contig ID
                  154849 1.R1040
5'-most EST
                  g4303828
Method
                  BLASTX
NCBI GI
                  g4455369
BLAST score
                  284
E value
                  6.0e-25
Match length
                  85
```

NCBI Description (AL035524) hypothetical protein [Arabidopsis thaliana]

BLAST score

```
Seq. No.
                  27416
                  154849 2.R1040
Contig ID
5'-most EST
                  fC-gmro700564066z3
Method
                  BLASTX
                  q4455369
NCBI GI
BLAST score
                  646
                  2.0e-67
E value
                  170
Match length
% identity
                  74
                  (AL035524) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27417
                  154866 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy077a09b1
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                . 41
E value
                  1.0e-13
Match length
                  158
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  27418
                  154874 1.R1040
Contig ID ''
5'-most EST
                  jC-qmle01810073e12a1
Method
                  BLASTN
NCBI GI
                  q1707656
BLAST score
                  53
E value
                  7.0e-21
Match length
                  125
% identity
NCBI Description P.sativum mRNA for DnaJ-like protein
                  27419
Seq. No.
Contig ID
                  154904 1.R1040
5'-most EST
                  kmv700743355.h1
                  27420
Seq. No.
Contig ID
                  154940 1.R1040
5'-most EST
                  jex700906705.hl
Seq. No.
                  27421
Contig ID
                  154955 1.R1040
5'-most EST
                  jC-gmro02910074d04a1
                  27422
Seq. No.
Contig ID
                  154980 1.R1040
5'-most EST
                  hrw701061966.hl
                  27423
Seq. No.
Contig ID
                  154995 1.R1040
5'-most EST
                  pcp700995712.h1
Method
                  BLASTX
NCBI GI
                  q3176684
```

Contig ID

```
E value
                   1.0e-10
Match length
                   77
% identity
                   44
                   (AC003671) Contains similarity to equilibratiave nucleoside
NCBI Description
                   transporter 1 gb U81375 from Homo sapiens. ESTs gb N65317,
                   gb T20785, gb AA586285 and gb AA712578 come from this gene.
                   [Arabidopsis thaliana]
                  27424
Seq. No.
                 _ 155009 1.R1040
Contig ID
                  zhf700962113.h1
5'-most EST
                  BLASTN
Method
                  g3116019
NCBI GI
BLAST score
                   208
E value
                   1.0e-113
Match length
                   331
                   91
% identity
                  Pisum sativum mRNA for ftsZ gene
NCBI Description
                   27425
Seq. No.
Contig ID
                   155013 1.R1040
5'-most EST
                   fC-qmse700842410f1
Method
                  BLASTX
NCBI GI
                   q2492515
BLAST score ...
                   148
                   2.0e-09
E value
Match length
                   39
% identity
NCBI Description
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
                   >qi 2129924 pir S58298 ATPase - pepper (fragment)
                   >gi_929013_emb_CAA62084 (X90472) ATPase [Capsicum annuum]
Seq. No.
                   27426
Contig ID
                   155014 1.R1040
5'-most EST
                  pcp700995734.h1
Seq. No.
                   27427
Contig ID
                   155027 1.R1040
5'-most EST
                  pcp700995753.h1
Method
                  BLASTX
NCBI GI
                   q2262116
BLAST score
                   155
E value
                   5.0e-10
Match length
                   131 ·
% identity
NCBI Description
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
Contig ID
                   155028 1.R1040
5'-most EST
                  gsv701\overline{0}50132.h1
                   27429
Seq. No.
Contig ID
                   155063 1.R1040
5'-most EST
                  pcp700995804.h1
                   27430
Seq. No.
```

155066 1.R1040

```
5'-most EST
                   pcp700995808.h1
Method
                   BLASTX
NCBI GI
                   q3550982
BLAST score
                   568
E value
                   1.0e-58
Match length
                   127
% identity
NCBI Description
                   (AB010690) mutM homologue-1 [Arabidopsis thaliana]
Seq. No.
                   27431
                   155084 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220132aa08a1
Method
                   BLASTX
NCBI GI
                   g3426037
BLAST score
                   518
E value
                   1.0e-52
Match length
                   161
% identity
                   63
                   (ACO05168) putative ABC transporter protein [Arabidopsis
NCBI Description
Seq. No.
                   27432
Contig ID
                   155141 1.R1040
5'-most EST
                   kmv700737722.h1
Method
                   BLASTX
                   g3776557
NCBI GI-
BLAST score
                   319
E value
                   2.0e-29
Match length
                   112
% identity
NCBI Description
                   (AC005388) Contains similarity to gi 2924495 hypothetical
                   protein Rv1920 from Mycobacterium tuberculosis genome
                   gb AL022020. [Arabidopsis thaliana]
Seq. No.
                   27433
Contig ID
                   155145 1.R1040
5'-most EST
                   kmv700739054.h1
Seq. No.
                   27434
Contig ID
                   155146 1.R1040
5'-most EST
                   q43976\overline{5}9
Seq. No.
                   27435
Contig ID
                   155156 1.R1040
5'-most EST
                   kmv700737739.h1
Seq. No.
                   27436
Contig ID
                   155165 1.R1040
5'-most EST
                  gsv701046071.hl
Method
                  BLASTX
NCBI GI
                  q3005590
BLAST score
                  215
E value
                   3.0e-17
Match length
                  50
% identity
NCBI Description (AF051326) rRNA methylase [Arabidopsis thaliana]
```

Seq. No.

```
27437
Seq. No.
                 155167 1.R1040
Contig ID
                  k11701\overline{2}13878.h1
5'-most EST
Seq. No.
                   27438
                   155174 1.R1040
Contig ID
                  kmv700737763.h1
5'-most EST
                   27439
Seq. No.
                   155198 1.R1040
Contig ID
5'-most EST
                   kmv700737793.h1
                  BLASTX
Method
                  g3047111
NCBI GI
BLAST score
                   271
E value
                   5.0e-35
Match length
                   171
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27440
Contig ID
                   155214 1.R1040
                   kmv700737815.h1
5'-most EST
Seq. No.
                  27441
Contig ID
                  155218 1.R1040
5'-most EST
                  zpv700762681.hl
                  27442
Seq. No.
Contig ID
                   155247 1.R1040
5'-most EST
                   kmv700737967.hl
Method
                  BLASTX
NCBI GI
                  g3184061
BLAST score
                  143
E value
                   3.0e-09
Match length
                  77
% identity
NCBI Description
                   (AL023776) atp dependent helicase [Schizosaccharomyces
                  pombe]
                  27443
Seq. No.
Contig ID
                  155267 1.R1040
5'-most EST
                  sat701009238.h1
Method
                  BLASTX
NCBI GI
                  q4388717
BLAST score
                  821
E value
                   4.0e-88
Match length
                  199
% identity
NCBI Description
                   (AC006413) putative nuclear phosphoprotein (contains
                  multiple TPR repeats prosite:QDOC50005) [Arabidopsis
                  thaliana]
                  27444
Seq. No.
Contig ID
                  155284 1.R1040
5'-most EST
                  jsh701068504.h1
```

Contiq ID

5'-most EST

```
155297 1.R1040
Contig ID
                   kmv700737947.hl
5'-most EST
Seq. No.
                   27446
                   155305_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810082g07a1
                   BLASTX
Method
                   g1172586
NCBI GI
BLAST score
                   502
E value
                   4.0e-91
Match length
                   384
% identity
                   43
                   POLYPHENOL OXIDASE A1 PRECURSOR (PPO) (CATECHOL OXIDASE)
NCBI Description
                   >gi 22029 emb CAA77764 (Z11702) polyphenol oxidase [Vicia
                   27447
Seq. No.
Contiq ID
                   155318 1.R1040
5'-most EST
                   zsg701127589.h1
Seq. No.
                   27448
Contig ID
                   155318 2.R1040
5'-most EST
                   zzp700836030.h1
                   27449
Seq. No.
Contig ID
                   155334 1.R1040
5'-most EST
                   kmv700738015.h1
                   27450
Seq. No.
Contig ID
                   155340 1.R1040
5'-most EST
                  xpa700795933.h1
Seq. No.
                   27451
Contig ID
                   155347 1.R1040
5'-most EST
                   zhf700962131.h1
                   27452
Seq. No.
Contig ID
                   155347 2.R1040
5'-most EST
                  k11701215047.h1
                   27453
Seq. No.
Contig ID
                   155351 1.R1040
5'-most EST
                   kmv700738039.h1
Method
                  BLASTX
NCBI GI
                  q416651
BLAST score
                   328
                   7.0e-31
E value
                  93
Match length
% identity
                   71
NCBI Description
                  PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
                   PCNT103) >gi_100301_pir__S16269 auxin-induced protein
                   (clone pCNT103) - common tobacco >gi_19791_emb_CAA39704_
                   (X56263) auxin-induced protein [Nicotiana tabacum]
Seq. No.
                  27454
```

155406 1.R1040 kmv700738134.h1

Match length

```
Method
                  BLASTX
NCBI GI
                  g3293547
BLAST score
                  159
E value
                  1.0e-10
Match length
                  120
% identity
                  33
NCBI Description
                  (AF072709) putative oxidoreductase [Streptomyces lividans]
Seq. No.
                  27455
Contig ID
                  155415 1.R1040
5'-most EST
                  g5607167
Method
                  BLASTX
NCBI GI
                  g3738298
BLAST score
                  440
E value
                  6.0e-43
Match length
                  346
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  >gi 4249394 (AC006072) unknown protein [Arabidopsis
                  thaliana]
                  27456
Seq. No.
Contig ID
                  155437 1.R1040
5'-most EST
                  zhf700964234.h1
Seq. No. -
                  27457
Contig ID
                  155438 1.R1040
5'-most EST
                  kmv700738178.h1
Method
                  BLASTX
NCBI GI
                  q3176726
BLAST score
                  243
E value
                  5.0e-21
Match length
                  73
% identity
NCBI Description
                  (AC002392) putative serine proteinase [Arabidopsis
                  thaliana]
Seq. No.
                  27458
Contig ID
                  155458 1.R1040
5'-most EST
                  kmv700738215.h1
Method
                  BLASTX
NCBI GI
                  q4559332
BLAST score
                  198
                  3.0e-15
E value
Match length
                  44
% identity
NCBI Description
                  (AC007087) putative phosphoenolpyruvate carboxylase
                  [Arabidopsis thaliana]
                  27459
Seq. No.
Contig ID
                  155462 1.R1040
5'-most EST
                  kmv700738220.h1
Method
                  BLASTX
NCBI GI
                  q4006868
BLAST score
                  330
E value
                  3.0e - 31
```

Match length

```
76 .
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   27460
Seq. No.
                   155479 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910034d07a1
Method
                   BLASTX
NCBI GI
                   g1652280
                   293
BLAST score
                   2.0e-26
E value
                   143
Match length
% identity
                   44
NCBI Description (D90904) ribonuclease II [Synechocystis sp.]
Seq. No.
                   27461
                   155489 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}30346.h1
                   27462
Seq. No.
Contig ID
                   155508 1.R1040
5'-most EST
                   kmv700738303.h1
                   27463
Seq. No.
                   155526 1.R1040
Contig ID
5'-most EST
                   kmv700740217.h1
                   27464
Seq. No.
                   155552 1.R1040
Contig ID
5'-most EST
                   zhf700962503.h1
                   27465
Seq. No.
Contig ID
                   155557 1.R1040
5'-most EST
                   kmv700738379.h1
                   27466
Seq. No.
                   155560 1.R1040
Contig ID
5'-most EST
                   kl1701215236.hl
                   27467
Seq. No.
                   155560 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810028f10a1
Method
                   BLASTX
NCBI GI
                   g2828290
BLAST score
                   313
E value
                   1.0e-28
Match length
                   116
% identity
NCBI Description (AL021687) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                   27468
                   155564 1.R1040
Contig ID
                   pmv700888237.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1171577
BLAST score
                   296
E value
                   6.0e-40
```

5'-most EST

```
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                   27469
                   155584 1.R1040
Contig ID
5'-most EST
                   kmv700738433.h1
Seq. No.
                   27470
                   155593 1.R1040
Contig ID
5'-most EST
                   kmv700738455.h1
Seq. No.
                   27471
                   155608 1.R1040
Contig ID
5'-most EST
                   kmv700739961.h1
Seq. No.
                   27472
Contig ID
                   155667 1.R1040
                   jC-gmle01810091f05a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4508076
BLAST score
                   168
E value
                   8.0e-12
Match length
                   100
% identity
                   33
NCBI Description
                   (AC005882) 55659 [Arabidopsis thaliana]
Seq. No.
                   27473
                   155687 1.R1040
Contig ID
                   jsh701\overline{0}68458.h1
5'-most EST
Seq. No.
                   27474
Contig ID
                   155706 1.R1040
5'-most EST
                   kmv700738615.h1
Seq. No.
                   27475
Contig ID
                   155720 1.R1040
                   fua701\overline{0}39127.h1
5'-most EST
Seq. No.
                   27476
Contig ID
                   155750 1.R1040
5'-most EST
                   k11701\overline{2}14463.h1
Method
                   BLASTX
NCBI GI
                   q1546694
BLAST score
                   528
E value
                   8.0e-54
Match length
                   144
% identity
NCBI Description
                   (X98806) peroxidase ATP20a [Arabidopsis thaliana]
Seq. No.
                   27477
Contig ID
                   155815 1.R1040
5'-most EST
                   kmv700738766.h1
Seq. No.
                   27478
Contig ID
                   155874 1.R1040
```

kmv700738846.h1

E value

```
Seq. No.
                  27479
Contig ID
                  155883 1.R1040
5'-most EST
                  epx701107287.h1
Method
                  BLASTX
                  q3135611
NCBI GI
BLAST score
                  221
                   5.0e-18
E value
Match length
                  119
% identity
NCBI Description
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
                  27480
Seq. No.
                  155897 1.R1040
Contig ID
                  kmv700738875.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367519
BLAST score
                  463
E value
                   3.0e-46
Match length
                  139
% identity
NCBI Description
                   (AC004392) Contains similarity to gb U51898
                  Ca2+-independent phospholipase A2 from Rattus norvegicus.
                  [Arabidopsis thaliana]
Seq. No.
                  27481
Contig ID
                  155911 1.R1040
5'-most EST
                  uC-gmrominsoy174a06b1
Method
                  BLASTX
NCBI GI
                  g3859112
BLAST score
                  247
E value
                  3.0e-22
Match length
                  88
% identity
NCBI Description
                  (AF031607) male sterility MS5 [Arabidopsis thaliana]
Seq. No.
Contig ID
                  155924 1.R1040
5'-most EST
                  uC-gmronoir051d06b1
                  27483
Seq. No.
Contig ID
                  155994 1.R1040
5'-most EST
                  kmv700739006.h1
Method
                  BLASTX
NCBI GI
                  g2244912
BLAST score
                  265
E value
                  2.0e-29
Match length
                  142
% identity
NCBI Description (Z97339) similar to transketolase [Arabidopsis thaliana]
Seq. No.
                  27484
Contig ID
                  155996 1.R1040
5'-most EST
                  kmv700739008.h1
Method
                  BLASTX
NCBI GI
                  q3859944
BLAST score
                  172
```

4.0e-12

% identity

```
Match length
                   47
                   70
% identity
                   (AF084570) FKBP12 interacting protein [Arabidopsis
NCBI Description
                   thaliana]
                   27485
Seq. No.
                   155996 2.R1040
Contig ID
                   smc700\overline{7}46270.h1
5'-most EST
                   27486
Seq. No.
                   156013 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}46457.h1
                   27487
Seq. No.
Contig ID
                   156019 1.R1040
5'-most EST
                   fC-gmle700739040a1
Method
                   BLASTX
                   g3450842
NCBI GI
BLAST score
                   612
E value
                   1.0e-63
Match length
                   128
% identity
                   89
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
Seq. No.
                   27488
                   156091 1.R1040
Contig ID
5'-most EST
                   fC-gmle700739163a1
Method
                   BLASTX
NCBI GI
                   g3122671
BLAST score
                   702
E value
                   2.0e-74
Match length
                   145
% identity
                   86
                  HYPOTHETICAL RAE1-LIKE PROTEIN >gi 2129676 pir S71241
NCBI Description
                   probable export protein - Arabidopsis thaliana >gi 1297188
                   (U53501) Theoretical protein with similarity to Swiss-Prot
                   Accession Number P41838 poly A+ RNA export protein
                   [Arabidopsis thaliana]
Seq. No.
                   27489
                   156136 1.R1040
Contig ID
5'-most EST
                   pxt700940920.h1
Seq. No.
                   27490
                   156216 1.R1040
Contig ID
5'-most EST
                   kmv700739404.h1
                   27491
Seq. No.
                   156217 1.R1040
Contig ID
5'-most EST
                   kmv700739405.h1
Method
                   BLASTX
NCBI GI
                   g2262158
BLAST score
                   408
                   6.0e-40
E value
Match length
                   114
```

```
(AC002329) putative mitochondrial phosphate translocator
 NCBI Description
                   protein [Arabidopsis thaliana]
                   27492
 Seq. No.
                   156223 1.R1040
 Contig ID
                   awf700840272.hl
 5'-most EST
                   27493
Seq. No.
                   156256 1.R1040
 Contig ID
                   kmv700741147.h1
 5'-most EST
                   27494
 Seq. No.
                   156259 1.R1040
 Contig ID
 5'-most EST
                   kmv700739469.h1
 Method
                   BLASTX
                   g4510389
NCBI GI
 BLAST score
                   479
E value
                   2.0e-48
Match length
                   128
 % identity
                   72
NCBI Description
                   (AC007017) putative solute carrier protein [Arabidopsis
                   thaliana]
Seq. No.
                   27495
Contig ID
                   156263 1.R1040
 5'-most EST
                   rca700998391.h1
Method
                   BLASTX
NCBI GI
                   q3334667
BLAST score
                   138
E value
                   1.0e-08
Match length
                   36
 % identity
NCBI Description
                   (Y10493) putative cytochrome P450 [Glycine max]
Seq. No.
                   27496
Contig ID
                   156267 1.R1040
5'-most EST
                   fde700875994.h1
                   27497
Seq. No.
Contig ID
                   156267 2.R1040
5'-most EST
                   fC-gmle700739489a1
Seq. No.
                   27498
Contig ID
                   156285 1.R1040
 5'-most EST
                   awf700836661.hl
Method
                   BLASTX
NCBI GI
                   q1076318
BLAST score
                   219
E value
                   3.0e-18
Match length
                   78
% identity
NCBI Description
                   dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
                   precursor - Arabidopsis thaliana (fragment)
                   >gi 559395 emb CAA86300 (Z46230) dihydrolipoamide
                   acetyltransferase (E2) subunit of PDC [Arabidopsis
```

thalianal

Method

BLASTX

```
Seq. No.
                   27499
Contig ID
                   156287 1.R1040
5'-most EST
                   kmv700739545.h1
Method
                   BLASTX
NCBI GI
                   g3377803
BLAST score
                   191
                   3.0e-14
E value
Match length
                   51
% identity
                   63
                   (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
                   27500
Seq. No.
Contig ID
                   156292 1.R1040
5'-most EST
                   uC-gmrominsoy198c07b1
Method
                   BLASTX
NCBI GI
                   q3935168
BLAST score
                   1100
E value
                   1.0e-120
Match length
                   281
% identity
                   79
                   (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27501
                   156301 1.R1040
Contig ID
5'-most EST
                   g5677515
Method
                   BLASTX
NCBI GI
                   g3236235
BLAST score
                   302
E value
                   3.0e-27
Match length
                   88
% identity
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
                   >qi 4056501 (AC005896) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   27502
Contig ID
                   156305 1.R1040
5'-most EST
                   leu701145416.h1
Seq. No.
                   27503
                   156309 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810009h02a1
Method
                   BLASTX
NCBI GI
                   q1184075
BLAST score
                   715
E value
                   2.0e-75
Match length
                   349
% identity
NCBI Description
                   (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
                   >gi_1587673 prf 2207203A Cf-2 gene [Lycopersicon
                   esculentum]
Seq. No.
                   27504
Contig ID
                   156316 1.R1040
                   kmv700739687.h1
5'-most EST
```

BLAST score

```
NCBI GI
                   g3402689
BLAST score
                   303
                   6.0e-28
E value ·
Match length
                   81
% identity
                   73
                   (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                   27505
Seq. No.
                   156338 1.R1040
Contig ID
5'-most EST
                   leu701154128.h1
                   27506
Seq. No.
Contig ID
                   156345 1.R1040
5'-most EST
                   g5605837
Seq. No.
                   27507
                   156351 1.R1040
Contig ID
                   kmv700\overline{7}39670.h1
5'-most EST
Seq. No.
                   27508
Contig ID
                   156375 1.R1040
5'-most EST
                   kmv700739711.h1
Seq. No.
                   27509
Contig ID
                   156391 1.R1040
5'-most EST
                   kmv700739779.h1
Seq. No.
                   27510
Contig ID
                   156393 1.R1040
5'-most EST
                   fC-gmse7000754533f1
Method
                   BLASTX
NCBI GI
                   q3367568
BLAST score
                   643
E value
                   3.0e-67
Match length
                   174
% identity
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                   thaliana]
Seq. No.
                   27511
Contig ID
                   156412 1.R1040
5'-most EST
                   uC-gmrominsoy169b01b1
Seq. No.
Contig ID
                   156412 2.R1040
5'-most EST
                   bth700848345.hl
Seq. No.
                   27513
Contig ID
                   156425 1.R1040
5'-most EST
                   kmv700741476.h1
                   27514
Seq. No.
Contig ID
                   156447 1.R1040
5'-most EST
                   fC-gmle700739836a1
Method
                   BLASTN
NCBI GI
                   a495658
```

```
E value
                   4.0e-85
Match length
                   377
% identity
                   86
                  Pisum sativum aspartate carbamoyltransferase (pyrB1) mRNA,
NCBI Description
                   complete cds
                   27515
Seq. No.
Contig ID
                  156448 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220077f06d1
Method
                   BLASTX
NCBI GI
                  g2804280
BLAST score
                   198
                   3.0e-15
E value
Match length
                   63
% identity
                   57
                   (AB003687) 6-4 photolyase [Arabidopsis thaliana]
NCBI Description
                   >gi 3929918 dbj BAA34711 (AB017331) 6-4 photolyase
                   [Arabidopsis thaliana]
Seq. No.
                   27516
Contig ID
                   156458 1.R1040
                   kmv700739866.h1
5'-most EST
Seq. No.
                   27517
                   156473 1.R1040
Contig ID
5'-most EST
                   eep700867371.hl
Method
                  BLASTX
NCBI GI
                   g4455363
BLAST score
                   313
E value
                   2.0e-28
Match length
                   142
% identity
                   40
                   (AL035524) Medicago nodulin N21-like protein (Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   27518
Contig ID
                   156506 1.R1040
5'-most EST
                  g5666770
Method
                  BLASTX
NCBI GI
                  q4490316
BLAST score
                  212
E value
                   5.0e-17
Match length
                  96
% identity
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                  27519
Contig ID
                  156520 1.R1040
5'-most EST
                  fC-gmle700739977a1
Method
                  BLASTX
NCBI GI
                  g2997593
BLAST score
                  259
E value
                  9.0e-23
Match length
                  89
% identity
NCBI Description
                  (AF020816) glucose-6-phosphate/phosphate-translocator
```

precursor [Solanum tuberosum]

5'-most EST

```
27520
Seq. No.
                  156551 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810009a03d1
Method
                  BLASTX
NCBI GI
                  g3080402
BLAST score
                  175
                  1.0e-12
E value
Match length
                  44
% identity
                  75
                   (AL022603) putative NADPH quinone oxidoreductase
NCBI Description
                   [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_
                   (AL035527) putative NADPH quinone oxidoreductase
                  [Arabidopsis thaliana]
Seq. No.
                  27521
Contig ID
                  156581 1.R1040
                  kmv700740079.h1
5'-most EST
Seq. No.
                  27522
Contig ID
                  156588 1.R1040
5'-most EST
                  kmv700740093.h1
                  27523
Seq. No.
Contig ID
                  156593 1.R1040
5'-most EST
                  sat701\overline{0}03618.h1
Method
                 BLASTX
NCBI GI
                  q2832649
BLAST score
                  406
E value
                  6.0e-40
Match length
                  101
% identity
NCBI Description
                  (AL021710) adenylosuccinate lyase - like protein
                  [Arabidopsis thaliana]
                  27524
Seq. No.
Contig ID
                  156634 1.R1040
5'-most EST
                  jC-gmro02910024d03a1
                  27525
Seq. No.
Contig ID
                  156651 1.R1040
5'-most EST
                  fC-gmle700740186a1
Method
                  BLASTX
NCBI GI
                  g4510406
BLAST score
                  475
E value
                  2.0e-47
Match length
                  147
% identity
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  27526
Contig ID
                  156665 1.R1040
5'-most EST
                  eep700865943.h1
Seq. No.
                  27527
Contig ID
                  156692 1.R1040
```

jC-gmst02400057f01d1

Seq. No.

27538

```
27528
Seq. No.
Contig ID
                   156708 1.R1040
5'-most EST
                   fua701039591.h1
                   27529
Seq. No.
                   156728 1.R1040
Contig ID
5'-most EST
                   kmv700740492.h1
                   27530
Seq. No.
                   156800 1.R1040
Contig ID
                   kmv700740391.h1
5'-most EST
                   27531
Seq. No.
Contig ID
                   156869 1.R1040
5'-most EST
                   kmv700740491.h1
Method
                   BLASTX
                   g4218126
NCBI GI
BLAST score
                   283
                   2.0e-25
E value
Match length
                   88
% identity
                   55
NCBI Description
                   (AL035353) putative protein [Arabidopsis thaliana]
Seq. No.
                   27532
Contig ID
                   156872 1.R1040
                   kmv700740494.h1
5'-most EST
Seq. No.
                   27533
Contig ID
                   156877 1.R1040
5'-most EST
                   zhf700956784.h1
Seq. No.
                   27534
Contig ID
                   156880 1.R1040
5'-most EST
                   asn701140433.h1
Method
                  BLASTX
NCBI GI
                   g4522004
BLAST score
                   204
E value
                   3.0e-16
Match length
                   86
% identity
NCBI Description
                   (AC007069) putative histidine kinase, sensory transduction
                   [Arabidopsis thaliana]
Seq. No.
                   27535
Contig ID
                  156898 1.R1040
5'-most EST
                  bth700848106.hl
Seq. No.
                  27536
Contig ID
                  156905 1.R1040
5'-most EST
                  zhf700953760.h1
Seq. No.
                  27537
Contig ID
                  156909 1.R1040
                  kmv700740557.h1
5'-most EST
```

5'-most EST

```
Contig ID
                  156939 1.R1040
5'-most EST
                  kmv700740625.h1
                  27539
Seq. No.
                  156942 1.R1040
Contig ID
                  kmv700740628.hl
5'-most EST
                  BLASTX
Method
                  q3894172
NCBI GI
BLAST score
                  532
E value
                  3.0e-54
Match length
                  194
                   48
% identity
                   (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  27540
Seq. No.
                  156969 1.R1040
Contig ID
                  kmv700740688.h1
5'-most EST
Seq. No.
                  27541
Contig ID
                  156974 1.R1040
                  bth700849423.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1296805
BLAST score
                  428
E value
                  2.0e-42
Match length
                  117
% identity
                  70
NCBI Description
                  (X90929) C-terminal peptidase of the D1 protein [Hordeum
                  vulgare]
                  27542
Seq. No.
Contig ID
                  156980 1.R1040
5'-most EST
                  leu701153567.h1
Seq. No.
                  27543
Contig ID
                  157021 1.R1040
5'-most EST
                  g5607109
                  27544
Seq. No.
Contig ID
                  157046 1.R1040
                  kmv700740817.h1
5'-most EST
Seq. No.
                  27545
Contig ID
                  157070 1.R1040
5'-most EST
                  kmv700740864.h1
Method
                  BLASTX
NCBI GI
                  g2244910
BLAST score
                  176
E value
                  1.0e-12
Match length
                  85
% identity
NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  27546
Contig ID
                  157075 1.R1040
```

 $jsh701\overline{0}64103.h1$

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   g4115914
BLAST score
                   508
E value
                   9.0e-67
Match length
                   214
% identity
                   60
NCBI Description
                   (AF118222) contains similarity to Iron/Ascorbate family of
                   oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85,
                  N=1) [Arabidopsis thaliana] >gi 4539410 emb CAB40043.1
                   (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis
                   thaliana]
                   27547
Seq. No.
Contig ID
                   157088 1.R1040
                   kmv700743634.h1
5'-most EST
Seq. No.
                   27548
Contig ID
                  157090 1.R1040
5'-most EST
                  leu701147124.h1
Seq. No.
                  27549
Contig ID
                  157095 1.R1040
5'-most EST
                   zpv700760606.hl
Method
                  BLASTX
NCBI GI
                  g2213597
BLAST score
                   607
E value
                   4.0e-63
Match length
                   170
% identity
                   (AC000348) T7N9.17 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27550
Contig ID
                   157123 1.R1040
5'-most EST
                   fC-qmle700741352a1
Seq. No.
                   27551
Contig ID
                   157158 1.R1040
5'-most EST
                   kmv700740995.h1
Seq. No.
                   27552
Contig ID
                   157181 1.R1040
5'-most EST
                  gsv701052712.hl
Seq. No.
                  27553
Contig ID
                  157191 1.R1040
5'-most EST
                  jC-gmle01810071e10a1
Seq. No.
                  27554
Contig ID
                  157215 1.R1040
5'-most EST
                  kmv700741072.hl
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                  177
E value
                  2.0e-23
Match length
                  69
% identity
```

(AC005499) putative elongation factor [Arabidopsis

Seq. No.

27563

27555 Seq. No. 157220 1.R1040 Contig ID 5'-most EST hrw701061188.h1 27556 Seq. No. Contig ID 157221 1.R1040 5'-most EST rca700997763.h1 Method BLASTX NCBI GI g3319713 BLAST score 1046 E value 1.0e-114 Match length 272 % identity NCBI Description (AJ006992) chitinase precursor [Canavalia ensiformis] 27557 Seq. No. Contig ID 157237 1.R1040 kmv700741105.h1 5'-most EST 27558 Seq. No. 157244 1.R1040 Contig ID kmv700741112.h1 5'-most EST 14 1 1 Seq. No. 27559 Contig ID 157324 1.R1040 5'-most EST uC-gmflminsoy099b09b1 Seq. No. 27560 Contig ID 157332 1.R1040 5'-most EST $bnu700\overline{9}67559.h1$ Seq. No. 27561 Contig ID 157336 1.R1040 5'-most EST smc700747435.h1 Method BLASTX NCBI GI g2501296 BLAST score 217 E value 6.0e-18 Match length 87 % identity 49 NCBI Description DNA GYRASE SUBUNIT B >gi 1652801 dbj BAA17720 (D90908) DNA gyrase B subunit [Synechocystis sp.] Seq. No. 27562 Contig ID 157345 1.R1040 5'-most EST kmv700741250.h1 Method BLASTX NCBI GI g3493253 BLAST score 159 E value 3.0e-11 Match length 64 % identity

thaliana]

NCBI Description (AF076156) catechol-O-methyltransferase [Mus musculus]

```
157355 1.R1040
Contig ID
5'-most EST
                   kmv700741261.h1
Method
                  BLASTN
NCBI GI
                  g510546
BLAST score
                   324
E value
                  0.0e + 00
Match length
                  589
% identity
                  89
NCBI Description P.sativum mRNA for starch branching enzyme II
                  27564
Seq. No.
Contig ID
                  157442 1.R1040
5'-most EST
                  smc700749730.hl
                  BLASTX
Method
                  g4204311
NCBI GI
BLAST score
                  181
                  1.0e-13
E value
Match length
                   65
                  57
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  27565
                  157495 1.R1040
Contig ID
5'-most EST
                  kmv700741453.h1
                  27566
Seq. No.
Contig ID
                  157496 1.R1040
5'-most EST
                  zsg701123053.hl
                  27567
Seq. No.
                  157496 2.R1040
Contig ID
5'-most EST
                  fde700875595.h1
                  27568
Seq. No.
                  157516 1.R1040
Contig ID
5'-most EST
                  kmv700741487.h1
                  BLASTX
Method
                  g404688
NCBI GI
BLAST score
                  266
E value
                  1.0e-23
Match length
                  97
% identity
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
                  27569
Seq. No.
Contig ID
                  157539 1.R1040
5'-most EST
                  kmv700741519.h1
Method
                  BLASTX
NCBI GI
                  g1708972
BLAST score
                  333
E value
                  8.0e-31
Match length
                  158
% identity
NCBI Description
                   (R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR
                   (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi 1262279
                   (U51562) (R)-(+)-mandelonitrile lyase isoform MDL3
```

```
precursor [Prunus serotina] >gi_2343181 (AF013161)
                  (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus
                  serotina]
                  27570
Seq. No.
                  157541 1.R1040
Contig ID
5'-most EST
                  kmv700741521.h1
Seq. No.
                  27571
Contig ID
                  157557 1.R1040
5'-most EST
                  pmv700894256.hl
Seq. No.
                  27572
Contig ID
                  157585 1.R1040
5'-most EST
                  gsv701045237.h1
Seq. No.
                  27573
Contig ID
                  157633 1.R1040
5'-most EST
                  kmv700741674.h1
Method
                  BLASTX
NCBI GI
                  q4539369
BLAST score
                  182
E value
                  1.0e-23
Match length
                  88
% identity
NCBI Description
                  (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  27574
Contig ID
                  157640 1.R1040
5'-most EST
                  bth700844817.h1
Seq. No.
                  27575
                  157651 1.R1040
Contig ID
5'-most EST
                  zpv700761954.h1
Seq. No.
                  27576
Contig ID
                  157651 2.R1040
5'-most EST
                  kmv700741709.h1
Seq. No.
                  27577
Contig ID
                  157686 1.R1040
                  kmv700741760.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4539343
BLAST score
                  231
E value
                  3.0e-19
Match length
                  121
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                  27578
Seq. No.
                  157688 1.R1040
Contig ID
5'-most EST
                  sat701011341.hl
```

27579

157700 1.R1040

jC-qmle01810057d04d1

Seq. No.

Contig ID 5'-most EST

NCBI Description

```
27580
Seq. No.
Contig ID
                   157712 1.R1040
5'-most EST
                   jC-gmst02400049h05d1
                   27581
Seq. No.
                   157713 1.R1040
Contig ID
5'-most EST
                   kmv700743793.h1
Method
                   BLASTX
                   g3775987
NCBI GI
BLAST score
                   173
                   7.0e-13
E value
                   51
Match length
                   65
% identity
                   (AJ010457) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   27582
Seq. No.
                   157728 1.R1040
Contig ID
5'-most EST
                   kmv700741821.h1
Method
                   BLASTN
NCBI GI
                   g4519184
BLAST score
                   53
                   4.0e-21
E value
Match length
                   117
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K15F13, complete sequence
Seq. No.
                   27583
Contig ID
                   157739 1.R1040
                   xzm700763715.h1
5'-most EST
Seq. No.
                   27584
                   157754 2.R1040
Contig ID
                   cle700\overline{9}67748.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3063455
BLAST score
                   313
E value
                   6.0e-29
Match length
                   72
% identity
NCBI Description
                   (AC003981) F22013.17 [Arabidopsis thaliana]
Seq. No.
                   27585
Contig ID
                   157782 1.R1040
                   smc700748556.hl
5'-most EST
Seq. No.
                   27586
Contig ID
                   157783 1.R1040
5'-most EST
                   jC-gmro02910038f02a1
Method
                   BLASTX
NCBI GI
                   g3080401
BLAST score
                   337
E value
                   1.0e-31
Match length
                   95
% identity
```

(AL022603) putative protein [Arabidopsis thaliana]

```
>gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 27587
Contig ID 157801_1.R1040
5'-most EST kmv700741935.h1
```

Seq. No. 27588

Contig ID 157830_1.R1040

5'-most EST jC-gmro02800031e05a1

Seq. No. 27589

Contig ID 157843_1.R1040 5'-most EST kmv700742008.h1

Seq. No. 27590

Contig ID 157865_1.R1040 5'-most EST kmv700742049.h1

Method BLASTN
NCBI GI g510545
BLAST score 157
E value 6.0e-83
Match length 285
% identity 89

NCBI Description P.sativum mRNA for starch branching enzyme I

 Seq. No.
 27591

 Contig ID
 157870_1.R1040

 5'-most EST
 smc700747937.h1

Method BLASTX
NCBI GI g2388561
BLAST score 543
E value 1.0e-55
Match length 165
% identity 66

NCBI Description (AC000098) Similar to Arabidopsis hypothetical protein

PID:e326839 (gb Z97337). [Arabidopsis thaliana]

_

 Seq. No.
 27592

 Contig ID
 157913_1.R1040

 5'-most EST
 kmv700742131.h1

Seq. No. 27593

Contig ID 157920 1.R1040 5'-most EST kmv700742139.h1

Method BLASTX
NCBI GI g1168235
BLAST score 185
E value 2.0e-14
Match length 41
% identity 88

NCBI Description 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING

>gi_1073800_pir__C64077 6-phosphogluconate dehydrogenase,
decarboxylating (gnd) homolog - Haemophilus influenzae
(strain Rd KW20) >gi_1573539 (U32737) 6-phosphogluconate

dehydrogenase, decarboxylating (gnd) [Haemophilus

influenzae Rd]

```
27594
Seq. No.
Contig ID
                  157926 1.R1040
5'-most EST
                  kmv700742157.h1
                  27595
Seq. No.
Contig ID
                  157941 1.R1040
5'-most EST
                  jC-qmf102220127h11a1
                  27596
Seq. No.
                  157973 1.R1040
Contig ID
                  pmv700890770.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g537404
BLAST score
                   335
                  1.0e-31
E value
Match length
                  66
                  89
% identity
                   (D26537) WSI76 protein induced by water stress [Oryza
NCBI Description
                  27597
Seq. No.
                  157991 1.R1040
Contig ID
                  pxt700945008.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3402687
BLAST score
                  394
E value
                   6.0e-38
Match length
                  151
% identity
                  53
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                  27598
Contig ID
                  158003 1.R1040
5'-most EST
                   fC-gmle700742323a1
Method
                  BLASTX
NCBI GI
                  g126334
BLAST score
                  168
E value
                   1.0e-11
Match length
                   177
% identity
                   33
NCBI Description
                  LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)
                  >gi 79925 pir A24075 lipase precursor - Staphylococcus
                  hyicus >gi 47136 emb CAA26602 (X02844) precursor
                   [Staphylococcus hyicus]
Seq. No.
                  27599
Contig ID
                  158036 1.R1040
5'-most EST
                  zhf700960242.h1
Method
                  BLASTN
NCBI GI
                  g1694899
BLAST score
                  103
E value
                  6.0e-51
Match length
                  271
% identity
                  85
```

NCBI Description P.sativum mRNA for Copl protein

```
27600
Seq. No.
Contig ID
                   158066 1.R1040
5'-most EST
                   jC-gmle01810044h01d1
                   27601
Seq. No.
Contig ID
                   158088 1.R1040
5'-most EST
                   kmv700742511.h1
Method
                   BLASTX
                   g401213
NCBI GI
BLAST score
                   376
E value
                   3.0e-36
Match length
                   127
% identity
                   64
NCBI Description
                   ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792
                   (M96073) phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana] >gi_445600_prf 1909347A
                   phosphoribosylanthranilate transferase [Arabidopsis
                   thaliana]
                   27602
Seq. No.
Contig ID
                   158097 1.R1040
5'-most EST
                   vzy700751779.h1
Seq. No.
                   27603
Contig ID
                   158122 1.R1040
5'-most EST
                   kmv700742589.h1
Seq. No.
                   27604
Contig ID
                   158141 1.R1040
5'-most EST
                   g5753461
Seq. No.
                   27605
Contig ID
                   158162 1.R1040
5'-most EST
                   kmv700742669.h1
Seq. No.
                   27606
Contig ID
                   158207 1.R1040
5'-most EST
                   jC-qmle01810093f01a1
Method
                  BLASTX
NCBI GI
                   q2245095
BLAST score
                   446
E value
                   8.0e-57
Match length
                   143
% identity
NCBI Description
                  (Z97343) formyltransferase purU homolog [Arabidopsis
                  thaliana]
Seq. No.
                  27607
Contig ID
                  158255 1.R1040
5'-most EST
                  jex700904465.hl
Seq. No.
                  -27608
Contig ID
                  158289 1.R1040
5'-most EST
                  pmv700891478.h1
Seq. No.
                  27609
Contig ID
                  158291 1.R1040
```

```
5'-most EST
                  jC-gmle01810084f03a1
Method
                  BLASTX
                  g3377517
NCBI GI
                  670
BLAST score
                  2.0e-70
E value
                  208
Match length
% identity
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
                  27610
Seq. No.
                  158355 1.R1040
Contig ID
                  kmv700743045.h1
5'-most EST
                  27611
Seq. No.
                  158379_1.R1040
Contig ID
5'-most EST
                  gsv701049990.h1
                  BLASTX
Method
                  q3201635
NCBI GI
BLAST score
                  296
                  4.0e-27
E value
Match length
                  75
% identity
                  76
                  (AC004669) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  27612
Seq. No.
Contig ID
                  158407 1.R1040
                  kmv700743124.h1
5'-most EST
Seq. No.
                  27613
Contig ID
                  158438 1.R1040
                  rlr700895959.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2827661
BLAST score
                  244
E value
                  3.0e-21
Match length
                  59
% identity
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
                  27614
Seq. No.
Contig ID
                  158440 1.R1040
5'-most EST
                  uC-qmflminsoy044b10b1
Seq. No.
                  27615
                  158473 1.R1040
Contig ID
                  kmv700743250.h1
5'-most EST
Seq. No.
                  27616
                  158558 1.R1040
Contig ID
5'-most EST
                  kmv700743410.h1
                  27617
Seq. No.
Contig ID
                  158571 1.R1040
5'-most EST
                  fde700874744.h1
Method
                  BLASTX
```

g3510254

260

NCBI GI BLAST score

E value

4.0e-45

```
E value
                   5.0e-23
Match length
                   67
% identity
                   75
NCBI Description
                   (AC005310) putative zinc transporter [Arabidopsis thaliana]
                   27618
Seq. No.
                   158599 1.R1040
Contig ID
5'-most EST
                   fC-qmle700743470a1
Method '
                   BLASTX
                   g4102600
NCBI GI
BLAST score
                   544 ·
                   6.0e-56
E value
Match length
                   123
% identity
                   80
NCBI Description
                   (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   27619
                   158627 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy030c01b1
Seq. No.
                   27620
                   158667 1.R1040
Contig ID
5'-most EST
                   rca700997551.hl
Method
                   BLASTX
                   g2347199
NCBI GI
                                       ...
BLAST score
                   522
E value
                   7.0e-53
Match length
                   225
% identity
NCBI Description
                   (AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                   27621
                   158695 1.R1040
Contiq ID
5'-most EST
                   leu701150633.h1
Seq. No.
                   27622
Contig ID
                   158727 2.R1040
5'-most EST
                   jC-gmst02400049e02d1
Seq. No.
                   27623
Contig ID
                   158736 1.R1040
5'-most EST
                   jC-qmst02400066b05a2
Method
                   BLASTX
NCBI GI
                   q2088658
BLAST score
                   366
E value
                   6.0e-35
Match length
                   120
% identity
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                   27624
Seq. No.
                   158751 1.R1040
Contig ID
                                                           ~~··· .·.
5'-most EST
                   q5605744
Method
                  BLASTX
NCBI GI
                   q4567247
BLAST score
                   454
```

NCBI GI

```
138
Match length
% identity
                   62
NCBI Description
                   (AC007070) unknown protein [Arabidopsis thaliana]
                   27625
Seq. No.
                   158768 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}60112.h1
Seq. No.
                   27626
Contig ID
                   158804 1.R1040
5'-most EST
                   kmv700743942.hl
                   BLASTX
Method
                   g1903360
NCBI GI
BLAST score
                   188
E value
                   4.0e-14
Match length
                   123
% identity
                   37
                   (ACO00104) Similar to Arabidopsis 2A6 (gb X83096). EST
NCBI Description
                   gb T76913 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                   27627
                   158842 1.R1040
Contig ID
                   kmv700744008.h1
5'-most EST
                   27628
Seq. No.
Contig ID
                   158954 1.R1040
                   rca700996387.hl
5'-most EST
Seq. No.
                   27629
                   158989 1.R1040
Contig ID
5'-most EST
                   uC-qmronoir057f06b1
                   27630
Seq. No.
                   158994 1.R1040
Contig ID
                   leu701148728.h1
5'-most EST
Seq. No.
                   27631
                   158997 1.R1040
Contig ID
5'-most EST
                   smw700\overline{6}46229.h1
Seq. No.
                   27632
                   159036 1.R1040
Contig ID
5'-most EST
                   ary700764309.h1
Method
                   BLASTX
NCBI GI
                   q3377803
BLAST score
                   601
E value
                   2.0e-62
Match length
                   200
% identity
                   (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   27633
Contig ID
                   159055 1.R1040
5'-most EST
                   smc700744206.hl
Method
                   BLASTX
```

g4263704

5'-most EST

```
BLAST score
                   166
                   3.0e-11
E value
Match length
                   78
% identity
                   38
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                   27634
Seq. No.
                   159080 1.R1040
Contig ID
5'-most EST
                 fC-gmro700744539a1
Seq. No.
                   27635
                   159153 1.R1040
Contig ID
5'-most EST
                   smc700744305.h1
Seq. No.
                   27636
Contig ID
                   159161 1.R1040
                   smc700744314.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2213594
BLAST score
                   219
E value
                   3.0e-19
Match length
                   84
% identity
NCBI Description (ACO00348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                   27637
Contig ID
                   159171 1.R1040
5'-most EST
                   smc700744327.h1
                   27638
Seq. No.
Contig ID
                   159179 1.R1040
5'-most EST
                   smc700747036.hl
                   27639
Seq. No.
Contig ID
                   159182 1.R1040
5'-most EST
                  uC-gmrominsoy0001a08b1
                   27640
Seq. No.
Contig ID
                   159203 1.R1040
5'-most EST
                   smc700747068.hl
Method
                  BLASTN
NCBI GI
                   g4519193
BLAST score
                   35
                   2.0e-10
E value
Match length
                   91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
                  27641
Seq. No.
                  159274 1.R1040
Contig ID
5'-most EST
                  smc700744564.hl
Seq. No.
                  27642
                  159284 1.R1040
Contig ID
```

pmv700888323.hl

Seq. No.

27648

```
Method
                  BLASTX
NCBI GI
                  g4455359
BLAST score
                  348
E value
                   4.0e-33
Match length
                  106
% identity
                   64
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  27643
Seq. No.
Contig ID
                  159317 1.R1040
5'-most EST
                  smc700744707.h1
Method
                  BLASTX
NCBI GI
                  g2244763
BLAST score
                  339
E value
                   4.0e-37
Match length
                  104
% identity
NCBI Description
                  (Z97335) A6 anther-specific protein [Arabidopsis thaliana]
                  27644
Seq. No.
                  159354 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy050a03b1
Method
                  BLASTX
NCBI GI
                  g2827699
BLAST score
                  150
                  2.0e-09
E value
Match length
                  84
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
                  27645
Seq. No.
                  159363 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400027c08a1
Method
                  BLASTX
                  q4467111
NCBI GI
BLAST score
                  518
                  2.0e-60
E value
Match length
                  163
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  27646
Seq. No.
Contig ID
                  159414 1.R1040
5'-most EST
                  hrw701061205.hl
                  27647
Seq. No.
                  159468 1.R1040
Contig ID
5'-most EST
                  smc700745014.hl
Method
                  BLASTX
NCBI GI
                  g4433381
BLAST score
                  211
E value
                  3.0e-17
Match length
                  75
% identity
NCBI Description (D50034) 4-coumarate:CoA ligase [Nicotiana tabacum]
```

Seq. No.

27655

```
159475 1.R1040
 Contig ID
 5'-most EST
                    smc700745049.h1
Seq. No.
                    27649
                    159490 1.R1040
 Contig ID
 5'-most EST
                    kl1701210978.h1
 Method
                    BLASTX
                    q1931640
 NCBI GI
BLAST score
                    511
 E value
                    4.0e-52
Match length
                    114
 % identity
                    77
                    (U95973) Serine carboxypeptidase isolog [Arabidopsis
 NCBI Description
 Seq. No.
                    27650
 Contig ID
                    159500 1.R1040
 5'-most EST
                    uC-gmflminsoy001d04b1
Method
                    BLASTX
NCBI GI
                    q4038034
BLAST score
                    295
 E value
                    2.0e-26
Match length
                    77
 % identity
                    74
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                    27651
 Contig ID
                    159536 1.R1040
 5'-most EST
                    qsv701\overline{0}49536.h1
Method
                    BLASTX
NCBI GI
                    g4544412
BLAST score
                    150
E value
                    2.0e-09
Match length
                    101
 % identity
NCBI Description
                    (AC006955) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
 Contig ID
                    159606 2.R1040
 5'-most EST
                    eep700866025.h1
Seq. No.
                    27653
 Contig ID
                    159614 1.R1040
 5'-most EST
                   pxt700946155.h1
                    27654
Seq. No.
Contig ID
                    159632 1.R1040
 5'-most EST
                    smc700745377.h1
Method
                   BLASTX
NCBI GI
                   q3075398
BLAST score
                    576
E value
                    3.0e-59
Match length
                   199
% identity
NCBI Description
                   (AC004484) unknown protein [Arabidopsis thaliana]
```

```
Contig ID
                   159685 1.R1040
 5'-most EST
                   jex700\overline{9}09716.h1
 Seq. No.
                   27656
 Contig ID
                   159701 1.R1040
 5'-most EST
                   pmv700891919.h1
Seq. No.
                   27657
Contig ID
                   159756 1.R1040
 5'-most EST
                   uC-gmrominsoy230e08b1
Method
                   BLASTX
NCBI GI
                   g1946371
BLAST score
                   373
E value
                   9.0e-36
Match length
                   129
% identity
                   59
NCBI Description
                  (U93215) regulatory protein Viviparous-1 isolog
                   [Arabidopsis thaliana]
Seq. No.
                   27658
Contig ID
                   159823 1.R1040
5'-most EST
                   smc700745818.hl
Method
                   BLASTX
NCBI GI
                   g1086263
BLAST score
                   195
E value
                   7.0e-15
Match length
                   141
% identity
                   33
NCBI Description
                  TMV resistance protein N - tobacco (Nicotiana glutinosa)
                   >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   27659
Contig ID
                   159837 1.R1040
5'-most EST
                   smc700745847.h1
Method
                   BLASTX
NCBI GI
                   g3367568
BLAST score
                   379
E value
                  2.0e-36
Match length
                  113
% identity
                   62
NCBI Description
                  (AL031135) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  27660
Contig ID
                  159847 1.R1040
5'-most EST
                  smc700745871.h1
Seq. No.
                  27661
Contig ID
                  159851 1.R1040
5'-most EST
                  uC-gmrominsoy284d04b1
Seq. No.
                  27662
Contig ID
                  159884 1.R1040
5'-most EST
                  smc700745936.h1
Method
                  BLASTX
NCBI GI
                  g3776573
BLAST score
                  533
```

5'-most EST

```
E value
                   2.0e-54
Match length
                   173
% identity
                   58
NCBI Description
                   (AC005388) Similar to nodulins and lipase homolog F14J9.5
                   gi 3482914 from Arabidopsis thaliana BAC qb AC003970.
                  Alternate first exon from 72258 to 72509. [Arabidopsis
                  thaliana]
                   27663
Seq. No.
Contig ID
                   159920 1.R1040
                   smc700746027.hl
5'-most EST
Seq. No.
                   27664
Contig ID
                   159922 1.R1040
5'-most EST
                   smc700746031.h1
Method
                  BLASTX
NCBI GI
                  q2129933
BLAST score
                   153
E value
                   2.0e-10
Match length
                   47
% identity
NCBI Description
                  myb-related transcription factor TMH27 - tomato
                  >qi 1167484 emb CAA64614 (X95296) transcription factor
                   [Lycopersicon esculentum]
Seq. No.
                  27665
Contig ID
                   159925 1.R1040
5'-most EST
                  leu701149294.h1
Seq. No.
                  27666
Contig ID
                  159930 1.R1040
5'-most EST
                  qsv701054304.h1
Method
                  BLASTX
NCBI GI
                  q3036840
BLAST score
                  232
E value
                  2.0e-19
Match length
                  91
% identity
NCBI Description
                   (AJ222967) cystinosin [Homo sapiens]
                  >gi 3036851 emb CAA75882 (Y15924) cystinosin [Homo
                  sapiens]
Seq. No.
                  27667
Contig ID
                  159951 1.R1040
5'-most EST
                  dpv701101389.h1
Seq. No.
                  27668
Contig ID
                  159970 1.R1040
5'-most EST
                  hrw701\overline{0}62059.h1
Seq. No.
                  27669
Contig ID
                  159984 1.R1040
5'-most EST
                  smc700747140.hl
Seq. No.
                  27670
Contig ID
                  159988 1.R1040
```

asn701139351.h1

Seq. No.

Contig ID

27679

160087 1.R1040 -

```
Method
                   BLASTX
NCBI GI
                   g3172025
BLAST score
                   210
E value
                   6.0e-17
Match length
                   70
% identity
                   66
                   (AB005805) aldehyde oxidase [Arabidopsis thaliana]
NCBI Description
                   27671
Seq. No.
Contig ID
                   159993 1.R1040
                   zhf700951771.h1
5'-most EST
Seq. No.
                   27672
Contig ID
                   160011 1.R1040
5'-most EST
                   k11701\overline{2}06372.h1
Method
                   BLASTX
NCBI GI
                   q3355464
BLAST score
                   246
E value
                   5.0e-21
Match length
                   118
% identity
                   47
                   (AC004218) putative ATP-binding-cassette protein, 3'
NCBI Description
                   partial [Arabidopsis thaliana]
Seq. No.
                   27673
Contig ID
                   160016 1.R1040
5'-most EST
                   smc700746184.h1
Seq. No.
                   27674
Contig ID
                   160042 1.R1040
5'-most EST
                   smc700746222.h1
Seq. No.
                   27675
Contig ID
                   160049 1.R1040
5'-most EST
                   smc700746233.h1
Seq. No.
                   27676
Contig ID
                   160064 1.R1040
5'-most EST
                   smc700746265.hl
Seq. No.
                   27677
Contig ID
                   160071 1.R1040
5'-most EST
                   q5753341
Method
                   BLASTX
NCBI GI
                   q2288982
BLAST score
                   357
E value
                   8.0e-34
Match length
                   111
% identity
                   (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   160071 2.R1040
5'-most EST
                   jex700\overline{9}08256.h1
```

% identity

- 38

```
5'-most EST
                   jC-gmro02800042a02a1
Method
                   BLASTX
NCBI GI
                   g4097522
BLAST score
                   689
                   2.0e-72
E value
Match length
                   213
% identity
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                   ananassa]
                   27680
Seq. No.
                   160087 2.R1040
Contig ID
5'-most EST
                   fC-gmro700749247a2
Method
                   BLASTX
NCBI GI
                   g4097522
BLAST score
                   598
E value
                   4.0e-62
Match length
                   170
% identity
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                   ananassa]
Seq. No.
                   27681
Contig ID
                   160101 1.R1040
5'-most EST
                   jC-gmst02400016d01d1
Seq. No.
                   27682
Contig ID
                   160103 1.R1040
5'-most EST
                   epx701\overline{1}05621.h1
Method
                   BLASTX
NCBI GI
                   q3661610
BLAST score
                   711
E value
                   2.0e-75
Match length
                   145
% identity
                   (AF092565) splicing factor Prp8 [Homo sapiens]
NCBI Description
Seq. No.
                   27683
Contig ID
                   160104 1.R1040
5'-most EST
                   jC-qmf102220081e06a1
Method
                   BLASTX
                   q4539314
NCBI GI
BLAST score
                   238
E value
                   1.0e-19
Match length
                   282
% identity
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.
                   27684
                   160104 2.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy082c05b1
Method
                   BLASTX
NCBI GI
                   g4539314
BLAST score
                   160
E value
                   7.0e-11
Match length
                   132
```

```
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                   27685
Seq. No.
                   160107 1.R1040
Contig ID
5'-most EST
                   zzp700833586.h1
Seq. No.
                   27686
Contig ID
                   160111 1.R1040
5'-most EST
                   jC-gmro02800035c06a1
Method
                  BLASTX
NCBI GI
                  g4467125
BLAST score
                   604
E value
                   3.0e-81
Match length
                   200
% identity
                  73
NCBI Description
                   (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  27687
Contig ID
                  160129 1.R1040
5'-most EST
                  pmv700889726.h1
Method
                  BLASTX
NCBI GI
                  q4426611
BLAST score
                  156
E value
                   2.0e-10
Match length
                  106
% identity
NCBI Description (AF096897) pushover [Drosophila melanogaster]
                  27688
Seq. No.
Contig ID
                  160141 1.R1040
5'-most EST
                  smc700746360.h1
Seq. No.
                  27689
Contig ID
                  160148 1.R1040
5'-most EST
                  smc700746369.h1
Seq. No.
                  27690
Contig ID
                  160156 1.R1040
5'-most EST
                  dpv701\overline{0}99069.h1
Method
                  BLASTN
NCBI GI
                  q218261
BLAST score
                  92
E value
                  2.0e-44
Match length .
                  180
% identity
NCBI Description Soybean mRNA for early nodulin
                  27691
Seq. No.
Contig ID
                  160163 1.R1040
5'-most EST
                  zpv700759810.hl
Method
                  BLASTX
NCBI GI
                  g3193310
BLAST score
                  356
E value
                  1.0e-33
Match length
                  130
% identity
                  52
```

NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1

```
Seq. No.
                   27692
Contig ID
                   160174 1.R1040
5'-most EST
                   jC-qmst02400076q03a1
Seq. No.
                   27693
Contig ID
                   160179 1.R1040
5'-most EST
                   jex700908178.hl
Method
                   BLASTX
NCBI GI
                   q4490937
BLAST score
                   299
E value
                   7.0e-27
Match length
                   192
% identity
NCBI Description
                   (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
                   sapiens]
                   27694
Seq. No.
Contig ID
                  160195 1.R1040
5'-most EST
                   smc700746437.h1
                   27695
Seq. No.
Contig ID
                  160197 1.R1040
5'-most EST
                   jC-gmro02910016h01a1
Method
                  BLASTX
NCBI GI
                  q2980798
BLAST score
                   258
E value
                   4.0e-22
Match length
                  101
% identity
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  27696
                  160204 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910011d08d1
Method
                  BLASTX
NCBI GI
                  q4580463
BLAST score
                  157
E value
                  3.0e-10
Match length
                   47
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.
                  27697
                  160232 1.R1040
Contig ID
                  zhf700952347.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2132842
BLAST score
                  128
E value
                  3.0e-16
Match length
                  105
% identity
                  42
NCBI Description
                  probable membrane protein YOL077c - yeast (Saccharomyces
                  cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c
```

(GB:Y07563) [Arabidopsis thaliana]

[Saccharomyces cerevisiae]

1.

```
Seq. No.
                  27698
Contig ID
                  160238 1.R1040
5'-most EST
                  uC-gmflminsoy026d11b1
Method
                  BLASTX
NCBI GI
                  q2769642
BLAST score
                  429
                  3.0e-42
E value
Match length
                  150
% identity
NCBI Description
                   (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
                  esculentum]
Seq. No.
                  27699
Contig ID
                  160252 1.R1040
5'-most EST
                  smc700746519.h1
Seq. No.
                  27700
Contig ID
                  160260 1.R1040
5'-most EST
                  qsv701048360.hl
Method
                  BLASTX
NCBI GI
                  q4455175
BLAST score
                  143
E value
                   6.0e-09
Match length
                  81
% identity
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
                  27701
Seq. No.
Contig ID
                  160276 1.R1040
5'-most EST
                  jsh701066720.hl
Method
                  BLASTX
NCBI GI
                  q4263704
BLAST score
                  207
E value
                  1.0e-16
Match length
                  65
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
                  27702
Seq. No.
Contig ID
                  160287 1.R1040
5'-most EST
                  smc700746568.hl
Seq. No.
                  27703
Contig ID
                  160287 2.R1040
5'-most EST
                  zzp700831088.hl
                  27704
Seq. No.
Contig ID
                  160297 1.R1040
5'-most EST
                  smc700746585.h1
Method
                  BLASTX
NCBI GI
                  g3980412
BLAST score
                  428
E value
                  1.0e-42
Match length
                  95
% identity
```

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

```
27705
Seq. No.
Contig ID
                  160303 1.R1040
5'-most EST
                  smc700746593.h1
Method
                  BLASTX
NCBI GI
                  q2244990
BLAST score
                  482
                  7.0e-49
E value
Match length
                  105
% identity
                  95
                  (297340) similarity to LIM homeobox protein -
NCBI Description
                  Caenorhabditis [Arabidopsis thaliana]
Seq. No.
                  27706
Contig ID
                  160330 1.R1040
5'-most EST
                  smc700746653.hl
Method
                  BLASTN
NCBI GI
                  g4151924
BLAST score
                  40
                  4.0e-13
E value -
Match length
                  72
                  89
% identity
NCBI Description Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds
                  27707
Seq. No.
Contig ID
                  160356 1.R1040
5'-most EST
                  g4396418
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  622
E value
                  2.0e-64
Match length
                  232
% identity
                  (AL035526) putative protein (fragment) [Arabidopsis.
NCBI Description
                  thaliana]
Seq. No.
                  27708
                  160379 1.R1040
Contig ID
5'-most EST
                  dpv701100411.h1
Seq. No.
                  27709
                  160399 1.R1040
Contig ID
5'-most EST
                  uC-qmropic009d01b1
Method
                  BLASTX
NCBI GI
                  q4567194
BLAST score
                  262
E value
                  1.0e-22
Match length
                  75
% identity
NCBI Description
                  (AC007168) putative cytochrome p450 [Arabidopsis thaliana]
                  27710
Seq. No.
Contig ID
                  160478 1.R1040
5'-most EST
                  smc700746889.hl
                  27711
Seq. No.
```

160496 1.R1040

Contig ID

Contig ID

```
5'-most EST
                   zlv700807562.h1
Seq. No.
                   27712
Contig ID
                   160508 2.R1040
5'-most EST
                   smc700746930.hl
Seq. No.
                   27713
Contig ID
                   160511 1.R1040
5'-most EST
                   jC-qmle01810023c12a1
Method
                  BLASTX
NCBI GI
                   g2829864
BLAST score
                   298
E value
                   8.0e-48
Match length
                   221
% identity
NCBI Description
                   (ACO02396) similar to zinc metalloproteinases [Arabidopsis
                  thaliana]
                   27714
Seq. No.
Contig ID
                   160516 1.R1040
5'-most EST
                   jC-qmst02400030c03a1
Method
                  BLASTX
                  q4539324
NCBI GI
BLAST score
                   979
                   1.0e-106
E value
Match length
                   355
% identity
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                  27715
Seq. No.
                  160520 1.R1040
Contig ID
5'-most EST
                   zsg701125310.h1
Method
                  BLASTX
NCBI GI
                  g1345571
BLAST score
                   407
                  1.0e-39
E value
Match length
                  115
% identity
NCBI Description (X80010) starch branching enzyme II [Pisum sativum]
Seq. No.
                  27716
                  160524 1.R1040
Contig ID
5'-most EST
                  smc700747747.h1
Method
                  BLASTX
NCBI GI
                  g3482978
BLAST score
                  289
E value
                  3.0e-26
Match length
                  77
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27717
                  160541 1.R1040
Contig ID
5'-most EST
                  zzp700\overline{8}35619.h1
Seq. No.
                  27718
```

160563 1.R1040

BLAST score

148

```
5'-most EST
                   smc700748250.h1
                   27719
Seq. No.
Contig ID
                   160702 1.R1040
5'-most EST
                   sat701010058.h2
Method
                   BLASTX
NCBI GI
                   g3128210
BLAST score
                   483
E value
                   7.0e-49
Match length
                   111
% identity
                   81
NCBI Description
                   (AC004077) putative cytochrome P450 protein [Arabidopsis
                   thaliana] >gi 3337378 (AC004481) putative cytochrome P450
                   protein [Arabidopsis thaliana]
Seq. No.
                   27720
Contig ID
                   160703 1.R1040
                   smc700747185.hl
5'-most EST
Seq. No.
                   27721
Contig ID
                   160709 1.R1040
5'-most EST
                   smc700747193.hl
Seq. No.
                   27722
Contig ID
                   160712 1.R1040
5'-most EST
                   awf700840345.h1
Seq. No.
                   27723
Contig ID
                   160723 1.R1040
5'-most EST
                   asn701139051.h1
Seq. No.
Contig ID
                   160746 1.R1040
                   smc700747234.h1
5'-most EST
Seq. No.
                   27725
Contig ID
                   160765 1.R1040
5'-most EST
                   smc700\overline{7}47259.h1
                   27726
Seq. No.
Contig ID
                   160808 1.R1040
5'-most EST
                   uC-gmropic045e04b1
Method
                   BLASTX
NCBI GI
                   q4490319
BLAST score
                   161
                   1.0e-10
E value
Match length
                  141
% identity
                   (AL035678) metal-transporting P-type ATPase [Arabidopsis
NCBI Description
                  thaliana]
                   27727
Seq. No.
Contig ID
                   160818 1.R1040
5'-most EST
                  pmv700893763.h1
Method
                  BLASTX
NCBI GI
                  q285741
```

```
3.0e-09
E value
Match length
                   136
% identity
                   35
NCBI Description
                  (D14550) EDGP precursor [Daucus carota]
                  27728
Seq. No.
                  160823 1.R1040
Contig ID
5'-most EST
                   smc700747335.hl
Seq. No.
                   27729
                   160837 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy120h03b1
Seq. No.
                   27730
Contig ID
                   160844 1.R1040
5'-most EST
                   smc700747364.h1
Seq. No.
                   27731
                   160860 1.R1040
Contig ID
                   smc700747387.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2494898
BLAST score
                   235
E value
                   9.0e-20
Match length
                  115
% identity
                   40
                  PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG >qi 1545982 (U53346)
NCBI Description
                   PWP2H protein [Homo sapiens] >gi 1737066 (U56085) periodic
                  tryptophan protein 2 [Homo sapiens] >gi 1737072 (U56089)
                  periodic tryptophan protein 2 [Homo sapiens]
Seq. No.
                   27732
Contig ID
                  160874 1.R1040
5'-most EST
                   zhf700\overline{9}63734.h1
                  27733
Seq. No.
Contig ID
                  160918 1.R1040
5'-most EST
                  smc700747781.h1
                   27734
Seq. No.
Contig ID
                  160950 1.R1040
                  smc700749017.h1
5'-most EST
Seq. No.
                  27735
Contig ID
                  160950 2.R1040
5'-most EST
                  uC-gmrominsoy032a05b1
                  27736
Seq. No.
Contig ID
                  160972 1.R1040
5'-most EST
                  pmv700893606.h1
Method
                  BLASTX
NCBI GI
                  q2245069
BLAST score
                  575
E value
                  2.0e-59
Match length
                  147
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
```

NCBI GI

```
27737
 Seq. No.
 Contig ID
                    160983 1.R1040
 5'-most EST
                    smc700747596.h1
 Method
                    BLASTX
                    g1752734
 NCBI GI
 BLAST score
                    218
 E value
                    5.0e-18
 Match length
                    85
 % identity
                    49
                    (D78510) beta-glucan-elicitor receptor [Glycine max]
 NCBI Description
 Seq. No.
                    27738
 Contig ID
                    160985 1.R1040
 5'-most EST
                    uC-gmrominsoy320g06b1
 Seq. No.
                    27739
 Contig ID
                    160992 1.R1040
 5'-most EST
                    smc700747620.h1
                    27740
 Seq. No.
 Contig ID
                    161005 1.R1040
 5'-most EST
                    fde700871538.hl
                    27741
 Seq. No.
Contig ID
                    161006 1.R1040
 5'-most EST
                    jC-gmro02910007d03d1
                    27742
 Seq. No.
 Contig ID
                    161056 1.R1040
 5'-most EST
                    uC-gmropic008f11b1
 Method
                    BLASTX
 NCBI GI
                    q2088651
 BLAST score
                    349
 E value
                    6.0e-33
 Match length
                    121
                    55
 % identity
 NCBI Description
                    (AF002109) hypersensitivity-related gene 201 isolog
                    [Arabidopsis thaliana]
                    27743
 Seq. No.
 Contig ID
                    161065 1.R1040
 5'-most EST
                    zsg701128088.hl
 Method
                    BLASTX
 NCBI GI
                    q3550588
 BLAST score
                    277
                    2.0e-24
 E value
                    143
 Match length
 % identity
                    49
                    (AJ010643) heat shock transcription factor (HSFA) [Pisum
 NCBI Description
                    sativum]
                    27744
 Seq. No.
 Contig ID
                    161165 1.R1040
 5'-most EST
                    kl1701210268.h1
                    BLASTX
 Method
```

g3135265

```
BLAST score
                   216
                   6.0e-24
E value
Match length
                   114
% identity
                   50
NCBI Description
                   (AC003058) unknown protein [Arabidopsis thaliana]
                   27745
Seq. No.
Contig ID
                   161172 1.R1040
                   rca700\overline{9}98634.h1
5'-most EST
Seq. No.
                   27746
Contig ID
                   161183 1.R1040
5'-most EST
                   zhf700957607.h1
                   27747
Seq. No.
Contig ID
                   161199 1.R1040
5'-most EST
                   smc700747996.h1
Method
                   BLASTX
                   g4140691
NCBI GI
BLAST score
                   174
                   8.0e-13
E value
Match length
                   69
% identity
                   (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
NCBI Description
                   27748
Seq. No.
Contig ID
                   161214_1.R1040
5'-most EST
                   uC-gmropic102g11b1
Method
                   BLASTX
NCBI GI
                   g2129953
BLAST score
                   505
E value
                   3.0e-51
Match length
                   127
% identity
                   69
                   laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542).
NCBI Description
                   diphenol oxidase [Nicotiana tabacum]
                   27749
Seq. No.
                   161276 1.R1040
Contig ID
                   rca700997496.h1
5'-most EST
                   27750
Seq. No.
                   161302 1.R1040
Contig ID
5'-most EST
                   rca700\overline{9}98578.h1
Method
                   BLASTX
NCBI GI
                   g3319345
BLAST score
                   143
E value
                   3.0e-09
Match length
                   86
% identity
                   (AF077407) contains similarity to maize transposon MuDR
NCBI Description
                   (GB:M76978) [Arabidopsis thaliana]
                   27751
Seq. No.
                   161313 1.R1040'
Contig ID
```

zsg701126738.hl

BLASTX

5'-most EST Method

Method

BLASTX

```
q2264380
NCBI GI
BLAST score
                  391
                  9.0e-38
E value
Match length
                  89
% identity
                  88
NCBI Description
                   (AC002354) NAD+ dependent isocitrate dehydrogenase subunit
                  2 [Arabidopsis thaliana]
                  27752
Seq. No.
Contig ID
                  161326 1.R1040
5'-most EST
                  smc700748137.hl
Method
                  BLASTX
                  g2500547
NCBI GI
BLAST score
                  298
E value
                  5.0e-30
Match length
                  184
% identity
                  45
                  DIS3 PROTEIN >gi 2131990 pir S66704 hypothetical protein
NCBI Description
                  YOL021c - yeast (Saccharomyces cerevisiae)
                  >gi 1419801_emb_CAA99021_ (Z74763) ORF YOL021c
                  [Saccharomyces cerevisiae] >gi 1754617 dbj BAA11176
                   (D76430) DIS3 protein [Saccharomyces cerevisiae]
Seq. No.
                  27753
Contig ID
                  161340 1.R1040
5'-most EST
                  fC-gmro7000748156a1
Method
                  BLASTX
NCBI GI
                  q4539004
BLAST score
                  609
E value
                  2.0e-63
Match length
                  169
% identity
                  66
NCBI Description (ALO49481) putative protein kinase [Arabidopsis thaliana]
                  27754
Seq. No.
Contig ID
                  161362 1.R1040
5'-most EST
                  smc700748191.h1
Seq. No.
                  27755
Contig ID
                  161398 1.R1040
5'-most EST
                  smc700748247.h1
Method
                  BLASTX
NCBI GI
                  g3292821 .
BLAST score
                  146
E value
                  3.0e-09
Match length
                  67
% identity
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  161431 1.R1040
5'-most EST
                  zpv700763075.h1
Seq. No.
                  27757
Contiq ID
                  161435 1.R1040
5'-most EST
                  uC-gmflminsoy091e02b1
```

```
g4205079
NCBI GI
                   204
BLAST score
E value
                   1.0e-15
Match length
                   150
 % identity
                   (U70425) ankyrin repeat-containing protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   27758
Contig ID
                   161438 1.R1040
                   smc700749922.hl
5'-most EST
Seq. No.
                   27759
Contig ID
                   161443 1.R1040
5'-most EST
                   zhf700958132.hl
                   27760
Seq. No.
Contig ID
                   161460 1.R1040
5'-most EST
                  asn701133614.h2
                   27761
Seq. No.
Contig ID
                   161466 1.R1040
5'-most EST
                   jC-gmst02400055g07a1
                   BLASTX
Method
                   g3033388
NCBI GI
BLAST score
                   195
E value
                   8.0e-15
Match length
                   112
% identity
NCBI Description
                   (AC004238) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27762
Contig ID
                   161488 1.R1040
5'-most EST
                   fua701040684.hl
                   27763
Seq. No.
                   161490 1.R1040
Contig ID
5'-most EST
                   smc700748381.hl
Seq. No.
                   27764
Contig ID
                   161515_1.R1040
5'-most EST
                   fC-gmro7000748409f1
Method
                   BLASTX
NCBI GI
                   q2982431
                   199
BLAST score
E value
                   4.0e-15
Match length
                   155
% identity
                   (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   27765
Seq. No.
                   161531_1.R1040
Contig ID
5'-most EST
                   fC-gmro700847984r1
Method
                   BLASTX
                   g1236961
NCBI GI
```

285

BLAST score

Contig ID

```
2.0e-25
E value
Match length
                   68
% identity
                   75
NCBI Description
                   (U50201) prunasin hydrolase precursor [Prunus serotina]
Seq. No.
                   27766
                   161531 2.R1040
Contig ID
5'-most EST
                   smc700748435.hl
                   27767
Seq. No.
Contig ID
                  161545 1.R1040
5'-most EST
                  asn701139424.hl
                  BLASTX
Method
NCBI GI
                  q2829887
BLAST score
                   306
E value
                   3.0e-28
Match length
                   93
% identity
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  27768
Contig ID
                  161550 1.R1040
5'-most EST
                  fC-gmro7000748459f1
Method
                  BLASTX
NCBI GI
                  g2760839
BLAST score
                  260
E value
                  2.0e-22
Match length
                  169
                  25
% identity
NCBI Description
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
                  27769
Seq. No.
Contig ID
                  161570 1.R1040
5'-most EST
                  uC-gmronoir052g11b1
Method
                  BLASTX
NCBI GI
                  q3367578
BLAST score
                  464
E value
                  3.0e-46
Match length
                  120
% identity
                   69
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  27770
Contig ID
                  161576 1.R1040
5'-most EST
                  uC-gmrominsoy312h07b1
Method
                  BLASTN
NCBI GI
                  g3643588
BLAST score
                  52
E value
                  5.0e-20
Match length
                  116
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  27771
```

161577_1.R1040

```
5'-most EST
                  zhf700952184.h1
Method
                  BLASTX
                  g4455307
NCBI GI
BLAST score
                  542
                  2.0e-55
E value
Match length
                  106
% identity
                  91
                  (AL035528) methionyl-tRNA synthetase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  27772
Seq. No.
Contig ID
                  161604 1.R1040
5'-most EST
                  fC-gmro700748540a2
Method
                  BLASTX
NCBI GI
                  q4539320
BLAST score
                  562
E value
                  6.0e-58
Match length
                  152
% identity
NCBI Description
                  (AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis
                  thaliana]
Seq. No.
                  27773
Contig ID
                  161607 1.R1040
5'-most EST
                  smc700748580.hl
Seq. No.
                  27774
Contig ID
                  161610 1.R1040
5'-most EST
                  smc700748551.hl
                  27775
Seq. No.
Contig ID
                  161650 1.R1040
5'-most EST
                  smc700748596.h1
                  27776
Seq. No.
                  161667 1.R1040
Contig ID
5'-most EST
                  smc700748623.h1
                  27777
Seq. No.
Contig ID
                  161727 1.R1040
5'-most EST
                  bth700847982.h1
Method
                  BLASTX
NCBI GI
                  q112947
BLAST score
                  202
E value
                  8.0e-16
Match length
                  88
% identity
                  31
NCBI Description
                  AAC-RICH MRNA CLONE AAC3 PROTEIN >gi 84121 pir S05357
                  hypothetical protein (clone AAC3) - slime mold
                  (Dictyostelium discoideum) (fragment)
                  >gi 7176 emb CAA34531 (X16524) coding region (AA 1 - 437)
                  [Dictyostelium discoideum]
Seq. No.
                  27778
Contig ID
                  161758 1.R1040
```

smc700748749.hl

5'-most EST

Contig ID

```
27779
Seq. No.
Contig ID
                   161780 1.R1040
5'-most EST
                   smc700748780.hl
Seq. No.
                   27780
                   161788 1.R1040
Contig ID
5'-most EST
                   uC-qmropic016b02b1
Seq. No.
                   27781
Contig ID
                   161836 1.R1040
5'-most EST
                   jC-gmf102220108c08a1
Method
                   BLASTX
NCBI GI
                   g3850585
BLAST score
                   191
E value
                   2.0e-14
Match length
                   52
% identity
NCBI Description
                   (AC005278) ESTs gb_H36966, gb R65511, gb_T42324 and
                   gb T20569 come from this gene. [Arabidopsis thaliana]
                   27782
Seq. No.
Contig ID
                   161836 2.R1040
5'-most EST
                   qsv701\overline{0}50118.h1
Method
                   BLASTX
NCBI GI
                   g3850585
BLAST score
                   191
E value
                   2.0e-14
Match length
                   52
% identity
NCBI Description
                   (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and
                   gb_T20569 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   27783
Contig ID
                   161836 3.R1040
5'-most EST
                   jsh701\overline{0}66140.h1
Method
                   BLASTX
NCBI GI
                   q3850585
BLAST score
                   172
E value
                   2.0e-12
Match length
                   43
% identity
NCBI Description
                   (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and
                   gb T20569 come from this gene. [Arabidopsis thaliana]
                   27784
Seq. No.
Contig ID
                   161856 1.R1040
                   smc700748885.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2213592
BLAST score
                   211
E value
                   3.0e-17
Match length
                   85
% identity
NCBI Description
                  (AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.
                   27785
```

161859 1.R1040

```
5'-most EST
                   smc700748888.h1
Method
                   BLASTX
NCBI GI
                   g3786009
BLAST score
                   379
                   7.0e-37
E value
Match length
                   87
% identity
                   82
NCBI Description
                   (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   27786
                   161865 1.R1040
Contig ID
5'-most EST
                   gsv701047952.hl
                   27787
Seq. No.
Contig ID
                   161881 1.R1040
5'-most EST
                   fC-gmro7000748929a1
Method
                   BLASTX
                   g2760836
NCBI GI
BLAST score
                   202
E value
                   2.0e-15
Match length
                   111
% identity
                   40
NCBI Description
                   (AC003105) putative Ser/Thr protein kinase [Arabidopsis
Seq. No.
                   27788
Contig ID
                   161885 1.R1040
5'-most EST
                   zlv700807563.h1
Seq. No.
                   27789
Contig ID
                   161912 1.R1040
5'-most EST
                   smc700749012.h1
Seq. No.
                   27790
Contig ID
                   161913 1.R1040
5'-most EST
                   smc700749013.h1
Seq. No.
                   27791
                   161922 1.R1040
Contig ID
5'-most EST
                   smc700749027.h1
Method
                   BLASTX
NCBI GI
                   q995714
BLAST score
                   231
E value
                   3.0e-23
Match length
                   129
% identity
NCBI Description
                  (X91258) L3177 [Saccharomyces cerevisiae]
Seq. No.
                   27792
Contig ID
                   162005 1.R1040
5'-most EST
                   jsh701\overline{0}66291.h1
Seq. No.
                   27793
Contig ID
                   162025 1.R1040
5'-most EST
                   smc700749221.h1
Method
                   BLASTX
NCBI GI
                   q4249402
```

Method

BLASTX

```
BLAST score
                   219
E value
                   1.0e-17
Match length
                   153
% identity
                   39
NCBI Description
                   (AC006072) unknown protein [Arabidopsis thaliana]
                   27794
Seq. No.
                   162054 1.R1040
Contig ID
                   hrw701\overline{0}62841.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2388689
BLAST score
                   328
E value
                   2.0e-35
Match length
                   94
% identity
NCBI Description
                   (AF016633) GH1 protein [Glycine max]
Seq. No.
                   27795
Contig ID
                   162064 1.R1040
5'-most EST
                   pmv700895230.h1
Method
                   BLASTX
NCBI GI
                   q1076498
BLAST score
                   170
E value
                   6.0e-12
Match length
                   70
                   49
% identity
NCBI Description
                   zinc-finger protein (C-terminal) - soybean
                   >gi_558543_emb_CAA85320_ (Z36749) C-terminal zinc-finger
                   [Glycine max]
                   27796
Seq. No.
Contig ID
                   162154 1.R1040
5'-most EST
                   uC-qmronoir000h01b1
                   27797
Seq. No.
Contig ID
                   162179 1.R1040
5'-most EST
                   smc700749541.h1
                   27798
Seq. No.
Contig ID
                   162187 1.R1040
5'-most EST
                   smc700\overline{7}49560.h1
Seq. No.
                   27799
Contig ID
                   162206 1.R1040
5'-most EST
                   qsv701\overline{0}50671.h1
                   BLASTX
Method
NCBI GI
                   q3393062
BLAST score
                   338
E value
                   6.0e-32
Match length
                   80
% identity
NCBI Description
                   (Y17386) putative In2.1 protein [Triticum aestivum]
Seq. No.
Contig ID
                   162214 1.R1040
5'-most EST
                   jC-gmst02400057g05a1
```

```
g2739379
NCBI GI
BLAST score
                  165
                   2.0e-11
E value
Match length
                  107
% identity
                   54
                   (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  27801
Seq. No.
                  162269 1.R1040
Contig ID
5'-most EST
                  smc700749733.h1
Method
                  BLASTN
                  g3882144
NCBI GI
BLAST score
                  172
                   3.0e-92
E value
Match length
                  223
% identity
                   95
                  Homo sapiens mRNA for KIAA0712 protein, complete cds
NCBI Description
                  27802
Seq. No.
Contig ID
                  162278 1.R1040
5'-most EST
                   jC-qmro02910030a07a1
Method
                  BLASTX
NCBI GI
                  g3335357
BLAST score
                  597
E value
                   5.0e-62
Match length
                  123
% identity
NCBI Description
                   (AC003028) putative diphenol oxidase [Arabidopsis thaliana]
Seq. No.
                  162307 1.R1040
Contig ID
5'-most EST
                  eep700864855.hl
                  27804
Seq. No.
Contig ID
                  162329 1.R1040
5'-most EST
                  jC-gmro02910039g11a1
Seq. No.
                  27805
Contig ID
                  162329 2.R1040
5'-most EST
                  zhf700962763.h1
Seq. No.
                  27806
Contig ID
                  162333 1.R1040
5'-most EST
                  kl1701202535.h1
                  27807
Seq. No.
                  162346 1.R1040
Contig ID
5'-most EST
                  smc700749796.h1
Method
                  BLASTN
NCBI GI
                  q3309572
BLAST score
                  182
                  5.0e-98
E value
                  227
Match length
% identity
NCBI Description
                  Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA,
```

complete cds >gi_4505460_ref_NM_003633.1_NRPB_ Homo sapiens nuclear restricted protein, BTB domain-like (brain) (NRPB)

mRNA, and translated products

27808 Seq. No. Contig ID 162360 1.R1040 5'-most EST smc700749822.h1 Method BLASTX q3172025 NCBI GI BLAST score 559 1.0e-57 E value Match length 140 75 % identity (AB005805) aldehyde oxidase [Arabidopsis thaliana] NCBI Description 27809 Seq. No. Contig ID 162361 1.R1040 5'-most EST uC-gmronoir049h07b1 Seq. No. 27810 162414 1.R1040 Contig ID 5'-most EST uC-qmropic019e08b1 Seq. No. 27811 Contig ID 162419 1.R1040 5'-most EST pmv700893728.h1 Method BLASTX NCBI GI q4510377 BLAST score 146 E value 2.0e-09 Match length 76 % identity NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana] Seq. No. 27812 Contig ID 162420 1.R1040 5'-most EST dpv701101092.h1 Seq. No. 27813 Contig ID 162447 1.R1040 5'-most EST smc700749945.hl 27814 Seq. No. Contig ID 162452 1.R1040 5'-most EST smc700749951.h1 Method BLASTX NCBI GI q3413700 BLAST score 388 E value 1.0e-37 Match length 118 % identity NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana] Seq. No. 162457 1.R1040 Contig ID 5'-most EST smc700749958.hl

27816

162466 1.R1040

Seq. No.

Contig ID

E value

3.0e-28

```
5'-most EST
                   smc700749970.h1
                   27817 .
Seq. No.
                   162487 1.R1040
Contig ID
                   smc700750012.hl
5'-most EST
                   27818
Seq. No.
                   162502 1.R1040
Contig ID
5'-most EST
                   fC-qmro700750041a2
Method
                   BLASTX
                   g4138209
NCBI GI
BLAST score
                   309
                   3.0e-28
E value
Match length
                   140
% identity
                   43
NCBI Description
                   (AJ223071) serine/threonine kinase protein MSTK2L,long-form
                   [Mus musculus]
Seq. No.
                   27819
Contig ID
                   162513 1.R1040
5'-most EST
                   uC-gmropic108f03b1
Method
                   BLASTX
NCBI GI
                   g1946367
BLAST score
                   330
E value
                   3.0e-30
Match length
                   176
% identity
NCBI Description
                   (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   162513 2.R1040
5'-most EST
                   uC-gmropic037c12b1
Method
                   BLASTX
NCBI GI
                   g3738298
BLAST score
                   157
E value
                   9.0e-16
Match length
                   77
% identity
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
                   >gi 4249394 (AC006072) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   27821
Contig ID
                   162514 1.R1040
5'-most EST
                   uC-qmrominsoy128d07b1
Seq. No.
                   27822
Contig ID
                   162530 1.R1040
5'-most EST
                   uC-gmropic106c05b1
Seq. No.
                   27823
Contig ID
                   162532 1.R1040
5'-most EST
                   k11701\overline{2}14995.h1
Method
                   BLASTX
NCBI GI
                   q3063451
BLAST score
                   182
```

Contig ID

5'-most EST

```
Match length
                   143
% identity
                   51
NCBI Description
                   (AC003981) F22013.13 [Arabidopsis thaliana]
Seq. No.
                   27824
Contig ID
                   162540 1.R1040
5'-most EST
                   uC-gmflminsoy065h02b1
                   27825
Seq. No.
                   162543 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy138e10b1
                   27826
Seq. No.
                   162562 1.R1040
Contig ID
5'-most EST
                   fC-gmro700750148a2
Method
                   BLASTX
                   g2935300
NCBI GI
BLAST score
                   602
E value
                   1.0e-62
Match length
                   135
% identity
                   (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                   2 [Gossypium hirsutum]
Seq. No.
                   27827
Contig ID
                   162574 1.R1040
                   rca700\overline{9}98968.h1
5'-most EST
Seq. No.
                   27828
Contig ID
                   162582 1.R1040
5'-most EST
                   crh700851350.hl
Seq. No.
                   27829
Contig ID
                   162624 1.R1040
                   smc700750249.h1
5'-most EST
Seq. No.
                   27830
Contig ID
                   162632 1.R1040
5'-most EST
                   sat701009548.hl
Seq. No.
                   27831
Contig ID
                   162649 1.R1040
5'-most EST
                   fC-qmro700750285a2
Method
                  BLASTX
NCBI GI
                  q1888357
BLAST score
                   624
E value
                   7.0e-65
Match length
                  227
% identity
                   57
NCBI Description
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >qi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  27832
```

162661 1.R1040 kl1701212328.hl

5'-most EST

Method

```
Seq. No.
                   27833
                   162672 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220141e11a1
Seq. No.
                   27834
                   162680 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220085h08a1
Method
                   BLASTX
NCBI GI
                   g3402677
BLAST score
                   176
E value
                   1.0e-12
Match length
                   77
                   49
% identity
NCBI Description
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   27835
                   162703 1.R1040
Contig ID
                   smc700750385.h1
5'-most EST
                   27836
Seq. No.
Contig ID
                   162723 1.R1040
5'-most EST
                   smc700750417.h1
                   27837
Seq. No.
                   162762 2.R1040
Contig ID
5'-most EST
                  pmv700890418.h1
Method
                   BLASTX
NCBI GI
                   g2588895
BLAST score
                   216
E value
                   1.0e-17
Match length
                   91
% identity
NCBI Description (AB008515) RanBPM [Homo sapiens]
                   27838
Seq. No.
                   162775 1.R1040
Contig ID
5'-most EST
                   tku700646303.h1
                   27839
Seq. No.
                   162783 1.R1040
Contig ID
5'-most EST
                   sat701011406.hl
Seq. No.
                  27840
                  162784 1.R1040
Contig ID
5'-most EST
                  rca701000069.h1
Method
                  BLASTX
NCBI GI
                   q2654868
BLAST score
                   461
                  4.0e-46
E value
Match length
                  125
% identity
NCBI Description
                  (AF015301) RbohAp108 [Arabidopsis thaliana]
Seq. No.
                  27841
                  162807 1.R1040
Contig ID
```

uC-gmrominsoy125h06b1

BLASTX

Method

NCBI GI

BLASTX

q134889

```
NCBI GI
                   g3335060
BLAST score
                   632 ·
                   6.0e-66
E value
Match length
                   170
% identity
                   70
NCBI Description
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
                   thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma
                   membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                   27842
                   162810 1.R1040
Contig ID
5'-most EST
                   tku700646344.hl
Seq. No.
                   27843
Contig ID
                   162838 1.R1040
5'-most EST
                   fua701041113.hl
Seq. No.
                   27844
Contig ID
                   162841 1.R1040
                   k11701\overline{2}07057.h1
5'-most EST
Seq. No.
                   27845
Contig ID
                   162858 1.R1040
5'-most EST
                   awf700841108.h1
                   27846
Seq. No.
Contig ID
                   162885 1.R1040
5'-most EST
                   pxt700945733.h1
Method
                   BLASTX
NCBI GI
                   q3377802
BLAST score
                   449
E value
                   8.0e-45
Match length
                   122
% identity
NCBI Description
                   (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis
                   thaliana]
Seq. No.
                   27847
Contig ID
                   162943 1.R1040
5'-most EST
                   ujr700\overline{6}46531.h1
Seq. No.
                   27848
Contig ID
                   162946 1.R1040
5'-most EST
                   jC-gmst02400072d11a1
Method
                   BLASTX
NCBI GI
                   q1946367
BLAST score
                   328
E value
                   2.0e-30
Match length
                   86
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                   27849
Contig ID
                   162954 1.R1040
5'-most EST
                  qsv701047970.h1
```

```
BLAST score
                  249
E value
                  4.0e-21
Match length
                  165
% identity
                  35
NCBI Description
                  SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)
                  >gi 108065 pir S12981 68K protein - gray wolf
                  >gi 227342 prf 1702226A SRP68 protein [Canis familiaris]
Seq. No.
                  27850
Contig ID
                  162964 1.R1040
                  hrw701062474.hl
5'-most EST
Seq. No.
                  27851
Contig ID
                  162965 1.R1040
5'-most EST
                  pxt700945737.h1
Seq. No.
                  27852
Contig ID
                  162980 1.R1040
5'-most EST
                  jsh701068517.hl
Seq. No.
                  27853
Contig ID
                  162987 1.R1040
5'-most EST
                  zhf700963936.h1
                  27854
Seq. No.
Contig ID
                  162991 1.R1040
5'-most EST
                  uC-gmropic021g10b1
                  BLASTX
Method
NCBI GI
                  q1419036
BLAST score
                  438
E value
                  2.0e-43
Match length
                  116
% identity
NCBI Description
                  (X98421) delta-1-pyrroline-5-carboxylate synthase [Medicago
                  sativa]
                  27855
Seq. No.
Contig ID
                  162991 2.R1040
5'-most EST
                  jC-gmro02910066g03a1
                  BLASTX
Method
NCBI GI
                  q1709534
BLAST score
                  460
E value
                  4.0e-46
Match length
                  140
% identity
                  69
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                  (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                  (GLUTAMYL-GAMMA-SEMIALDE... >gi 2129572 pir S66637
                  delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis
                  thaliana >gi_829100_emb_CAA60740_ (X87330)
                  pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
                  >gi_870866 emb CAA60446 (X86777) pyrroline-5-carboxylate
                  synthetase A [Arabidopsis thaliana]
                  >gi_1041248_emb CAA61593 (X89414) pyrroline-5-carboxylate
```

synthase [Arabidopsis thaliana] >gi 2642162 (AC003000)

```
Seq. No.
                   27856
Contig ID
                   163015 1.R1040
5'-most EST
                   ujr700646622.hl
Seq. No.
                   27857
Contig ID
                   163018 1.R1040
5'-most EST
                   uC-gmrominsoy155b12b1
Seq. No.
                   27858
Contig ID
                   163055 1.R1040
5'-most EST
                   ujr700646676.h1
Seq. No.
                   27859
Contig ID
                   163069 1.R1040
5'-most EST
                  bth700844272.h1
                   27860-
Seq. No.
Contig ID
                   163071 1.R1040
5'-most EST
                  jC-gmro02910062c04a1
                   27861
Seq. No.
                   163080 1.R1040
Contig ID
5'-most EST
                   vzy700750670.hl
Method
                   BLASTN
NCBI GI
                   g1947070
BLAST score
                   229
E value
                   1.0e-126
Match length
                   245
% identity
NCBI Description
                  Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene,
                  complete cds
                   27862
Seq. No.
                  163094 1.R1040
Contig ID
5'-most EST
                  g5057812
Method
                  BLASTX
NCBI GI
                  q3643082
BLAST score
                   348
E value
                  2.0e-32
Match length
                  100
% identity
NCBI Description (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
Seq. No.
                  27863
                  163101 1.R1040
Contig ID
5'-most EST
                  vzy700750543.h1
Method
                  BLASTX
NCBI GI
                  q282881
BLAST score
                  237
E value
                  3.0e-20
Match length
                  82
% identity
                  56
NCBI Description receptor-like protein kinase precursor - Arabidopsis
```

delta-1-pyrroline 5-carboxylase synthetase, P5C1

[Arabidopsis thaliana]

```
thaliana >qi 166846 (M84658) receptor-like protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  27864
Contig ID
                  163102 1.R1040
```

uC-qmflminsoy030a08b1

Seq. No. 27865

5'-most EST

Contig ID 163147 1.R1040 5'-most EST vzy700750613.h1

Method BLASTX NCBI GI q4455171 BLAST score 185 E value 5.0e-14 Match length 73 % identity 62

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

27866 Seq. No.

Contig ID 163148 1.R1040 5'-most EST zsq701120644.h1 Method BLASTX

g3047111 NCBI GI BLAST score 536 E value 5.0e-55 Match length 125 % identity

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.

163154 1.R1040 Contig ID . 5'-most EST zhf700952519.h1

27868 Seq. No.

Contig ID 163165 1.R1040 5'-most EST vzy700750638.hl

Seq. No. 27869

Contig ID 163168 1.R1040 5'-most EST vzy700750650.h1

Seq. No.

Contig ID 163175 1.R1040 5'-most EST fC-qmse7000751147f1

Method BLASTX NCBI GI q120745 BLAST score 893 E value 2.0e-96 Match length 229 % identity

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI)

>gi 68450 pir NUBY glucose-6-phosphate isomerase (EC

5.3.1.9) - yeast (Saccharomyces cerevisiae)

>gi_4135_emb_CAA32158 (X13977) phosphoglucose isomerase (AA 1-554) [Saccharomyces cerevisiae] >gi 172142 (M37267) phosphoglucose isomerase (EC 5.3.1.9) [Saccharomyces

```
cerevisiae] >gi_172225 (M21696) phosophoglucoisomerase (EC 5.3.1.9) [Saccharomyces cerevisiae] >gi_311672_emb_CAA79683_ (Z21487) glycolytic enzyme phosphoglucoisomerase [Saccharomyces cerevisiae] >gi_536565_emb_CAA85158_ (Z36065) ORF YBR196c [Saccharomyces cerevisiae]
```

Seq. No. 27871

Contig ID 163178 1.R1040 5'-most EST zhf700955950.h1

Seq. No. 27872

Contig ID 163179_1.R1040 5'-most EST zsg701126321.h1

Seq. No. 27873

Contig ID 163195_1.R1040 5'-most EST zzp700831750.h1

Method BLASTN
NCBI GI 9871468
BLAST score 142
E value 4.0e-74
Match length 280
% identity 90

NCBI Description H.annuus mitochondrion genes trnH and trnE

Seq. No. 27874

Contig ID 163205_1.R1040 5'-most EST vzy700750716.h1

Seq. No. 27875

Contig ID 163225_1.R1040 5'-most EST awf700837938.h1

Seq. No. 27876

Contig ID 163241_1.R1040

5'-most EST uC-gmflminsoy117a12b1

Seq. No. 27877

Contig ID 163271 1.R1040 5'-most EST vzy700750891.h1

Seq. No. 27878

Contig ID 163277_1.R1040 5'-most EST vzy700750823.h1

Seq. No. 27879

Contig ID 163292_1.R1040 5'-most EST zhf700955919.h1

Seq. No. 27880

Contig ID 163294_1.R1040 5'-most EST vzy700750849.h1

Seq. No. 27881

Contig ID 163301_1.R1040 5'-most EST rca700996549.h1

Match length

```
Method
                    BLASTX
 NCBI GI
                    g4176531
 BLAST score
                    260
 E value
                    1.0e-22
 Match length
                    95
 % identity
                    47
 NCBI Description
                    (AL035263) weak similarity to chick phosphatidylcholine-ste
                    rol acetyltransferase [Schizosaccharomyces pombe]
Seq. No.
                    27882
Contig ID
                    163328 1.R1040
 5'-most EST
                    zzp700833379.h1
Seq. No.
                   27883
Contig ID
                   163340 1.R1040
5'-most EST
                   uC-gmrominsoy097a01b1
Seq. No.
                   27884
Contig ID
                   163362 1.R1040
5'-most EST
                   jC-gmf102220141e03a1
Seq. No.
                   27885
Contig ID
                   163376 1.R1040
5'-most EST
                   epx701\overline{1}06687.h1
Method
                   BLASTN
NCBI GI
                   g2218149
BLAST score
                   94
E value
                   2.0e-45
Match length
                   218
% identity
NCBI Description
                   Vigna unguiculata type IIIa membrane protein cp-wap11 mRNA,
                   complete cds
Seq. No.
                   27886
Contig ID
                   163387 1.R1040
5'-most EST
                   vzy700750993.h1
Seq. No.
                   27887
Contig ID
                   163395 1.R1040
5'-most EST
                   fde700876383.h1
Seq. No.
                   27888
Contig ID
                   163406 1.R1040
5'-most EST
                   vzy700751028.hl
Seq. No.
                   27889
Contig ID
                   163415 1.R1040
5'-most EST
                   zhf700953130.h1
Seq. No.
                   27890
Contig ID
                   163463 1.R1040
5'-most EST
                   vzy700751115.h1
Method
                   BLASTX
NCBI GI
                   q4115371
BLAST score
                   601
E value
                   4.0e-62
```

```
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                  163471 1.R1040
5'-most EST
                  vzy700751131.h1
                  27892
Seq. No.
Contig ID
                  163487 1.R1040
5'-most EST
                  vzy700751154.hl
Method
                  BLASTN
NCBI GI
                  q340697
BLAST score
                  331
                  0.0e + 00
E value
Match length
                  375
% identity
                  84
NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA
                  27893
Seq. No.
                  163491 1.R1040
Contig ID
5'-most EST
                  vzy700751160.h1
                  27894
Seq. No.
                  163497 1.R1040
Contig ID
5'-most EST
                  vzy700751180.hl
Method
                  BLASTN
NCBI GI
                  g392991
BLAST score
                  143
E value
                  9.0e-75
Match length
                  287
% identity
NCBI Description
                  Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete
                  27895
Seq. No.
                  163508 1.R1040
Contig ID
                  vzy700751201.hl
5'-most EST
Seq. No.
                  27896
                  163514 1.R1040
Contig ID
                  vzy700751208.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2388574
BLAST score
                  276
E value
                  4.0e-24
Match length
                  83
% identity
                  75
NCBI Description
                  (AC000098) Strong similarity to Phalaenopsis homeobox
                  protein (gb U34743). [Arabidopsis thaliana]
                  27897
Seq. No.
                  163557 1.R1040
Contig ID
                  vzy700751274.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2655008
BLAST score
                  150
```

4.0e-10

E value

Seq. No.

```
52
  Match length
                     46
  % identity
                     (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
  NCBI Description
                     esculentum]
  Seq. No.
                     27898
                     163558 1.R1040
  Contig ID
                     pmv700894549.h1
  5'-most EST
                     27899
  Seq. No.
  Contig ID
                     163567 1.R1040
                     bth700846161.h1
  5'-most EST
                     27900
  Seq. No.
                     163587 1.R1040
  Contig ID
  5'-most EST
                     awf700843147.hl
  Seq. No.
                     27901
                     163609 1.R1040
  Contig ID
                     pmv700888988.hl
  5'-most EST
                     27902
  Seq. No.
  Contig ID
                     163626 1.R1040
  5'-most EST
                     vzy700751413.hl
  Method
                     BLASTX
  NCBI GI
                     q3281850
  BLAST score
                     555
  E value
                     3.0e-57
  Match length
                     125
  % identity
                     81
                     (AL031004) monogalactosyldiacylglycerol synthase - like
  NCBI Description
                     protein [Arabidopsis thaliana]
  Seq. No.
                     27903
                     163633 1.R1040
  Contig ID
  5'-most EST
                     vzy700751420.hl
                     27904
  Seq. No.
  Contig ID
                     163645 1.R1040
  5'-most EST
                     vzy700751441.h1
                     27905
  Seq. No.
                     163695 1.R1040
  Contig ID
· 5'-most EST
                     vzy700751535.h1
  Seq. No.
                     27906
                     163712 1.R1040
  Contig ID
  5'-most EST
                     vzy700751804.h1
  Method
                     BLASTX
  NCBI GI
                     g32709
  BLAST score
                     288
                     3.0e-26
  E value
                     81
  Match length
  % identity
  NCBI Description
                    (X62570) IFP53 [Homo sapiens]
```

Match length

```
163733 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy076c09b1
Method
                   BLASTX
                   g4193320
NCBI GI
BLAST score
                   181
                   6.0e-17
E value
                   55
Match length
                   75
% identity
                   (AF045473) histone deacetylase [Zea mays]
NCBI Description
                   27908
Seq. No.
                   163733 2.R1040
Contig ID
                   awf700841470.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3023947
BLAST score
                   202
E value
                   7.0e-16
Match length
                   45
% identity
                   76
                   PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi 2665840
NCBI Description
                   (AF035815) putative histone deacetylase RPD3 [Zea mays]
Seq. No.
                   27909
Contig ID
                   163771 1.R1040
5'-most EST
                   zzp700833196.hl
Seq. No.
                   27910
Contig ID
                   163782 1.R1040
5'-most EST
                   fC-qmse700752579a1
Method
                   BLASTX
NCBI GI
                   q4140255
BLAST score
                   455
E value
                   4.0e-45
Match length
                   160
% identity
                   (AJ009973) hexokinase [Aspergillus niger]
NCBI Description
Seq. No.
                   27911
Contig ID
                   163811 1.R1040
5'-most EST
                   jsh701\overline{0}69592.h1
Seq. No.
                   27912
Contig ID
                   163814 1.R1040
5'-most EST
                   leu701149792.hl
                   27913
Seq. No.
Contig ID
                   163830 1.R1040
5'-most EST
                   vzy700756824.h1
                   27914
Seq. No.
Contig ID
                   163831 1.R1040
5'-most EST
                   jC-gmst02400053f04a1
Method
                   BLASTX
NCBI GI
                   q4107099
BLAST score
                   465
E value
                   2.0e-46
```

200

```
% identity
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi 4156245 dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
Seq. No.
                   27915
                   163866 1.R1040
Contig ID
5'-most EST
                   zsg701120567.hl
                   27916
Seq. No.
                   163877 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy045e04b1
Method
                  BLASTX
NCBI GI
                   q4539359
BLAST score
                   236
E value
                   1.0e-19
Match length
                   131
% identity
                   39
                   (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27917
                   163877 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy093b06b1
Method
                  BLASTX
                  g2244949
NCBI GI
BLAST score
                  206
E value
                   3.0e-16
Match length
                   98
                   48
% identity
NCBI Description
                   (Z97339) similarity to ORF - Lilium longiflorum
                   [Arabidopsis thaliana]
Seq. No.
                   27918
Contig ID
                   163877 3.R1040
5'-most EST
                  uC-gmflminsoy063b02b1
Method
                  BLASTX
NCBI GI
                  g2244949
BLAST score
                   152
E value
                   5.0e-10
Match length
                   80
% identity
                   45
                   (Z97339) similarity to ORF - Lilium longiflorum
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  27919
Contig ID
                  163883 1.R1040
                   vzy700751835.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2225877
BLAST score
                  201
E value
                   4.0e-16
Match length
                  81
% identity
                   (AB002406) TIP49 [Rattus norvegicus] >gi 4106528 (AF100694)
NCBI Description
                  Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_
```

(AB001581) DNA helicase p50 [Rattus norvegicus]

```
27920
Seq. No.
                   163898 1.R1040
Contig ID
                   vzy700751866.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g1778095
BLAST score
                   327
E value
                   3.0e-30
Match length
                   124
% identity
NCBI Description
                   (U64903) putative sugar transporter; member of major
                   facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
                   27921
Seq. No.
                  163906_1.R1040
Contig ID
5'-most EST
                  leu701\overline{1}50641.h1
                  27922
Seq. No.
Contig ID
                  163909 1.R1040
5'-most EST
                  zzp700829891.h1
Method
                  BLASTX
NCBI GI
                  g4559327
BLAST score
                  236
E value
                  8.0e-20
                  109
Match length
                   50
% identity
NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  27923
                  164014 1.R1040
Contig ID
                  vzy700752066.h1
5'-most EST
Seq. No.
                  27924
Contig ID
                  164056_1.R1040
5'-most EST
                  jC-qmle01810078f10a1
                  BLASTX
Method
NCBI GI
                 g1495259
BLAST score
                 490
E value
                  3.0e-49
Match length
                  204
                  46
% identity
NCBI Description (X97826) orf04 [Arabidopsis thaliana]
                  27925
Seq. No.
Contig ID
                  164102 1.R1040
5'-most EST
                  jC-gmf102220052f06a1
Method
                  BLASTX
NCBI GI
                  g2492792
BLAST score
                  692
                  6.0e-73
E value
Match length
                  187
                  73
% identity
NCBI Description LATE NODULIN 56 (N-56) >gi 532290 dbj BAA07212 (D38015)
                  soybean late nodulin [Glycine max]
Seq. No.
                  27926
```

164102 2.R1040

Contig ID

Contig ID

5'-most EST

```
5'-most EST
                   zpv700763092.h1
Method
                   BLASTX
NCBI GI
                   g2492792
BLAST score
                   294
E value
                   2.0e-26
Match length
                   93
% identity
NCBI Description
                   LATE NODULIN 56 (N-56) >gi 532290 dbj BAA07212 (D38015)
                   soybean late nodulin [Glycine max]
                   27927
Seq. No.
                   164154 1.R1040
Contig ID
                   epx701105636.h1
5'-most EST
                   27928
Seq. No.
Contig ID
                   164156 1.R1040
                   vzy700752270.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2668492
BLAST score
                   198
                   3.0e-15
E value
Match length
                   151
                   36
% identity
NCBI Description
                   (D89981) metal-transporting P-type ATPase [Arabidopsis
                   thaliana]
                   27929
Seq. No.
Contig ID
                   164175 1.R1040
5'-most EST
                   uC-gmropic035g09b1
Seq. No.
                   27930
Contig ID
                   164205 1.R1040
5'-most EST
                   zhf700953905.h1
                   27931
Seq. No.
                   164230 1.R1040
Contig ID
5'-most EST
                   epx701105604.h1
Seq. No.
                   27932
                   164235 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy215c09b1
                   27933
Seq. No.
Contig ID
                   164269 1.R1040
5'-most EST
                   jex700\overline{9}07685.h1
Method
                   BLASTX
NCBI GI
                   g3342798
                   305
BLAST score
E value
                   8.0e-28
Match length
                   105
% identity
                   58
                   (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                   papaya]
Seq. No.
                   27934
```

164269 2.R1040

fua701036923.hl

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   g3342798
BLAST score
                  199
E value
                   1.0e-15
Match length
                   49
% identity
                   78
NCBI Description
                   (AF061240) glutamine cyclotransferase precursor [Carica
                  papaya]
                   27935
Seq. No.
Contig ID
                   164270 1.R1040
5'-most EST
                   pmv700893975.h1
Method
                   BLASTX
NCBI GI
                   q4220512
BLAST score
                   1125
E value
                   1.0e-123
Match length
                   258
% identity
                   79
NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]
                   27936
Seq. No.
Contig ID
                   164277 1.R1040
5'-most EST
                  uC-gmrominsoy102h05b1
                   27937
Seq. No.
Contig ID
                   164278 1.R1040
5'-most EST
                   vzy700752453.hl
                  BLASTX
Method
NCBI GI
                  g3046815
BLAST score
                  214
E value
                   5.0e-18
Match length
                  130
% identity
                   41
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
                  27938
Seq. No.
                  164337 1.R1040
Contig ID
5'-most EST
                  zhf700958489.h1
Seq. No.
                   27939
                  164425_1.R1040
Contig ID
5'-most EST
                   jC-gmf102220093h03a1
Method
                  BLASTX
NCBI GI
                  q4220524
BLAST score
                  268
                  2.0e-23
E value
                  68
Match length
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  27940
Seq. No.
                  164446 1.R1040
Contig ID
                  vzy700752710.h1
5'-most EST
Seq. No.
                  27941
                  164497 2.R1040
Contig ID
```

vzy700753311.hl

Match length

```
27942
Seq. No.
Contig ID
                   164507 1.R1040
5'-most EST
                   jC-qmf102220071g03d1
Method
                   BLASTX
NCBI GI
                   g2109293
BLAST score
                   237
                   9.0e-20
E value
Match length
                   55
% identity
                   80
                   (U97568) serine/threonine protein kinase [Arabidopsis
NCBI Description
Seq. No.
                   27943
Contig ID
                   164524 1.R1040
5'-most EST
                   vzy700752812.hl
Method
                   BLASTX
NCBI GI
                   q2979562
BLAST score
                   194
E value
                   6.0e-15
Match length
                   88
% identity
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3386623 (AC004665) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   27944
                   164529 1.R1040
Contig ID
5'-most EST
                   vzy700752822.hl
                   27945
Seq. No.
Contig ID
                   164541 1.R1040
5'-most EST
                   jC-gmf102220051c03a1
                   BLASTX
Method
NCBI GI
                   q1621465
BLAST score
                   172
E value
                   2.0e-12
Match length
                   109
% identity
NCBI Description
                   (U73105) laccase [Liriodendron tulipifera]
Seq. No.
                   27946
Contig ID
                   164557 1.R1040
5'-most EST
                   vzy700752856.h1
                   27947
Seq. No.
                   164563 1.R1040
Contiq ID
5'-most EST
                   vzy700752865.hl
Seq. No.
                   27948
                   164598 1.R1040
Contig ID
5'-most EST
                   zzp700833255.h1
Method
                   BLASTX
NCBI GI
                   g2651308
BLAST score
                   151
                   8.0e-10
E value
```

5'-most EST

```
% identity
NCBI Description
                  (AC002336) putative myosin heavy chain [Arabidopsis
                  thaliana]
Seq. No.
                  27949
Contig ID
                  164602 1.R1040
5'-most EST
                  uC-gmrominsoy207f12b1
                  27950
Seq. No.
                  164608 1.R1040
Contig ID
5'-most EST
                  pmv700894015.h1
Method
                  BLASTX
                  g3157949
NCBI GI
BLAST score
                  860
E value
                  9.0e-93
Match length
                  189
% identity
                  84
NCBI Description
                  (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
                  precursor gb_Z28697 from Nicotiana tabacum. ESTs gb Z18185
                  and gb_AA605362 come from this gene. [Arabidopsis thaliana]
                  27951
Seq. No.
                  164614 1.R1040
Contig ID
5'-most EST
                  uC-gmropic039d10b1
Method
                  BLASTX
NCBI GI
                  g2196466
BLAST score
                  331
E value
                  1.0e-30
Match length
                  115
                  62
% identity
                  (Y13673) TATA binding protein-associated factor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  27952
                  164617 1.R1040
Contig ID
5'-most EST
                  vzy700752953.h1
                  BLASTX
Method
NCBI GI
                  g2190547
BLAST score
                  661
E value
                  2.0e-69
                  197
Match length
                  59
% identity
NCBI Description
                  (AC001229) ESTs
                  gb T43256,gb 46316,gb N64930,gb AA395255,gb AA404382 come
                  from this gene. [Arabidopsis thaliana]
                  27953
Seq. No.
                  164655 1.R1040
Contig ID
5'-most EST
                  leu701\overline{1}48730.h1
                  27954
Seq. No.
                  164655 2.R1040
Contig ID
5'-most EST
                  vzy700753025.hl
Seq. No.
                  27955
Contig ID
                  164664 1.R1040
```

vzy700753040.hl

```
27956
Seq. No.
Contig ID
                   164683 1.R1040
5'-most EST
                   pmv700890195.h1
Method
                   BLASTX
NCBI GI
                   g2244792
BLAST score
                   529
E value
                   3.0e-54
Match length
                   109
% identity
                   86
NCBI Description
                   (297336) ankyrin homolog [Arabidopsis thaliana]
                   27957
Seq. No.
Contig ID
                   164691 1.R1040
5'-most EST
                   leu701146647.hl
Seq. No.
                   27958
Contig ID
                   164693 1.R1040
5'-most EST
                   pmv700890724.h1
                   BLASTX
Method
NCBI GI
                   q4220529
BLAST score
                   349
E value
                   8.0e-57
Match length
                   144
% identity
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   27959
Seq. No.
                   164705 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy034g04b1
Seq. No.
                   27960
Contig ID
                   164755 1.R1040
5'-most EST
                   fC-qmse700753182a1
Method
                   BLASTX
NCBI GI
                   q2833378
BLAST score
                   652
E value ·
                   2.0e-68
                   194
Match length
% identity
                   HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis
NCBI Description
                   thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis
                   thaliana]
Seq. No.
                   27961
Contig ID
                   164774 1.R1040
5'-most EST
                   uC-gmropic106g09b1
Method
                   BLASTX
NCBI GI
                   g4325342
BLAST score
                   354
E value
                   1.0e-33
Match length
                  121
% identity
NCBI Description
                   (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                  27962
```

164816_1.R1040

Contig ID

Seq. No.

```
5'-most EST
                  pmv700889507.h1
                  27963
Seq. No.
Contig ID
                  164832 1.R1040
5'-most EST
                  fC-gmf1700902412f1
Method
                  BLASTX
                  q4558591
NCBI GI
BLAST score
                  1003
                  1.0e-109
E value
Match length
                  263
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  27964
Contig ID
                  164835 1.R1040
                  epx701108908.hl
5'-most EST
Seq. No.
                  27965
Contig ID
                  164844 1.R1040
5'-most EST
                  vzy700753308.hl
Method
                  BLASTX
NCBI GI
                  g3451071
BLAST score
                  622
E value
                  1.0e-64
Match length
                  151
% identity
NCBI Description
                   (AL031326) beta adaptin - like protein [Arabidopsis
                  thaliana]
                  27966
Seq. No.
Contig ID
                  164848 1.R1040
5'-most EST
                  vzy700753314.hl
                  27967
Seq. No.
Contig ID
                  164859 1.R1040
5'-most EST
                  jC-gmro02910012d03a1
Method
                  BLASTX
NCBI GI
                  g3834323
BLAST score
                  361
                  2.0e-34
E value
Match length
                  100
% identity
NCBI Description
                  (AC005679) F9K20.25 [Arabidopsis thaliana]
                  27968
Seq. No.
                  164876 1.R1040
Contig ID
5'-most EST
                  fC-qmse700753353a2
Method
                  BLASTX
NCBI GI
                  g2832304
BLAST score
                  189
                  9.0e-15
E value
                  60
Match length
% identity
NCBI Description
                  (AF044489) receptor-like protein kinase [Oryza sativa]
```

Contig ID

```
164883 1.R1040
Contig ID
5'-most EST
                   fC-gmse7000764856f1
Method
                   BLASTX
NCBI GI
                   g3093294
BLAST score
                   909
E value
                   2.0e-98
Match length
                   227
% identity
                   33
                   (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27970
Contig ID
                   164914 1.R1040
5'-most EST
                   zsg701\overline{1}24756.h1
Method
                   BLASTX
NCBI GI
                   g4406820
BLAST score
                   288
E value
                   1.0e-28
Match length
                   90
% identity
                   (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                   thaliana]
                   27971
Seq. No.
Contig ID
                   164922 1.R1040
5'-most EST
                   zhf700963488.h1
                   BLASTX
Method
NCBI GI
                   q3367534
BLAST score
                   256
                   2.0e-22
E value
Match length
                   51
% identity
                   (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                   thaliana]
                   27972
Seq. No.
                   164952 1.R1040
Contig ID
5'-most EST
                   hrw701059334.h1
                   27973
Seq. No.
                   164953 1.R1040
Contig ID
5'-most EST
                   vzy700753465.hl
Seq. No.
                   27974
                   164971 1.R1040
Contig ID
5'-most EST
                   gsv701047903.hl
                   27975
Seq. No.
Contig ID
                   164974 1.R1040
5'-most EST
                   q43976\overline{4}9
                   27976
Seq. No.
                   164979 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810064a01a1
                   27977
Seq. No.
                   165063 1.R1040
```

% identity

```
5'-most EST
                   vzy700753634.hl
Seq. No.
                   27978
Contig ID
                   165090 1.R1040
5'-most EST
                   fua701041406.h1
Method
                   BLASTX
NCBI GI
                   g3540207
BLAST score
                   240
E value
                   2.0e-20
Match length
                   64
% identity
NCBI Description
                   (AC004260) Putative protein kinase [Arabidopsis thaliana]
                   27979
Seq. No.
                   165093 1.R1040
Contig ID
5'-most EST
                   vzy700756828.hl
                   27980
Seq. No.
                   165096 1.R1040
Contig ID
                   vzy700753682.hl
5'-most EST
Method
                   BLASTX
                   g818849
NCBI GI
BLAST score
                   356
E value
                   4.0e-34
Match length
                   89
                   67
% identity
                   (U25430) nucleotide pyrophosphatase precursor [Oryza
NCBI Description
                   sativa]
                   27981
Seq. No.
                   165111 1.R1040
Contig ID
5'-most EST
                   vzy700753707.h1
Seq. No.
                   27982
Contig ID
                   165120 1.R1040
5'-most EST
                   vzy700753719.h1
Method
                   BLASTX
NCBI GI
                   g4102600
BLAST score
                   415
E value
                   2.0e-40
Match length
                   160
% identity
                   64
                   (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   27983
                   165121 1.R1040
Contig ID
5'-most EST
                   vzy700753721.hl
                   27984
Seq. No.
Contig ID
                   165146 1.R1040
5'-most EST
                  uC-gmrominsoy261c08b1
Method
                  BLASTX
NCBI GI
                  g3582436
BLAST score
                   429
E value
                   3.0e-42
Match length
                  129
```

Method

...<u>.</u>

```
NCBI Description
                   (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
Seq. No.
                   27985
Contig ID
                   165155 1.R1040
5'-most EST
                   uC-gmrominsoy218h10b1
Method
                   BLASTX
                   q3043529
NCBI GI
BLAST score
                   194
E value
                   8.0e-15
Match length
                   82
% identity
                   (AJ002204) polyamine oxidase [Zea mays]
NCBI Description
                   27986
Seq. No.
Contig ID
                   165155 2.R1040
5'-most EST
                   crh700853013.hl
Seq. No.
                   27987
Contig ID
                   165159 1.R1040
5'-most EST
                   vzy700753785.hl
Seq. No.
                   27988
Contig ID
                   165169 1.R1040
5'-most EST
                   vzy700755286.hl
Method
                   BLASTX
NCBI GI
                   g2924509
BLAST score
                   752
                   6.0e-80
E value
Match length
                   184
% identity
                   72
NCBI Description
                   (AL022023) subtilisin proteinase - like [Arabidopsis
                   thaliana]
                   27989
Seq. No.
                   165175 1.R1040
Contig ID
5'-most EST
                  vzy700753812.h1
Seq. No.
                   27990
                   165186 1.R1040
Contig ID
5'-most EST
                   fC-qmse700753825a1
                   BLASTX
Method
NCBI GI
                   q1783355
BLAST score
                   581
                   3.0e-60
E value
                  139
Match length
% identity
                   72
                  (Y10421) delta-9 fatty acid desaturase [Cryptococcus
NCBI Description
                  curvatus]
                  27991
Seq. No.
                  165193 1.R1040
Contig ID
5'-most EST
                  uC-gmropic101d11b1
Seq. No.
                  27992
Contig ID
                  165237 1.R1040
5'-most EST
                  vzy700753918.hl
```

BLASTX

```
NCBI GI
                   q1173063
BLAST score
                   281
                   2.0e-25
E value
                   78
Match length
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN YL17-B >gi 1071989 pir S56960
                   ribosomal protein L17.e.B, cytosolic - yeast (Saccharomyces
                   cerevisiae) >gi 1008376 emb CAA89472 (Z49452) ORF YJL177w
                   [Saccharomyces cerevisiae]
                   27993
Seq. No.
                   165255 1.R1040
Contig ID
5'-most EST
                   vzy700755902.hl
                   27994
Seq. No.
                   165306 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}51074.h1
                   BLASTX
Method
NCBI GI
                   g1916809
BLAST score
                   237
                   4.0e-20
E value
                   83
Match length
% identity
                   (U81163) auxin-binding protein [Prunus persica].
NCBI Description
                   27995
Seq. No.
                   165353 1.R1040
Contig ID
5'-most EST
                   fC-gmse700754105a1
Method
                   BLASTN
NCBI GI
                   g517257
BLAST score
                   66
                   2.0e-28
E value
Match length
                   118
% identity
                   89
NCBI Description
                   Z.mays MNBla mRNA for DNA-binding protein
                   27996
Seq. No.
                   165356 1.R1040
Contig ID
5'-most EST
                   jsh701066076.h1
                   27997
Seq. No.
                   165376 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}03230.h1
Method
                   BLASTX
NCBI GI
                   g4063743
BLAST score
                   402
E value
                   6.0e-39
                   147
Match length
% identity
                   58
NCBI Description
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
                   27998
Seq. No.
                   165427 1.R1040
Contig ID
                   sat701007081.h1
5'-most EST
                   27999
Seq. No.
```

165432 1.R1040

Contig ID

Match length

```
vzy700756123.h1
5'-most EST
Seq. No.
                   28000
Contig ID
                   165434 1.R1040
5'-most EST
                   fC-gmse700754216a2
                   BLASTX
Method
                   q3928095
NCBI GI
BLAST score
                   1029
E value
                   1.0e-112
Match length
                   258
% identity
                   (AC005770) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   165461 1.R1040
5'-most EST
                   sat701\overline{0}14070.h1
Method
                   BLASTX
NCBI GI
                   q3193306
BLAST score
                   381
E value
                   1.0e-36
Match length
                   120
% identity
NCBI Description
                   (AF069300) contains similarity to Arabidopsis
                   membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
Seq. No.
                   28002
Contig ID
                   165468 1.R1040
5'-most EST
                   asn701141825.h1
Method
                   BLASTN
NCBI GI
                   g3600062
BLAST score
                   111
E value
                   2.0e-55
Match length
                   363
% identity
NCBI Description
                  Arabidopsis thaliana BAC T25C13
Seq. No.
                   28003
Contig ID
                   165486 1.R1040
5'-most EST
                   bth700845218.h1
Method
                   BLASTX
                   g3114658
NCBI GI
BLAST score
                   234
                   2.0e-19
E value
Match length
                   108
% identity
NCBI Description
                   (AF060871) hypothetical alcohol dehydrogenase [Rhodococcus
                   rhodochrous]
                   28004
Seq. No.
                   165486 2.R1040
Contig ID
5'-most EST
                   vzy700754292.h1
Method
                   BLASTN
NCBI GI
                   q2264306
BLAST score
                   44
E value
                   2.0e-15
```

```
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   28005
Contig ID
                   165495 1.R1040
5'-most EST
                   hrw701058919.hl
Seq. No.
                   28006
Contig ID
                   165531 1.R1040
5'-most EST
                   ary700764358.h1
Method
                   BLASTX
NCBI GI
                   g3885334
BLAST score
                   250
E value
                   2.0e-43
Match length
                   136
% identity
NCBI Description
                   (AC005623) putative argonaute protein [Arabidopsis
                   thaliana]
                   28007
Seq. No.
Contig ID
                   165551 1.R1040
5'-most EST
                   zsq701\overline{1}29794.h1
Method
                   BLASTX
                   g3426038
NCBI GI
BLAST score
                   404
E value
                   2.0e-39
Match length
                   127
% identity
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   28008
Contig ID
                   165571 2.R1040
5'-most EST
                   fde700872101.hl
                   28009
Seq. No.
                   165591 1.R1040
Contig ID
5'-most EST
                   vzy700754437.hl
Method
                   BLASTX
NCBI GI
                   g2702273
BLAST score
                   324
E value
                   4.0e-30
Match length
                   114
% identity
                   (AC003033) carrot B2 protein-like [Arabidopsis thaliana]
NCBI Description
                   28010
Seq. No.
Contig ID
                   165599 1.R1040
5'-most EST
                   uC-gmflminsoy042e03b1
Method
                   BLASTX
                   g4558672
NCBI GI
BLAST score
                   428
E value
                   4.0e-42
Match length
                   171
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
```

thaliana]

NCBI Description

```
28011
Seq. No.
Contig ID
                   165619 1.R1040
5'-most EST
                   uC-gmropic078b09b1
Seq. No.
                   28012
                   165630 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}10418.h1
Seq. No.
                   28013
Contig ID
                   165639 1.R1040
5'-most EST
                   vzy700755930.h1
Method
                   BLASTX
NCBI GI
                   g2145358
BLAST score
                   378
E value
                   9.0e-37
Match length
                   80
% identity
                   90
NCBI Description
                   (Y10922) HD-Zip protein [Arabidopsis thaliana]
                   28014
Seq. No.
Contig ID
                   165673 1.R1040
5'-most EST
                   vzy700754582.h1
                   28015
Seq. No.
Contig ID
                   165705 1.R1040
5'-most EST
                   fC-gmse7000754553f1
                   28016
Seq. No.
Contig ID
                   165721 1.R1040
5'-most EST
                   fC-qmse700754614a2
Method
                   BLASTX
NCBI GI
                   q4522003
BLAST score
                   294
E value
                   2.0e-26
Match length
                   107
% identity
NCBI Description
                   (AC007069) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   165731 1.R1040
5'-most EST
                   uC-gmrominsoy084h10b1
Seq. No.
                   28018
Contig ID
                   165742 1.R1040
5'-most EST
                   k11701\overline{2}04535.h2
                   28019
Seq. No.
Contig ID
                   165748 1.R1040
5'-most EST
                   zzp700836267.h1
Method .
                   BLASTX
NCBI GI
                   g3367534
BLAST score
                   392
E value
                   4.0e-38
Match length
                   99
% identity
```

(AC004392) Strong similarity to coatamer alpha subunit

E value

```
thaliana]
Seq. No.
                   28020
Contig ID
                   165758 1.R1040
                   uC-gmflminsoy091g09b1
5'-most EST
Method
                  BLASTN
                   q1638836
NCBI GI
BLAST score
                   166
E value
                   3.0e-88
Match length
                   438
% identity
                   84
NCBI Description H.vulgare mRNA for alpha-tubulin
                   28021
Seq. No.
Contig ID
                   165763 1.R1040
5'-most EST
                   jC-qmf102220077b10a1
Method
                  BLASTX
NCBI GI
                   q3548808
BLAST score
                   221
E value
                   8.0e-18
Match length
                   89
% identity
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
                   28022
Seq. No.
Contig ID
                   165777 1.R1040
5'-most EST
                   vzy700754713.h1
Seq. No.
                   28023
Contig ID
                   165788 1.R1040
5'-most EST
                   fC-qmse700754725a2
Method
                   BLASTX
NCBI GI
                   q584882
BLAST score
                   380
E value
                   1.0e-36
Match length
                   131
% identity
                   54
                  CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL
NCBI Description
                   CYCLASE) >qi 452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
Seq. No.
                   28024
Contig ID
                   165835 1.R1040
5'-most EST
                   asn701138122.hl
Seq. No.
                   28025
Contig ID
                   165850 1.R1040
5'-most EST
                   jC-gmle01810086f01a1
Seq. No.
                   28026
Contig ID
                   165853 1.R1040
5'-most EST
                   vzy700754816.h1
Method
                  BLASTX
                   g3461848
NCBI GI
BLAST score
                   231
```

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

2.0e-19

Seq. No.

```
87
 Match length
 % identity
                   60
 NCBI Description
                   (AC005315) putative ATPase [Arabidopsis thaliana]
 Seq. No.
                   28027
                   165854 1.R1040
 Contig ID
                   vzy700754817.h1
5'-most EST
 Seq. No.
                   28028
 Contig ID
                   165866 1.R1040
                   hrw701063185.hl
 5'-most EST
 Seq. No.
                   28029
 Contig ID
                   165914 1.R1040
 5'-most EST
                   vzy700754893.h1
 Seq. No.
                   28030
 Contig ID
                   165924 1.R1040
 5'-most EST
                   fC-qmse700754910a2
Method
                   BLASTX.
 NCBI GI
                   q4204912
 BLAST score
                   407
                   6.0e-40
 E value
Match length
                   113
 % identity
 NCBI Description
                   (U58918) MEK kinase [Arabidopsis thaliana]
 Seq. No.
                   165987 1.R1040
 Contig ID
 5'-most EST
                   pmv700892680.h1
                   BLASTX
Method
 NCBI GI
                   q1352681
 BLAST score
                   210
                   6.0e-22
 E value
Match length
                   83
 % identity
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir S55457
NCBI Description
                   phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >gi 633028 dbj BAA07287 (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
 Seq. No.
                   28032
 Contig ID
                   166019 1.R1040
 5'-most EST
                   q5342541
Method
                   BLASTX
NCBI GI
                   a4038036
BLAST score
                   323
E value
                   9.0e-30
Match length
                   101
 % identity
NCBI Description
                   (AC005936) unknown protein [Arabidopsis thaliana]
                   28033
Seq. No.
 Contig ID
                   166048 1.R1040
 5'-most EST
                   jC-gmle01810044f05a1
```

Contig ID

.5'-most EST

```
Contig ID
                   166059 1.R1040
                   uC-gmflminsoy028e09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1263160
BLAST score
                   331
                   2.0e-30
E value
Match length
                   217
                   9
% identity
                   (X89226) leucine-rich repeat/receptor protein kinase [Oryza
NCBI Description
                   28035
Seq. No.
                   166125 1.R1040
Contig ID
5'-most EST
                   vzy700755190.hl
Seq. No.
                   28036
                   166176 1.R1040
Contig ID
                   vzy700755267.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1171481
                                                                                 BLAST score
                   104
E value
                   2.0e-51
Match length
                   260
% identity
                   85
NCBI Description
                  Nicotiana tabacum mRNA for nitrilase, complete cds
Seq. No.
                   28037
Contig ID
                   166191 1.R1040
5'-most EST
                   fC-gmst700888672d3
Seq. No.
                   28038
Contig ID
                   166206 1.R1040
5'-most EST
                   fC-qmse7000755316a1
Method
                   BLASTN
NCBI GI
                   g3860320
BLAST score
                   215
E value
                   1.0e-117
Match length
                   475
% identity
                  Cicer arietinum mRNA for beta-galactosidase, clone
NCBI Description
                  CanBGal-5
Seq. No.
                   28039
Contig ID
                   166216 1.R1040
5'-most EST
                   uC-gmrominsoy201h12b1
Method
                   BLASTX
NCBI GI
                   q1938424
BLAST score
                   190
E value
                   4.0e-14
Match length
                   97
% identity
                   49
NCBI Description
                   (U97002) similar to acyl-CoA dehydrogenases and epoxide
                  hydrolases [Caenorhabditis elegans]
Seq. No.
                  28040
```

 $\sigma_{i} = f_{i} f_{i}$

166229 1.R1040

uC-gmrominsoy106g01b1

Contig ID

```
Method
                   BLASTX
NCBI GI
                   g2864614
BLAST score
                   181
                   3.0e-13
E value
Match length
                   67
% identity
                   46
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   28041
                   166240 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy215h09b1
Method
                   BLASTX
                   g3056591
NCBI GI
BLAST score
                   234
E value
                   1.0e-19
Match length
                   87
% identity
                   48
NCBI Description
                   (AC004255) T1F9.12 [Arabidopsis thaliana]
                   28042
Seq. No.
Contig ID
                   166259 1.R1040
5'-most EST
                   uC-gmrominsoy260h09b1
                   28043
Seq. No.
                   166262 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910047f02a1
Seq. No.
                   28044
Contig ID
                   166298 1.R1040
5'-most EST
                   zzp700833791.h1
Seq. No.
                   28045
                   166352 1.R1040
Contig ID
5'-most EST
                  asj700967425.h1
Method
                  BLASTX
NCBI GI
                  g2460203
BLAST score
                   190
                   1.0e-14
E value
Match length
                  72
                   50
% identity
NCBI Description
                   (AF021244) coronatine-induced protein 1 [Arabidopsis
                  thaliana]
                  28046
Seq. No.
                  166370 1.R1040
Contig ID
5'-most EST
                  gsv701054482.hl
Seq. No.
                  28047
Contig ID
                  166399 1.R1040
5'-most EST
                  lus701\overline{0}15762.h1
                  28048
Seq. No.
Contig ID
                  166427 1.R1040
                  hrw701\overline{0}60518.h1
5'-most EST
                  28049
Seq. No.
```

166428 1.R1040

% identity

NCBI Description

```
5'-most EST
                    vzy700755673.h1
 Method
                    BLASTX
 NCBI GI
                    g1652082
 BLAST score
                    158
 E value
                    1.0e-10
 Match length
                    95
 % identity
                    41
                    (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase
 NCBI Description
                    [Synechocystis sp.]
 Seq. No.
                    28050
                    166428 2.R1040
 Contig ID
 5'-most EST
                    vzy700756093.hl
 Seq. No.
                    28051
 Contig ID
                    166497 1.R1040
 5'-most EST
                    vzy700755817.h1
 Seq. No.
                    28052
 Contig ID
                    166500 1.R1040
 5'-most EST
                    pmv700891978.h1
                    28053
 Seq. No.
 Contig ID
                    166545 1.R1040
5'-most EST
                    fde700873207.h1
 Seq. No.
                    28054
                    166567 1.R1040
 Contig ID
 5'-most EST
                    xpa700792682.h1
                    28055
 Seq. No.
                    166579 1.R1040
 Contig ID
 5'-most EST
                    xpa700798256.h1
                    28056
 Seq. No.
 Contig ID
                    166699 1.R1040
 5'-most EST
                    vzy700\overline{7}56121.h1
                    28057
 Seq. No.
 Contig ID
                    166735 1.R1040
 5'-most EST
                    g42905<del>5</del>2
 Seq. No.
                    28058
 Contig ID
                    166742 1.R1040
 5'-most EST
                    vzy700756182.hl
                    28059
Seq. No.
Contig ID
                    166759 1.R1040
 5'-most EST
                    hrw701060431.h1
                    BLASTX
Method
NCBI GI
                    g4567311
BLAST score
                    176
E value
                    1.0e-12
Match length
                    43
```

4....

(AC005956) putative protein kinase [Arabidopsis thaliana]

Contig ID

```
28060
Seq. No.
Contig ID
                  166790 1.R1040
5'-most EST
                  fde700871081.h1
Seq. No.
                  28061
                  166806 1.R1040
Contig ID
5'-most EST
                  fC-gmro700843710a3
Method
                  BLASTX
NCBI GI
                  q2754825
BLAST score
                  439
E value
                  4.0e-43
Match length
                  245
% identity
                  42
NCBI Description
                  (AF033097) NPH1-2 [Avena sativa]
Seq. No.
                  28062
Contig ID
                  166839 1.R1040
5'-most EST
                  vzy700756331.h1
Seq. No.
                  28063
Contig ID
                  166845 1.R1040
5'-most EST
                  q4397586
Method
                  BLASTX
NCBI GI
                  g2501182
BLAST score
                  695
E value
                  2.0e-73
Match length
                  164
                  73
% identity
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir JC5237
NCBI Description
                  osmotin-like protein - tomato >qi 1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
Seq. No.
                  28064
Contig ID
                  166851 1.R1040
5'-most EST
                  jC-qmst02400040h11a1
Method
                  BLASTX
NCBI GI
                  q4008006
BLAST score
                  175
E value
                  9.0e-13
Match length
                  92
% identity
NCBI Description
                  (AF084034) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  28065
Seq. No.
Contig ID
                  166889 1.R1040
5'-most EST
                  jC-gmro02910068h05a1
Method
                  BLASTX
NCBI GI
                  q4106395
BLAST score
                  166
E value
                  1.0e-18
Match length
                  100
% identity
NCBI Description
                  (AF073744) raffinose synthase [Cucumis sativus]
                  28066
Seq. No.
```

166891 1.R1040

E value

```
5'-most EST
                   vzy700756410.h1
Seq. No.
                   28067
Contig ID
                   166900 1.R1040
5'-most EST
                   vzy700756421.hl
                   28068
Seq. No.
Contig ID
                   166905 1.R1040
5'-most EST
                   hrw701063660.hl
                   28069
Seq. No.
                   166907 1.R1040
Contig ID
5'-most EST
                   vzy700756429.hl
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   270
                   6.0e-24
E value
Match length
                   105
% identity
                   52
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
                   28070
Seq. No.
Contig ID
                   166918 1.R1040
5'-most EST
                   jC-gmf102220081b08a1
Seq. No.
                   28071
Contig ID
                   166923 1.R1040
5'-most EST
                   jC-gmst02400065a11d1
Seq. No.
                   28072
                   166927 1.R1040
Contig ID
5'-most EST
                   vzy700756461.hl
                   28073
Seq. No.
                   166960 1.R1040
Contig ID
5'-most EST
                   leu701147985.h1
Seq. No.
                   28074
Contig ID
                   166976 1.R1040
5'-most EST
                   zhf700955028.h1
Method
                   BLASTX
NCBI GI
                   g3482978
BLAST score
                   277
                   8.0e-25
E value
Match length
                   108
% identity
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   28075
Seq. No.
Contig ID
                   167014 1.R1040
5'-most EST
                   fC-gmse7000756618f1
Method
                  BLASTX
NCBI GI
                  q4006924
BLAST score
                  1058
```

1.0e-116

```
Match length
                   247
                   79
% identity
NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis
                   thaliana]
                   28076
Seq. No.
                   167017 1.R1040
Contig ID
                   sat701\overline{0}12712.h1
5'-most EST
Method
                   BLASTX
                   g4490303
NCBI GI
                   306
BLAST score
                   4.0e-28
E value
Match length
                   94
% identity
                   63
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
                   28077
Seq. No.
                   167039 1.R1040
Contig ID
5'-most EST
                   sat701004384.h1
Seq. No.
                   28078
Contig ID
                   167083 1.R1040
5'-most EST
                   vzy700756695.hl
Seq. No.
                   28079
Contig ID
                   167086 1.R1040
5'-most EST
                   uC-gmropic057g02b1
Seq. No.
                   28080
Contig ID
                   167088 1.R1040
5'-most EST
                   jC-qmro02910006h02a1
Method
                   BLASTX
NCBI GI
                   q4538926
BLAST score
                   538
E value
                   8.0e-57
Match length
                   213
% identity
NCBI Description
                   (AL049483) putative phosphatidylserine decarboxylase
                   [Arabidopsis thaliana]
Seq. No.
                   28081
Contig ID
                   167111 1.R1040
5'-most EST
                   fC-qmse7000756739a1
Method
                   BLASTX
NCBI GI
                   q461538
BLAST score
                   474
E value
                   1.0e-47
Match length
                   158
% identity
NCBI Description
                   PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE,
                   PHENYLALANINE-INHIBITED (PHOSPHO-2-KETO-3-DEOXYHEPTONATE
                  ALDOLASE) (DAHP SYNTHETASE)
                   (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE)
                  >gi 478311 pir JN0865
                   3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase - yeast
                   (Candida albicans) >qi 410315 (L12217)
```

3-deoxy-D-arabinoheptulosonate-7-phosphate synthase

E value

Match length

2.0e-19

77

Seq. No. 28082 Contig ID 167113 1.R1040 .5'-most EST pmv700890784.h1 Seq. No. 28083 Contig ID 167116 1.R1040 5'-most EST asn701135289.hl Method BLASTX NCBI GI q3600036 BLAST score 190 E value 3.0e-14 Match length 175 35 % identity NCBI Description (AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana] 28084 Seq. No. 167152 1.R1040 Contig ID 5'-most EST vzy700756817.h1 Seq. No. 28085 167172 1.R1040 Contig ID zhf700960734.h1 5'-most EST Method BLASTX NCBI GI g631069 BLAST score 152 E value 3.0e-10 Match length 83 % identity 13 NCBI Description AF-1p protein - human >gi_470035_emb_CAA82305_ (Z29064) Highly similar to murine eps 15 GB A.N. L221768 [Homo sapiens] >gi 4503593 ref NP 001972.1 pEPS15 epidermal growth factor receptor pathway substrate 28086 Seq. No. Contig ID 167175 1.R1040 zhf700963525.h1 5'-most EST Method BLASTX NCBI GI g3243033 BLAST score 162 E value 4.0e-11 Match length 85 % identity NCBI Description (AF069765) signal recognition particle 72 [Homo sapiens] >gi 3335650 (AF077019) signal recognition particle 72 [Homo sapiens] 28087 Seq. No. 167195 1.R1040 Contig ID fua701042252.h1 5'-most EST Method BLASTX NCBI GI g2190419 BLAST score 233

[Candida albicans]

NCBI GI

```
% identity
                   (Y13632) dem [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   28088
Contig ID
                   167215 1.R1040
5'-most EST
                   euj700697912.hl
                   28089
Seq. No.
Contig ID
                   167220 1.R1040
5'-most EST
                   euj700\overline{6}97919.h1
                   28090
Seq. No.
                   167233 1.R1040
Contig ID
5'-most EST
                   zhf700957625.hl
Method
                   BLASTX
NCBI GI
                   q4467108
BLAST score
                   141
E value
                   9.0e-09
Match length
                   46
% identity
                   61
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28091
                   167238 1.R1040
Contig ID
5'-most EST
                   euj700\overline{6}97955.h1
Seq. No.
                   28092
                   167280 1.R1040
Contig ID
5'-most EST
                   euj700698032.hl
                   BLASTX
Method
NCBI GI
                   g2244807
BLAST score
                   175
E value
                   7.0e-13
Match length
                   73
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   28093
Seq. No.
                   167287 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy087b11b1
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   322
E value
                   8.0e-30
Match length
                   122
% identity
                   52
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
                   28094
Seq. No.
Contig ID
                   167396 1.R1040
5'-most EST
                   crh700851493.h1
                   28095
Seq. No.
                   167406 1.R1040
Contig ID
5'-most EST
                   zpv700757086.h1
Method
                   BLASTX
```

g2507426

```
BLAST score
                   438
                   2.0e-43
E value
Match length
                   110
% identity
                   78
NCBI Description
                  ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
                   (ALANINE--TRNA LIGASE) (ALARS) >gi 1673365 emb CAA80380
                   (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   28096
Contig ID
                   167461 1.R1040
5'-most EST
                   crh700851213.h1
Method
                  BLASTX
NCBI GI
                   q2459431
BLAST score
                   194
E value
                   7.0e-15
Match length
                  82
% identity
                   46
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28097
Seq. No.
Contig ID
                   167481 1.R1040
                  dpv701\overline{0}97070.h1
5'-most EST
Seq. No.
                  28098
                  167481 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy260b03b1
                  28099
Seq. No.
Contig ID
                  167498 1.R1040
                   zpv700757247.h1
5'-most EST
                  28100
Seq. No.
                  167518 1.R1040
Contig ID
                   zpv700757279.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2264302
BLAST score
                   69
E value
                  3.0e-30
Match length
                  205
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  28101
                  167545 1.R1040
Contig ID
5'-most EST
                  fC-gmse7000757329a1
                  BLASTX
Method
NCBI GI
                  g4567307
BLAST score
                  195
E value
                  7.0e-15
Match length
                  72
% identity
                   (AC005956) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

```
167556 1.R1040
Contig ID
5'-most EST
                    r1r700899695.h1
Method
                    BLASTX
NCBI GI
                    g4572676
BLAST score
                    316
                    6.0e-29
E value
Match length
                    187
% identity
                    36
                    (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    28103
Contig ID
                    167611 1.R1040
                    k11701\overline{2}09728.h1
5'-most EST
Seq. No.
                    28104
Contig ID
                    167613 1.R1040
5'-most EST
                    uC-gmronoir065c05b1
                    28105
Seq. No.
Contig ID
                    167641 1.R1040
5'-most EST
                    zpv700757524.h1
                    28106
Seq. No.
                    167673 1.R1040
Contig ID
5'-most EST
                    xpa700795867.h1
Seq. No.
                    28107
                    167692 1.R1040
Contig ID
5'-most EST
                    zpv700757614.hl
Method
                    BLASTX
NCBI GI
                    g3980413
BLAST score
                    364
                    4.0e-35
E value
Match length
                    94
% identity
                    (AC004561) pumilio-like protein [Arabidopsis thaliana]
NCBI Description
                    28108
Seq. No.
                    167727 1.R1040
Contig ID
5'-most EST
                    jC-gmle01810087a02d1
                    28109
Seq. No.
Contig ID
                    167745 1.R1040
5'-most EST
                    jC-gmro02910072e07a1
                    28110
Seq. No.
                    167756 1.R1040
Contig ID
5'-most EST
                    zpv700758462.hl
Method
                    BLASTX
NCBI GI
                    g1084950
BLAST score
                   195
E value
                    8.0e-15
Match length
                   143
                    29
% identity
                   probable membrane protein YPR029c - yeast (Saccharomyces
cerevisiae) >gi_809594_emb_CAA89283_ (Z49274) unknown
NCBI Description
```

[Saccharomyces cerevisiae] >gi 1314103 emb CAA95025

(Z71255) unknown [Saccharomyces cerevisiae] Seq. No. 28111 Contig ID 167774 1.R1040 fC-gmse7000757783f1 5'-most EST Method BLASTX NCBI GI g1076755 BLAST score 537 8.0e-76 E value Match length 175 % identity 79 protein kinase - rice >gi 450300 (L27821) protein kinase NCBI Description [Oryza sativa] Seq. No. 28112 Contig ID 167806 1.R1040 5'-most EST zpv700757855.h1 Method BLASTX NCBI GI q3212855 BLAST score 378 E value 5.0e-36 Match length 207 % identity (AC004005) hypothetical protein [Arabidopsis thaliana] NCBI Description 28113 Seq. No. Contig ID 167840 1.R1040 5'-most EST zhf700958356.h1 Method BLASTX NCBI GI q3831452 BLAST score 189 E value 5.0e-14 Match length 171 27 % identity (AC005700) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description 28114 Seq. No. Contig ID 167854 1.R1040 5'-most EST zhf700953487.h1 Seq. No. 28115 Contig ID 167860 1.R1040 5'-most EST zpv700757966.h1 Method BLASTX NCBI GI q4467158 BLAST score 169 E value 7.0e-12 108 Match length % identity NCBI Description (AL035540) putative protein [Arabidopsis thaliana] Seq. No. Contig ID 167944 1.R1040 5'-most EST zpv700758128.h1

28117

168079 1.R1040

Seq. No. Contig ID

Method

NCBI GI

BLASTX

q3548818

```
5'-most EST
                   jC-gmle01810054d10a1
Seq. No.
                   28118
Contig ID
                   168102 1.R1040
                   pmv700889065.h1
5'-most EST
                   28119
Seq. No.
                   168114 1.R1040
Contig ID
5'-most EST
                   sat701002912.h1
Seq. No.
                   28120
                   168121 1.R1040
Contig ID
5'-most EST
                   zpv700758467.hl
Method
                   BLASTN
NCBI GI
                   g169972
BLAST score
                   199
E value
                   1.0e-108
Match length
                   259
% identity
NCBI Description
                   Soybean glycinin A-la-B-x subunit mRNA, complete cds
Seq. No.
                   28121
Contig ID
                   168198 1.R1040
5'-most EST
                   jC-gmro02910071d07d1
Seq. No.
Contig ID
                   168211 1.R1040
5'-most EST
                   zpv700758640.hl
Seq. No.
                   28123
Contig ID
                   168257 1.R1040
5'-most EST
                   zpv700758723.h1
                   28124
Seq. No.
Contig ID
                   168394 1.R1040
5'-most EST
                   zpv700759012.h1
Seq. No.
                   28125
Contig ID
                   168417 1.R1040
5'-most EST
                   zhf700955494.h1
                   28126
Seq. No.
Contig ID
                   168460 1.R1040
5'-most EST
                   zpv700759109.hl
Method
                   BLASTX
NCBI GI
                   q4006887
BLAST score
                   244
                  7.0e-21
E value
Match length
                   60
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   28127
Seq. No.
Contig ID
                   168467 1.R1040
5'-most EST
                   leu701155432.hl
```

NCBI Description

```
BLAST score
                   200
                   1.0e-15
E value
Match length
                   49
                   78
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28128
Seq. No.
                   168505 1.R1040
Contig ID
5'-most EST
                   rlr700896855.h1
                   28129
Seq. No.
                   168538 1.R1040
Contig ID
5'-most EST
                   pmv700890049.h1
Seq. No.
                   28130
Contig ID
                   168594 1.R1040
5'-most EST
                   zpv700759541.h1
Method
                   BLASTX
                   g1906830
NCBI GI
BLAST score
                   662
E value
                   1.0e-69
Match length
                   168
% identity
                   76
                  (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   168598 1.R1040
5'-most EST
                   sat701\overline{0}08969.h1
Seq. No.
                   28132
Contig ID
                   168601 1.R1040
5'-most EST
                   q4314150
Method
                   BLASTX
NCBI GI
                   q3257262
BLAST score
                   162
E value
                   4.0e-11
Match length
                   66
% identity
NCBI Description
                   (AP000003) 450aa long hypothetical fmu protein [Pyrococcus
                   horikoshii]
Seq. No.
                   28133
Contig ID
                   168619 1.R1040
5'-most EST
                   kl1701203142.h1
                   28134
Seq. No.
                   168679 1.R1040
Contig ID
5'-most EST
                   crh700853122.h1
Method
                   BLASTN
NCBI GI
                   q2605511
BLAST score
                   168
E value
                   2.0e-89
Match length
                   389
% identity
```

complete cds

Glycine max mRNA for beta subunit of beta conglycinin,

```
Seq. No.
                   28135
Contig ID
                   168704 1.R1040
5'-most EST
                   zpv700759841.h1
Seq. No.
                   28136
Contig ID
                   168760 1.R1040
5'-most EST
                   zpv700760005.h1
Seq. No.
                   28137
Contig ID
                   168790 1.R1040
5'-most EST
                   zpv700760103.hl
Method
                   BLASTX
NCBI GI
                   g461753
BLAST score
                   178
E value
                   4.0e-13
Match length
                   56
% identity
NCBI Description
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                   PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB
                   proteinase regulatory chain homolog precursor, chloroplast
                   - garden pea >gi 169128 (L09547) nuclear encoded precursor
                   to chloroplast protein [Pisum sativum]
Seq. No.
                   28138
Contig ID
                   168809 1.R1040
5'-most EST
                   q4396542
Method
                   BLASTX
NCBI GI
                   q3377822
BLAST score
                   289
E value
                   6.0e-26
Match length
                   96
% identity
                   53
NCBI Description
                   (AF076275) contains similarity to Caenorhabditis elegans
                  MEL-26 (GB:U67737) [Arabidopsis thaliana]
Seq. No.
                   28139
Contig ID
                   168851 1.R1040
5'-most EST
                   g5677098
Seq. No.
                   28140
Contig ID
                   168940 1.R1040
5'-most EST
                   zpv700760448.hl
Seq. No.
                   28141
                   168982 1.R1040
Contiq ID
5'-most EST
                   zpv700760532.h1
Seq. No.
                   28142
Contig ID
                  168994 1.R1040
5'-most EST
                   zpv700760559.h1
Method
                  BLASTX
NCBI GI
                  q1001312
BLAST score
                  204
E value
                  7.0e-16
Match length
                  59
% identity
```

NCBI Description (D64006) hypothetical protein [Synechocystis sp.]

Contig ID

```
Seq. No.
                  28143
Contig ID
                   169024 1.R1040
5'-most EST
                   zhf700956343.hl
Method
                  BLASTX
NCBI GI
                  q4539321
BLAST score
                   166
                  8.0e-12
E value
Match length
                   58
% identity
                   52
                  (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                  28144
Seq. No.
                   169045 1.R1040
Contig ID
5'-most EST
                   zpv700763458.hl
Seq. No.
                  28145
Contig ID
                  169159 1.R1040
5'-most EST
                  jC-gmf102220075a09d1
Seq. No.
                  28146
Contig ID
                  169260 1.R1040
5'-most EST
                  zpv700761194.hl
Seq. No.
                  28147
Contig ID
                  169354 1.R1040
5'-most EST
                  zpv700761405.hl
                  28148
Seq. No.
Contig ID
                  169360 1.R1040
5'-most EST
                  zpv700761423.h1
Seq. No.
                  28149
Contig ID
                  169365 1.R1040
5'-most EST
                  sat701004686.hl
                  28150
Seq. No.
Contig ID
                  169429 2.R1040
5'-most EST
                  jC-gmst02400060a10a1
                  28151
Seq. No.
Contig ID
                  169443 1.R1040
5'-most EST
                  sat701004844.hl
Method
                  BLASTX
NCBI GI
                  g4559388
BLAST score
                  697
E value
                  2.0e-73
Match length
                  248
% identity
NCBI Description
                  (AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  169450 1.R1040
5'-most EST
                  leu701145131.hl
Seq. No.
                  28153
```

169497_1.R1040

```
- 5'-most EST
                     zpv700761731.h1
 Method
                    BLASTX
 NCBI GI
                    g3790677
 BLAST score
                    143
 E value
                    6.0e-09
 Match length
                    103
 % identity
                    33
 NCBI Description
                    (AF099002) similar to human 5'-nucleotidase (SW:P49902)
                    [Caenorhabditis elegans]
 Seq. No.
                    28154
 Contig ID
                    169560 1.R1040
 5'-most EST
                    uC-gmrominsoy029h01b1
 Method
                    BLASTN
 NCBI GI
                    g2924733
 BLAST score
                    41
 E value
                    2.0e-13
 Match length
                    61
 % identity
                    92
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MUF9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    28155
 Contig ID
                    169613 1.R1040
 5'-most EST
                    zpv700762023.h1
 Method
                    BLASTX
 NCBI GI
                    g3372671
 BLAST score
                    432
 E value
                    6.0e-43
 Match length
                    105
 % identity
                    83
 NCBI Description
                    (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
 Seq. No.
 Contig ID
                    169680 1.R1040
 5'-most EST
                    epx701\overline{1}10086.h1
Seq. No.
Contig ID
                    169712 1.R1040
5'-most EST
                    \verb"jC-gmf102220079g12a1"
Seq. No.
                   28158
Contig ID
                    169719 1.R1040
5'-most EST
                   uC-gmflminsoy046h06b1
Method
                   BLASTN
NCBI GI
                   g975703
BLAST score
                   55
E value
                   6.0e-22
Match length
                   174
% identity
                   88
NCBI Description
                   P.sativum GR gene
Seq. No.
                   28159
Contig ID
                   169719 2.R1040
5'-most EST
                   epx701107025.hl
Method
```

BLASTN

g975703

NCBI GI

NCBI GI

BLAST score

g287567

47

```
BLAST score
                   43
E value
                   6.0e-15
                  91
Match length
                  87
% identity
NCBI Description P.sativum GR gene
Seq. No.
                  28160
                  169744 1.R1040
Contig ID
5'-most EST
                  pmv700889274.h1
                  28161
Seq. No.
Contig ID
                  169760 1.R1040
5'-most EST
                  zpv700762329.h1
Seq. No.
                  28162
Contig ID
                  169818 1.R1040
5'-most EST
                  jC-gmro02910033a10a1
                  28163
Seq. No.
                  169832 1.R1040
Contig ID
5'-most EST
                  fC-qmse7000762491f1
Method
                  BLASTN
NCBI GI
                  g1806143
BLAST score
                  287
E value
                  1.0e-160
Match length
                  519
% identity
                  89
NCBI Description M.sativa mRNA for cdc2 kinase homologue, cdc2MsE
Seq. No.
                  28164
Contig ID
                  169845 1.R1040
5'-most EST
                  zpv700762525.h1
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  318
E value
                  8.0e-30
Match length
                  81
% identity
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  28165
Contig ID
                  169895 1.R1040
5'-most EST
                  zpv700762633.h1
Method
                  BLASTX
NCBI GI
                  q4249402
BLAST score
                  171
E value
                  2.0e-12
Match length
                  66
% identity
NCBI Description
                  (AC006072) unknown protein [Arabidopsis thaliana]
Seq. No.
                  28166
Contig ID
                  169896 1.R1040
5'-most EST
                  jC-qmle01810021b01d1
Method
                  BLASTN
```

Contig ID

```
3.0e-17
E value
Match length
                   75
% identity
NCBI Description
                   Vigna radiata auxin-regulated mRNA
Seq. No.
                   28167
Contig ID
                   169917 1.R1040
5'-most EST
                   bth700846108.h1
                   28168
Seq. No.
Contig ID
                   169926 1.R1040
5'-most EST
                   sat701005108.h1
                   BLASTN
Method
NCBI GI
                   g2760172
BLAST score
                   44
E value
                   1.0e-15
Match length
                   182
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUB3, complete sequence [Arabidopsis thaliana]
                   28169
Seq. No.
                   170013 1.R1040
Contig ID
                   sat701\overline{0}08610.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4262226
                                                      BLAST score
                   173
E value
                   2.0e-12
Match length
                   78
% identity
NCBI Description
                  (AC006200) putative protein kinase [Arabidopsis thaliana]
                   28170
Seq. No.
                   170062 1.R1040
Contig ID
                   zpv700763005.h1
5'-most EST
Seq. No.
                   28171
Contig ID
                  170091 1.R1040
                   hrw701\overline{0}63395.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g123534
BLAST score
                   336
E value
                   1.0e-31
Match length
                   73
% identity
                   88
NCBI Description
                   17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3)
                   >gi 71493 pir HHSY17 heat shock protein 17 - soybean
                   >gi_18656_emb_CAA25578_ (X01104) heat shock protein 6871
(aa 1-153) [Glycine max] >gi_224205_prf__1012218B protein
                   6871, heat shock [Glycine max]
                   28172
Seq. No.
                   170100 1.R1040
Contig ID
5'-most EST
                   zpv700763069.h1
Seq. No.
                   28173
```

170154 1.R1040

Match length

264

```
5'-most EST
                    jC-gmf102220106g10a1
 Seq. No.
                    28174
 Contig ID
                    170195 1.R1040
 5'-most EST
                    zpv700763257.h1
 Method
                    BLASTX
 NCBI GI
                    g3763916
 BLAST score
                    532
                    3.0e-54
E value
 Match length
                    190
 % identity
                    54
 NCBI Description
                    (AC004450) unknown protein [Arabidopsis thaliana]
                    >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
 Seq. No.
                    28175
 Contig ID
                    170233 1.R1040
 5'-most EST
                   jC-gmf102220092a11a1
 Seq. No.
                    28176
 Contig ID
                    170309 1.R1040
 5'-most EST
                    zpv700763470.h1
 Seq. No.
                   28177
 Contig ID
                   170397 1.R1040
 5'-most EST
                    zpv700763625.hl
 Seq. No.
                   28178
                   170449 1.R1040
 Contig ID
 5'-most EST
                   eep700863716.h1
 Method
                   BLASTX
 NCBI GI
                   q1710401
 BLAST score
                   777
                    5.0e-83
 E value
 Match length
                   165
                   89
 % identity
                   RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
 NCBI Description
                    (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                   >gi 1044912 emb CAA63194 (X92443) ribonucleotide reductase
                   R2 [Nicotiana tabacum]
                   28179
 Seq. No.
 Contig ID
                   170451 1.R1040
 5'-most EST
                   jC-gmle01810094d11d1
                   28180
 Seq. No.
                   170477 1.R1040
 Contig ID
 5'-most EST
                   eep700863816.h1
 Seq. No.
                   28181
                   170486 1.R1040
 Contig ID
 5'-most EST
                   fC-gmro700863840a3
Method
                   BLASTX
NCBI GI
                   g1743354
BLAST score
                   747
E value
                   1.0e-109
```

NCBI Description

thaliana]

```
% identity
NCBI Description
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
Contiq ID
                   170486 2.R1040
5'-most EST
                   dpv701099622.h1
Method
                   BLASTX
NCBI GI
                   q4056462
BLAST score
                   791
E value
                   1.0e-137
Match length
                   320
% identity
                   78
NCBI Description
                   (AC005990) Strong similarity to gb_Y09876 aldehyde
                   dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                   the aldehyde dehydrogenase family PF_00171. ESTs
                   gb_F15117, gb R83958 and gb 586262 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   28183
Contig ID
                   170490 1.R1040
5'-most EST
                   eep700863849.h1
Method
                   BLASTX
NCBI GI
                   q2842478
BLAST score
                   220
                   3.0e-18
E value
Match length
                   86
% identity
NCBI Description
                   (AL021749) receptor protein kinase like protein
                   [Arabidopsis thaliana]
Seq. No.
                   28184
Contig ID
                   170520 1.R1040
5'-most EST
                   rca701\overline{0}00811.h1
Method
                   BLASTX
NCBI GI
                   q1698548
BLAST score
                   317
                   9.0e-29
E value
Match length
                   135
% identity
                   47
NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]
Seq. No.
                   28185
Contig ID
                   170574 1.R1040
5'-most EST
                  pxt700942627.h1
Seq. No.
                   28186
                   170576 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}55167.h1
Method
                  BLASTX
NCBI GI
                   q4558672
BLAST score
                   347
E value
                   9.0e-33
Match length
                  88
% identity
```

(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

Match length

139

```
28187
Seq. No.
                   170588 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400057h01a1
Method
                   BLASTX
NCBI GI
                   g1871185
BLAST score
                   554
                   9.0e-57
E value
Match length
                   125
% identity
                   (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
                   28188
Seq. No.
Contig ID
                   170647 1.R1040
5'-most EST
                   eep700864290.h1
Seq. No.
                   28189
                   170677 1.R1040
Contig ID
5'-most EST
                   eep700867106.hl
Seq. No.
                   28190
Contig ID
                   170695 1.R1040
5'-most EST
                   fC-qmro700864412a3
Method
                   BLASTX
NCBI GI
                   g4038030
BLAST score
                   419
E value
                   1.0e-40
Match length
                   196
% identity
NCBI Description
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
Seq. No.
                   28191
Contig ID
                   170705 1.R1040
5'-most EST
                   eep700864431.h1
Seq. No.
                   28192
Contig ID
                   170730 1.R1040
5'-most EST
                   eep700864515.h1
Method
                   BLASTX
NCBI GI
                   g547706
BLAST score
                   233
                   4.0e-19
E value
Match length
                   190
% identity
                   32
                   INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN
NCBI Description
                   PROTEASE) >qi 347022 pir S29509 insulinase (EC 3.4.99.45)
                   - rat >gi 564\overline{9}2 emb \overline{C}AA4\overline{76}89 (X67269) insulin-degrading
                   enzyme [Rattus norvegicus]
Seq. No.
                   28193
Contig ID
                   170743 1.R1040
5'-most EST
                   eep700864542.hl
Method
                   BLASTX
NCBI GI
                   g3540204
BLAST score
                   523
E value
                   3.0e-53
```

```
% identity
NCBI Description
                   (AC004260) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   170763 1.R1040
5'-most EST
                   yza700763910.h1
Method
                   BLASTX
NCBI GI
                   g1706956
BLAST score
                   181
E value
                   3.0e-27
Match length
                   121
                   57
% identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   28195
Seq. No.
Contig ID
                   170766 1.R1040
5'-most EST
                   jC-gmst02400005d11d1
Seq. No.
                   28196
Contig ID
                   170799 1.R1040
5'-most EST
                   eep700864693.h1
Method
                   BLASTX
NCBI GI
                   q3757822
BLAST score
                   212
E value
                   6.0e-17
Match length
                   117
% identity
                   41
NCBI Description
                   (AF044195) IkappaB kinase complex associated protein; IKAP
                   [Homo sapiens] >gi_4504629_ref_NP_003631.1_pIKBKAP_
                   inhibitor of kappa light polypeptide gene enhancer in
                   B-cells, kinase complex-associated protein; IKAP
Seq. No.
                   28197
                   170816 1.R1040
Contig ID
                   dpv701\overline{0}98520.h1
5'-most EST
Seq. No.
                   28198
                  170823 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}03808.h1
Method
                   BLASTX
NCBI GI
                   g3800951
BLAST score
                   153
E value
                   6.0e-10
Match length
                   57
% identity
                   (AF100657) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   28199
                   170831 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}56216.h1
                   28200
Seq. No.
Contig ID
                   170838 1.R1040
5'-most EST
                   uC-gmronoir004b07b1
```

Seq. No.

```
170844 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}06615.h1
Method
                   BLASTX
NCBI GI
                   q457517
BLAST score
                   261
E value
                   1.0e-22
Match length
                   126
% identity
NCBI Description
                   (L12579) alternatively spliced [Homo sapiens]
                   >gi 4503169 ref NP 001904.1 pCUTL1 cut (Drosophila)-like 1
                   (CCAAT displacement protein)
                   28202
Seq. No.
Contig ID
                   170862 1.R1040
5'-most EST
                   pxt700944333.hl
Seq. No.
                   28203
Contig ID
                   170870 1.R1040
5'-most EST
                   zzp700834111.h1
                   BLASTN
Method
                   q4235150
NCBI GI
BLAST score
                   46
                   7.0e-17
E value
                   130
Match length
% identity
                   84
                   Arabidopsis thaliana chromosome I BAC T25B24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   28204
Seq. No.
Contig ID
                   170873 1.R1040
5'-most EST
                   eep700866455.h1
Seq. No.
                   28205
                   170876 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400049b04a1
Method
                   BLASTX
NCBI GI
                   g1707642
BLAST score
                   703
                   6.0e-74
E value
                   249
Match length
% identity
NCBI Description
                   (Y07748) TMK [Oryza sativa]
Seq. No.
Contig ID
                   170919 1.R1040
5'-most EST
                   hrw701\overline{0}57932.h1
Seq. No.
Contig ID
                   170928 1.R1040
5'-most EST
                   uC-gmrominsoy258c09b1
                   28208
Seq. No.
                   170935 1.R1040
Contig ID
5'-most EST
                   eep700\overline{8}64995.h1
                   28209
Seq. No.
                   170952 1.R1040
Contig ID
```

Match length

90

```
5'-most EST
                   zzp700830712.h1
Seq. No.
                   28210
Contig ID
                   170953 1.R1040
5'-most EST
                   eep700865030.hl
                   28211
Seq. No.
Contig ID
                   170954 1.R1040
5'-most EST
                   fC-qmro700865034a4
Method
                   BLASTX
NCBI GI
                   q4262226
BLAST score
                   246
E value
                   3.0e-20
Match length
                   166
% identity
NCBI Description
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   28212
                   171008 1.R1040
Contig ID
5'-most EST
                   eep700870119.hl
                   BLASTX
Method
NCBI GI
                   q1777443
BLAST score
                   297
                   5.0e-27
E value
                   71
Match length
                   75
% identity
NCBI Description
                   (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
                   DNA-binding protein CCA1 [Arabidopsis thaliana] >gi 4090569
                   (U79156) CCA1 [Arabidopsis thaliana]
Seq. No.
                   28213
                   171025 1.R1040
Contig ID
5'-most EST
                   fC-qmro700865758a3
Method
                   BLASTX
                   q1930081
NCBI GI
BLAST score
                   556
                   1.0e-56
E value
Match length
                   247
% identity
                   53
                   (U92878) acyl-ACP thioesterase [Garcinia mangostana]
NCBI Description
Seq. No.
                   28214
Contig ID
                   171074 1.R1040
5'-most EST
                   eep700865319.h1
Seq. No.
                   28215
                   171078 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}57058.h1
Seq. No.
                   28216
                   171101 1.R1040
Contig ID
5'-most EST
                   eep700865363.h1
                   BLASTX
Method
NCBI GI
                   q3646450
BLAST score
                   230
                   2.0e-19
E value
```

```
% identity
NCBI Description
                   (AL031603) conserved hypothetical protein.
                   [Schizosaccharomyces pombe]
Seq. No.
                   28217
Contig ID
                   171107 1.R1040
5'-most EST
                   rca700995907.h1
Method
                   BLASTX
NCBI GI
                   q3953463
BLAST score
                   360
E value
                   1.0e-34
Match length
                   95
% identity
NCBI Description
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.
                   28218
Contig ID
                   171111 1.R1040
5'-most EST
                   eep700865381.h1
Seq. No.
                   28219
                   171125 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy077d10b1
Method
                   BLASTX
NCBI GI
                   q4263770
BLAST score
                   242
E value
                   2.0e-20
Match length
                   96
% identity
                   56
NCBI Description (AC006218) unknown protein [Arabidopsis thaliana]
Seq. No.
                   28220
                   171128 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}51170.h1
Method
                   BLASTX
NCBI GI
                   g3193293
BLAST score
                   322
E value
                   7.0e-30
Match length
                   122
% identity
NCBI Description
                   (AF069298) contains a short region of similarity to another
                   Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                   [Arabidopsis thaliana]
Seq. No.
                   28221
                   171136 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220053a06d1
Seq. No.
                   28222
Contig ID
                   171147 1.R1040
5'-most EST
                   uC-gmropic041f02b1
                   28223
Seq. No.
                   171162_1.R1040
Contig ID
5'-most EST
                   fC-gmro700865482a3
Method
                   BLASTX
NCBI GI
                   g136753
```

BLAST score

BLAST score

E value

275

4.0e-24

```
1.0e-113
E value
Match length
                   345
% identity
                   60
NCBI Description
                   GLYCOGEN (STARCH) SYNTHASE, ISOFORM 1
                   >qi 101338 pir A38326 UDPqlucose--starch
                   glucosyltransferase (EC 2.4.1.11) 1 - yeast (Saccharomyces
                   cerevisiae) >qi 172870 (M60919) qlycogen synthase
                   [Saccharomyces cerevisiae] >qi 836770 dbj BAA09254
                   (D50617) glycogen synthase isoform 1 [Saccharomyces
                   cerevisiae] >gi 1122228 dbj BAA08032 (D44599) Glycogen
                   synthase GSY1 [Saccharomyces cerevisiae]
                   28224
Seq. No.
Contig ID
                   171254 1.R1040
5'-most EST
                   eep700865645.h1
Seq. No.
                   28225
Contig ID
                   171298 1.R1040
5'-most EST
                   a5057577
                   28226
Seq. No.
Contig ID
                   171319 1.R1040
5'-most EST
                   eep700865761.h1
Seq. No.
                   28227
                   171328 1.R1040
Contig ID
5'-most EST
                   eep700865773.hl
Seq. No.
                   28228
Contig ID
                   171346 1.R1040
                   eep700\overline{8}65813.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539327
BLAST score
                   172
                   8.0e-13
E value
Match length
                   47
% identity
NCBI Description
                   (AL035679) putative proton pump [Arabidopsis thaliana]
                   28229
Seq. No.
                   171379 1.R1040
Contig ID
5'-most EST
                   eep700\overline{8}65879.h1
Method
                   BLASTX
NCBI GI
                   g3077640
BLAST score
                   846
E value
                   6.0e-91
                   279
Match length
% identity
NCBI Description
                   (AJ223151) O-methyltransferase [Prunus dulcis]
Seq. No.
                   28230
                   171388 1.R1040
Contig ID
                  pxt700945512.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3608261
```

% identity

47

```
59
Match length
% identity
                   78
NCBI Description
                   (AB017564) dof zinc finger protein [Arabidopsis thaliana]
Seq. No.
                   28231
Contig ID
                   171401 1.R1040
5'-most EST
                   zsq701127091.hl
                   BLASTX
Method
NCBI GI
                   g729273
BLAST score
                   432
E value
                  7.0e-43
                   111
Match length
                   77
% identity
                  CYPRO4 PROTEIN >gi_322804_pir__$28592 cypro4 protein -
NCBI Description
                   cardoon >gi_17959_emb_CAA49354 (X69672) cypro4 [Cynara
                   cardunculus]
Seq. No.
                   28232
                   171422 1.R1040
Contig ID
                   asn701136905.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2829887
BLAST score
                  164
E value
                   2.0e-11
Match length
                  105
                   37
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  28233
Seq. No.
                  171429 1.R1040
Contig ID
5'-most EST
                  eep700865982.hl
Method
                  BLASTX
NCBI GI
                  g4314358
BLAST score
                   400
E value
                   4.0e-39
Match length
                  110
                   69
% identity
                   (AC006340) putative kinesin heavy chain protein
NCBI Description
                   [Arabidopsis thaliana]
                  28234
Seq. No.
                  171468 1.R1040
Contig ID
5'-most EST
                  awf700837144.hl
Seq. No.
                  28235
                  171486 1.R1040
Contig ID
5'-most EST
                  fde700873229.h1
                  28236
Seq. No.
Contig ID
                  171494 1.R1040
5'-most EST
                  eep700866113.h1
                  BLASTX
Method
NCBI GI
                  g3236253
BLAST score
                  231
E value
                  6.0e-19
Match length
                  121
```

```
NCBI Description
                   (AC004684) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   28237
Contig ID
                   171514 1.R1040
5'-most EST
                   jC-qmf102220115f12d1
Method
                   BLASTN
NCBI GI
                   q4336139
BLAST score
                   41
E value
                   1.0e-13
Match length
                   89
% identity
                   87
NCBI Description
                  Arabidopsis thaliana serine/threonine protein phosphatase
                   2A 65 kDa A regulatory subunit alpha isoform gene, promoter
                   region
Seq. No.
                   28238
Contig ID
                   171520 1.R1040
5'-most EST
                   jC-qmle01810068e09a1
Method
                   BLASTX
NCBI GI
                   a2827160
BLAST score
                   149
                   1.0e-09
E value
                   103
Match length
% identity
                   28
NCBI Description (AF032667) rexo70 [Rattus norvegicus]
Seq. No.
                   28239
                   171524 1.R1040
Contig ID
5'-most EST
                  eep700866164.h1
Seq. No.
                   28240
Contig ID
                   171534 1.R1040
5'-most EST
                   zhf700\overline{9}65012.h1
Seq. No.
                   28241
                   171578 1.R1040
Contig ID
5'-most EST
                   zsg701120879.h1
                  BLASTX
Method
NCBI GI
                  g3810676
BLAST score
                  234
E value
                   1.0e-19
Match length
                  71
% identity
NCBI Description (AJ223357) SKOR [Arabidopsis thaliana]
Seq. No.
                   28242
                  171580 1.R1040
Contig ID
5'-most EST
                  eep700866259.h1
Seq. No.
                  28243
                  171584 1.R1040
Contig ID
                  gsv701\overline{0}51394.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4539291
BLAST score
                  340
```

5.0e-32

E value

```
Match length
                   129
% identity
                   53
                   (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28244
                   171592 1.R1040
Contig ID
5'-most EST
                   fde700875827.h1
                   28245
Seq. No.
                   171598 1.R1040
Contig ID
5'-most EST
                   epx701108483.hl
Method
                   BLASTX
NCBI GI
                   g2979543
BLAST score
                   254
E value
                   7.0e-22
Match length
                   102
% identity
                   53
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28246
Seq. No.
Contig ID
                   171603 1.R1040
5'-most EST
                   jC-qmf\overline{1}02220054c12a1
Seq. No.
                   28247
Contig ID
                   171605 1.R1040
5'-most EST
                   zsg701122004.h1
Method
                   BLASTX
NCBI GI
                   g3402690
BLAST score
                   166
                   3.0e-19
E value
Match length
                   107
% identity
                   52
                   (AC004697) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
                   28248
Seq. No.
Contig ID
                   171609 1.R1040
5'-most EST
                   eep700866305.h1
                   28249
Seq. No.
Contig ID
                   171627 1.R1040
5'-most EST
                   g5058235
                   28250
Seq. No.
                   171631 1.R1040
Contig ID
5'-most EST
                   eep700866336.hl
Method
                   BLASTX
NCBI GI
                   g2131161
BLAST score
                   115
                   8.0e-12
E value
Match length
                   64
% identity
                   61
NCBI Description
                   4-nitrophenylphosphatase (EC 3.1.3.41) - yeast
                   (Saccharomyces cerevisiae) >gi 1431400 emb CAA98816
                   (Z74284) ORF YDL236w [Saccharomyces cerevisiae]
```

Seq. No.

```
171634 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400065e10a2
                   28252
Seq. No.
                   171640 1.R1040
Contig ID
5'-most EST
                   eep700866353.h1
                   28253
Seq. No.
Contig ID
                   171693 1.R1040
5'-most EST
                   eep700866907.h1
                   28254
Seq. No.
                   171693 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy215e09b1
Method
                   BLASTX
NCBI GI
                   g3395440
BLAST score
                   219
                   2.0e-18
E value
                   71
Match length
                   59
% identity
NCBI Description
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
                   28255
Seq. No.
                   171732 1.R1040
Contig ID
5'-most EST
                   eep700866533.h1
Seq. No.
                   28256
                   171734 1.R1040
Contig ID
5'-most EST
                   rca700998788.hl
Seq. No.
                   28257
Contig ID
                   171742 1.R1040
5'-most EST
                   jC-qmle01810087e03d1
Seq. No.
                   28258
Contig ID
                   171746 1.R1040
5'-most EST
                   eep700866563.hl
Method .
                   BLASTX
NCBI GI
                   g3047085
BLAST score
                   277
                   2.0e-24
E value
Match length
                   121
% identity
                   (AF058914) No definition line found [Arabidopsis thaliana]
NCBI Description
                   28259
Seq. No.
                   171746 2.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}69885.h1
Method
                   BLASTX
                   g3047085
NCBI GI
BLAST score
                   152
                   3.0e-10
E value
Match length
                   40
% identity
                  (AF058914) No definition line found [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
Contig ID
                   171752 1.R1040
5'-most EST
                   zhf700\overline{9}59861.h1
Seq. No.
                   28261
                   171753 1.R1040
Contig ID
5'-most EST
                   zhf700958583.h1
                   28262
Seq. No.
                   171770 1.R1040
Contig ID
                   leu701156953.hl
5'-most EST
                   28263
Seq. No.
                   171791 1.R1040
Contig ID
5'-most EST
                   eep700866649.h1
Seq. No.
                   28264
                   171793 1.R1040
Contig ID
5'-most EST
                   eep700866653.hl
Method
                   BLASTX
                   q4454052
NCBI GI
BLAST score
                   192
                   8.0e-15
E value
Match length
                   87
% identity
NCBI Description (AL035394) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28265
Contig ID
                   171819 1.R1040
5'-most EST
                   eep700866701.h1
Seq. No.
                   28266
Contig ID
                   171855 1.R1040
5'-most EST
                   fua701042719.hl
Method
                   BLASTX
NCBI GI
                   q4006829
BLAST score
                   673
E value
                   6.0e-71
Match length
                   145
% identity
NCBI Description
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   171860 1.R1040
5'-most EST
                   kl1701212235.h1
Seq. No.
Contig ID
                   171875 1.R1040
5'-most EST
                   leu701148609.hl
Method
                   BLASTX
                   g3176707
NCBI GI
BLAST score
                   157
E value
                   9.0e-11
Match length
                   86
% identity
NCBI Description
                  (AC002392) putative proline-rich protein APG [Arabidopsis
```

thaliana]

```
Seq. No.
                   28269
Contig ID
                   171887 1.R1040
5'-most EST
                   eep700866850.hl
Method
                   BLASTX
NCBI GI
                   g4508079
BLAST score
                   417
                   3.0e-41
E value
Match length
                   98
% identity
                   77
NCBI Description
                   (AC005882) 66284 [Arabidopsis thaliana]
                   28270
Seq. No.
                   171889 1.R1040
Contig ID
5'-most EST
                   cks700764749.hl
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   573
E value
                   3.0e-59
Match length
                   132
% identity
                   83
NCBI Description
                   (AF013294) similar to nucleolin protein [Arabidopsis
                   thalianal
Seq. No.
                   28271
Contig ID
                   171890 1.R1040
5'-most EST
                   eep700866853.hl
Method
                   BLASTX
NCBI GI
                   q1841475
BLAST score
                   281
E value
                   2.0e-25
Match length
                   71
% identity
NCBI Description (Y11105) Myb26 [Pisum sativum]
Seq. No.
                   28272
Contig ID
                   171894 1.R1040
5'-most EST
                   jC-gmst02400029g09a1
Method
                   BLASTX
NCBI GI
                   q3334162
BLAST score
                   200
E value
                   2.0e-15
Match length
                   117
% identity
                   35
NCBI Description
                   DOWN SYNDROME CRITICAL REGION PROTEIN A
                   >gi 2588993 dbj BAA23270 (AB001990) Dcra [Mus musculus]
Seq. No.
                   28273
Contig ID
                   171894 2.R1040
5'-most EST
                   leu701\overline{1}49436.h1
Method
                   BLASTX
NCBI GI
                   q3334162
BLAST score
                   221
E value
                   4.0e-18
Match length
                   87
% identity
                   44
NCBI Description
                   DOWN SYNDROME CRITICAL REGION PROTEIN A
```

>gi 2588993 dbj BAA23270 (AB001990) Dcra [Mus musculus]

```
28274
Seq. No.
                   171907 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400073f11a1
                   28275
Seq. No.
                   171908 1.R1040
Contig ID
                   leu701146451.h1
5'-most EST
Method
                   BLASTN
                   g2143322
NCBI GI
BLAST score
                   42
                   2.0e-14
E value
Match length
                   82
% identity
                   88
NCBI Description
                  P.deltoides chloroplast DNA for psbB operon
Seq. No.
                   28276
Contiq ID
                   171916 1.R1040
                   sat701002934.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2760830
BLAST score
                   597
E value
                   3.0e-62
Match length
                   123
% identity
NCBI Description
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
                   28277
Seq. No.
Contig ID
                   171917 1.R1040
5'-most EST
                  pmv700891158.h1
Seq. No.
                   28278
Contig ID
                   171929 1.R1040
5'-most EST
                   eep700867235.h1
Method
                  BLASTX
NCBI GI
                   g2346978
BLAST score
                   147
E value
                   1.0e-09
                   74
Match length
% identity
NCBI Description
                   (AB006601) ZPT2-14 [Petunia x hybrida]
Seq. No.
                   28279
                   171930 1.R1040
Contig ID
5'-most EST
                   eep700867282.h1
Method
                  BLASTX
NCBI GI
                  q4038055
BLAST score
                  261
                   5.0e-23
E value
                  88
Match length
% identity
                   (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  >gi 4557077 gb AAD22516.1 AC007045 16 (AC007045) putative
                  cytochrome p450 [Arabidopsis thaliana]
```

Seq. No.

```
Contig ID
                    171976 1.R1040
 5'-most EST
                    asn701140943.h1
 Seq. No.
                    28281
 Contig ID
                    171977 1.R1040
 5'-most EST
                    leu701156653.h1
 Method
                    BLASTX
 NCBI GI
                    g4454567
 BLAST score
                    124
                    3.0e-10
 E value
 Match length
                    118
 % identity
                    44
                   (AF128407) lipase homolog [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   28282
 Contig ID
                   171980 1.R1040
 5'-most EST
                   leu701146017.h1
 Seq. No.
                   28283
 Contig ID
                   172016_1.R1040
 5'-most EST
                   pmv700894106.h1
 Seq. No.
                   28284
 Contig ID
                   172026_1.R1040
 5'-most EST
                   eep700867125.h1
Seq. No.
                   28285
Contig ID
                   172036 1.R1040
5'-most EST
                   uC-gmrominsoy170d05b1
Seq. No.
                   28286
Contig ID
                   172037 1.R1040
5'-most EST
                   eep700867149.h1
Method
                   BLASTX
NCBI GI
                   g1769903
BLAST score
                   164
E value
                   1.0e-11
Match length
                   82
% identity
                   41
                   (X95738) proline transporter 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28287
Contig ID
                   172073 1.R1040
5'-most EST
                   jC-gmro02910026d02a1
Seq. No.
                   28288
Contig ID
                   172081_1.R1040
5'-most EST
                   eep700867239.h1
Seq. No.
                   28289
Contig ID
                  172086 1.R1040
5'-most EST
                  bth700848572.h1
Method
                  BLASTX
NCBI GI
                  g3402697
BLAST score
                  423
E value
                  2.0e-41
Match length
```

17.4

5'-most EST

```
% identity
                   (AC004261) putative phosphatidylinositol-4-phosphate
NCBI Description
                   5-kinase [Arabidopsis thaliana]
Seq. No.
                   28290
Contig ID
                   172145 1.R1040
5'-most EST
                   dpv701097666.hl
Seq. No.
                   28291
Contig ID
                   172159 1.R1040
5'-most EST
                   eep700867465.h1
Method
                  BLASTX
NCBI GI
                   g4099833
BLAST score
                   162
E value
                   2.0e-11
Match length
                  77
% identity
                   42
NCBI Description
                   (U90265) bifunctional nuclease [Zinnia elegans]
Seq. No.
                  172168 1.R1040
Contig ID
5'-most EST
                  eep700867487.h1
Seq. No.
                  28293
                  172173 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220148c08a1
Method
                  BLASTX
NCBI GI
                  q4165861
BLAST score
                  536
E value
                   9.0e-55
Match length
                  164
% identity
                  29
NCBI Description
                  (AF006603) histone deacetylase mHDA2 [Mus musculus]
Seq. No.
                  28294
                  172181 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910054a03d1
Seq. No.
                  28295
                  172192 1.R1040
Contig ID
5'-most EST
                  eep700867563.hl
Seq. No.
                  28296
                  172212 1.R1040
Contig ID
                  asn701131028.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3775999
BLAST score
                  291
E value
                  2.0e-26
Match length
                  66
% identity
                  (AJ010463) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  28297
Seq. No.
Contig ID
                  172218 1.R1040
```

eep700867656.h1

% identity

69

```
28298
Seq. No.
                   172224 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}37416.h1
Method
                   BLASTX
                   g3511285
NCBI GI
BLAST score
                   555
                   3.0e-57
E value
Match length
                   121
% identity
                   (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                   tremula]
                   28299
Seq. No.
Contig ID
                   172227 1.R1040
5'-most EST
                   eep700869572.h1
                   28300
Seq. No.
                   172245 1.R1040
Contig ID
5'-most EST
                   rlr700899532.hl
Method
                   BLASTN
NCBI GI
                   q1142620
BLAST score
                   150
E value
                   8.0e-79
Match length
                   358
% identity
                   89
NCBI Description
                   Phaseolus vulgaris phaseolin G-box binding protein PG2
                   (PG2) mRNA, partial cds
Seq. No.
                   28301
Contig ID
                   172264 1.R1040
5'-most EST
                   eep700870273.hl
Seq. No.
                   28302
Contig ID
                   172267 1.R1040
5'-most EST
                   zsq701123293.h1
Seq. No.
                   28303
Contig ID
                   172278 1.R1040
                   fua701040559.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2507198
BLAST score
                   343
E value
                   3.0e-32
Match length
                   121
% identity
                   57
                  PROTEIN KINASE CEK1 >qi 1853976 dbj BAA06551 (D31773)
NCBI Description
                  protein kinase [Schizosaccharomyces pombe]
Seq. No.
                   28304
Contig ID
                   172301 1.R1040
5'-most EST
                   jC-gmst02400043f07d1
Method
                   BLASTX
NCBI GI
                   g3341687
BLAST score
                   150
E value
                   1.0e-09
Match length
                   45
```

```
NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.
                  28305
Contig ID
                  172304 1.R1040
                  crh700855002.hl
5'-most EST
                  28306
Seq. No.
                  172305 1.R1040
Contig ID
                  eep700867833.hl
5'-most EST
Method
                  BLASTX
                  g4454550
NCBI GI
BLAST score
                  201
E value
                   1.0e-15
Match length
                   104
% identity
                   23
NCBI Description
                   (AF113002) silencing mediator of retinoic acid and thyroid
                  hormone receptor beta [Mus musculus]
                  28307
Seq. No.
Contig ID
                  172318 1.R1040
5'-most EST
                  leu701153303.hl
                  28308
Seq. No.
Contig ID
                  172335 1.R1040
5'-most EST
                  eep700867882.hl
Seq. No.
                  28309
Contig ID
                  172354 1.R1040
5'-most EST
                   eep700867926.hl
Method
                  BLASTX
NCBI GI
                  g4204283
BLAST score
                  271
E value
                   4.0e-24
                  71
Match length
% identity
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  28310
                  172361 1.R1040
Contig ID
5'-most EST
                  pxt700941884.hl
                  BLASTX
Method
NCBI GI
                  g285741
BLAST score
                  228
                   4.0e-19
E value
                  87
Match length
% identity
NCBI Description (D14550) EDGP precursor [Daucus carota]
Seq. No.
                  28311
                  172373 1.R1040
Contig ID
                  fua701038295.hl
5'-most EST
                 BLASTX
Method
                  g399427
NCBI GI
BLAST score
                  519
E value
                  5.0e-53
                  121
Match length
```

% identity

Contig ID

5'-most EST

```
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_99392_pir__S24996
                   phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas
                   reinhardtii >gi 18143 emb CAA47043 (X66412) enolase
                   [Chlamydomonas reinhardtii]
Seq. No.
                   28312
Contig ID
                   172383 1.R1040
5'-most EST
                   kl1701213623.hl
Seq. No.
                   28313
Contig ID
                   172388 1.R1040
5'-most EST
                   eep700868002.hl
Method
                   BLASTX
NCBI GI
                   q3063448
BLAST score
                   344
E value
                   1.0e-32
Match length
                   101
% identity
NCBI Description
                   (AC003981) F22013.10 [Arabidopsis thaliana]
Seq. No.
                   28314
                   172398 1.R1040
Contig ID
5'-most EST
                   rlr700902336.h1
                   BLASTX
Method
NCBI GI
                   g1943751
BLAST score
                   726
                   4.0e-77
E value
                   149
Match length
% identity
                   95
NCBI Description
                   (U93845) Arabidopsis thaliana ER-type calcium pump
                   protein, complete sequence >gi 2078292 (U96455) ER-type
                   Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                   28315
Seq. No.
                   172412 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}17349.h1
Seq. No.
                   28316
                   172445 1.R1040
Contig ID
5'-most EST
                   eep700\overline{8}68125.h1
Seq. No.
                   28317
                   172453 1.R1040
Contiq ID
                   xpa700797315.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4102600
BLAST score
                   213
                   2.0e-17
E value
Match length
                   46
% identity
NCBI Description
                   (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   28318
```

172480 1.R1040

eep700868196.h1

```
28319
  Seq. No.
  Contig ID
                      172510 1.R1040
  5'-most EST
                      eep700\overline{8}68455.h1
  Seq. No.
                      28320
  Contig ID
                      172511 1.R1040
  5'-most EST
                      zhf700965043.h1
  Method
                      BLASTX
  NCBI GI
                      q3329368
·: BLAST score
                      326
  E value
                      2.0e-30
  Match length
                      103
  % identity
                      (AF031244) nodulin-like protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
  Contig ID
                      172541 1.R1040
  5'-most EST
                      zhf700961577.h1
  Method
                     BLASTX
  NCBI GI
                      q2583118
  BLAST score
                      227
  E value
                      4.0e-28
  Match length
                      105
  % identity
  NCBI Description
                      (AC002387) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                      28322
  Contig ID
                      172593 1.R1040
  5'-most EST
                      sat701\overline{0}07218.h2
                      28323
  Seq. No.
  Contig ID
                      172603 1.R1040
  5'-most EST
                      eep700868417.h1
                     BLASTX
  Method
  NCBI GI
                     q3287695
  BLAST score
                      454
  E value
                      5.0e-84
  Match length
                      316
  % identity
                      (AC003979) Similar to hypothetical protein C34B7.2
  NCBI Description
                     gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                     thaliana]
  Seq. No.
                     28324
                     172630 1.R1040
  Contig ID
  5'-most EST
                     dpv701\overline{0}97185.h1
                     28325
  Seq. No.
  Contig ID
                     172645 1.R1040
  5'-most EST
                     epx701\overline{1}04373.h1
  Method
                     BLASTX
  NCBI GI
                     q1710587
  BLAST score
                     194
  E value
                     3.0e-15
  Match length
                     53
  % identity
```

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic

ribosomal protein PO [Glycine max]

```
Seq. No.
                    28326
 Contig ID
                    172654_1.R1040
 5'-most EST
                    jex700\overline{9}07645.h1
 Method
                    BLASTX
 NCBI GI
                    q4567197
 BLAST score
                    172
 E value
                    2.0e-12
 Match length
                    37
 % identity
                    78
 NCBI Description
                   (AC007168) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    28327
 Contig ID
                    172670 1.R1040
 5'-most EST
                    jC-gmro02910007b10a1
 Seq. No.
                    28328
 Contig ID
                    172672 1.R1040
 5'-most EST
                    gsv701048066.h1
 Method
                    BLASTN
 NCBI GI
                    g2624382
 BLAST score
                    74
E value
                    1.0e-33
Match length
                    217
 % identity
                    83
NCBI Description
                   P.vulgaris mRNA for cinnamate 4-hydroxylase
Seq. No.
                   28329
Contig ID
                   172676 1.R1040
5'-most EST
                   eep700868519.hl
Method
                   BLASTX
NCBI GI
                   g2832304
BLAST score
                   181
E value
                   2.0e-13
Match length
                   93
% identity
NCBI Description
                   (AF044489) receptor-like protein kinase [Oryza sativa]
Seq. No.
                   28330
Contig ID
                   172694 1.R1040
5'-most EST
                   eep700868542.hl
Seq. No.
                   28331
Contig ID
                   172703 1.R1040
5'-most EST
                   g4396761
Seq. No.
                   28332
Contig ID
                   172707 1.R1040
5'-most EST
                   zhf700953295.h1
Method
                   BLASTX
NCBI GI
                   g3928090
BLAST score
                   320
E value
                   9.0e-30
Match length
                   100
% identity
                   58
NCBI Description
                  (AC005770) putative MTN3 protein [Arabidopsis thaliana]
```

BLAST score

E value

185

4.0e-14

28333 Seq. No. Contig ID 172716 1.R1040 5'-most EST eep700868582.h1Seq. No. 28334 Contig ID 172720 1.R1040 5'-most EST uC-gmrominsoy040f09b1 Method BLASTX NCBI GI g3287696 BLAST score 517 E value 1.0e-52 Match length 158 % identity NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana] 28335 Seq. No. Contig ID 172725 1.R1040 5'-most EST $jex700\overline{9}05667.h1$ Method **BLASTX** NCBI GI g2443886 BLAST score 156 4.0e-10 E value Match length 117 % identity (AC002294) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 28336 172738 1.R1040 Contig ID 5'-most EST eep700868615.h128337 Seq. No. Contig ID 172748 1.R1040 5'-most EST pmv700890005.h1 28338 Seq. No. Contig ID 172761 1.R1040 5'-most EST $eep700\overline{8}68657.h1$ Seq. No. 28339 Contig ID 172770 1.R1040 5'-most EST uC-gmrominsoy202h02b1 28340 Seq. No. Contig ID 172773 1.R1040 5'-most EST eep700868688.h128341 Seq. No. Contig ID 172798 1.R1040 5'-most EST eep700868740.h1Method BLASTX NCBI GI g2191136

Contig ID

28350

172995 1.R1040

```
88
Match length
% identity
                   41
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   28342
Seq. No.
                   172811 1.R1040
Contig ID
5'-most EST
                   eep700868770.h1
Method
                   BLASTX
NCBI GI
                   g4580472
BLAST score
                   423
                   5.0e-42
E value
Match length
                   92
% identity
                   86
                   (AC006081) DNA binding protein; similar to CDC27 and nuclear
NCBI Description
                   scaffold proteins [Arabidopsis thaliana]
                                                                 : ; •
Seq. No.
                   28343
Contig ID
                   172849 1.R1040
5'-most EST
                   uC-gmflminsoy081h07b1
Seq. No.
                   28344
Contig ID
                   172907 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220063d07a1
Seq. No.
                   28345
Contig ID
                   172914 1.R1040
5'-most EST
                   eep700870123.h1
Seq. No.
                   28346
Contig ID
                   172932 1.R1040
5'-most EST
                   fC-amro700846765d3
Method
                   BLASTN
NCBI GI
                   g1416513
BLAST score
                   56
E value
                   2.0e-22
                                     د أو در سي
Match length
                   112
% identity
NCBI Description
                  Brassica napus mRNA for CTP:phosphocholine
                   cytidylyltransferase, complete cds
Seq. No.
                   28347
Contig ID
                   172955 1.R1040
5'-most EST
                   eep700869078.hl
Seq. No.
Contig ID
                  172971 1.R1040
5'-most EST
                  eep700869104.hl
Seq. No.
                  28349
Contig ID
                  172982 1.R1040
5'-most EST
                  eep700869123.h1
```

Contig ID

28356

173085 1.R1040

```
eep700869140.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3482917
BLAST score
                   456
E value
                   9.0e-71
Match length
                   214
% identity
NCBI Description
                   (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
                   gi_2276344, gi_2829880, gi 2352919 and others. [Arabidopsis
                   thaliana]
                   28351
Seq. No.
Contig ID
                   173013 1.R1040
5'-most EST
                   q56780\overline{6}8
Method
                   BLASTX
NCBI GI
                   q3367568
BLAST score
                   272
E value
                   3.0e-36
Match length
                   117
% identity
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                   thaliana]
                   28352
Seq. No.
                   173020 1.R1040
Contig ID
5'-most EST
                   eep700869182.h1
                   28353
Seq. No.
Contig ID
                   173034 1.R1040
5'-most EST
                   leu701\overline{1}55874.h1
Method
                   BLASTX
NCBI GI
                   g2827631
BLAST score
                   420
E value
                   2.0e-41
Match length
                   95
% identity
                   (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                   28354
Seq. No.
                   173048 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy093d04b1
Method
                   BLASTX
NCBI GI
                   g3193306
BLAST score
                   403
                   2.0e-39
E value
Match length
                   116
% identity
                   70
NCBI Description
                   (AF069300) contains similarity to Arabidopsis
                   membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
Seq. No.
                   28355
                   173065_1.R1040
Contig ID
5'-most EST
                   eep700869336.hl
```

28364

```
5'-most EST
                   eep700869339.hl
Seq. No.
                   28357
Contig ID
                   173092 1.R1040
5'-most EST
                   uC-gmrominsoy264g09b1
Method
                   BLASTX
NCBI GI
                   q2191136
BLAST score
                   151
E value
                   8.0e-10
Match length
                   76
% identity
                   43
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   28358
Seq. No.
Contig ID
                   173102 1.R1040
5'-most EST
                   eep700869377.hl
Seq. No.
                   28359
Contig ID
                   173108 1.R1040
5'-most EST
                   q43003\overline{6}5
                   28360
Seq. No.
Contig ID
                   173127 1.R1040
5'-most EST
                   jC-gmr002910014a04d1
                   28361
Seq. No.
Contig ID
                   173149 1.R1040
5'-most EST
                   jC-gmf\(\bar{1}\)02220126g11a1
Seq. No.
                   28362
Contig ID
                   173150 1.R1040
5'-most EST
                   pmv700894867.hl
Method
                   BLASTX
NCBI GI
                   q1685005
BLAST score
                   390
E value
                   8.0e-38
Match length
                   132
% identity
                   (U32644) immediate-early salicylate-induced
NCBI Description
                   glucosyltransferase [Nicotiana tabacum]
Seq. No.
                   28363
Contig ID
                   173162 1.R1040
5'-most EST
                   jC-qmro02910009e07a1
Method
                   BLASTX
NCBI GI
                   q4249419
BLAST score
                   412
E value
                   4.0e-40
Match length
                   240
% identity
NCBI Description
                   (AC006072) hypothetical protein, 3' partial [Arabidopsis
                   thaliana]
```

```
173176 1.R1040
Contig ID
5'-most EST
                   eep700869562.h1
Seq. No.
                   28365
Contig ID
                   173210 1.R1040
5'-most EST
                   g4313501
Method
                   BLASTX
NCBI GI
                   q1706189
BLAST score
                   186
E value
                   2.0e-13
Match length
                   111
% identity
                   35
NCBI Description
                   LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2)
                   (CAT2) (TEA PROTEIN) (T-CELL EARLY ACTIVATION PROTEIN)
                   (20.5) >gi 627850 pir A54011 CAT1/ecoR protein - mouse
                   >gi 293315 (L11600) cationic amino acid transporter-2 [Mus
                   musculus] >gi_517493 (L29006) membrane protein [Mus
                  musculus]
Seq. No.
                   28366
Contig ID
                   173216 1.R1040
5'-most EST
                   jC-qmro02910052h01a1
                   28367
Seq. No.
Contig ID
                   173220 1.R1040
5'-most EST
                   jC-gmst02400056h01d1
Method
                   BLASTX
NCBI GI
                   q3281867
BLAST score
                   183
E value
                   2.0e-13
Match length
                   42
% identity
NCBI Description
                   (AL031004) putative protein [Arabidopsis thaliana]
                   28368
Seq. No.
Contig ID
                   173220 2.R1040
5'-most EST
                   eep700869660.h1
Method
                  BLASTX
NCBI GI
                  g3281867
BLAST score
                  291
E value
                   1.0e-26
Match length
                  85
% identity
NCBI Description
                   (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                  28369
Contig ID
                  173243 1.R1040
5'-most EST
                  eep700869954.h1
Method
                  BLASTX
NCBI GI
                  q1084334
BLAST score
                  367
E value
                  2.0e-35
Match length
                  92
% identity
NCBI Description
                  calcium-dependent protein kinase (EC 2.7.1.-) 1 -
                  Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
```

calcium-dependent protein kinase [Arabidopsis thaliana]

BLAST score

303

```
Seq. No.
                  28370
                  173253 1.R1040
Contig ID
5'-most EST
                  eep700869735.h1
Method
                  BLASTX
                  g4038043
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
                  100
Match length
% identity
                   37
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  28371
Seq. No.
Contig ID
                  173289 1.R1040
5'-most EST
                  eep700869833.h1
Seq. No.
                  28372
Contig ID
                   173305 1.R1040
5'-most EST
                   jC-qmle01810049a03d1
Method
                  BLASTX
NCBI GI
                  q3176715
BLAST score
                  240
E value
                   4.0e-20
Match length
                   69
% identity
NCBI Description
                   (AC002392) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   28373
Contig ID
                  173308 1.R1040
5'-most EST
                   zsq701124666.h1
Method
                  BLASTX
NCBI GI
                  q3687223
BLAST score
                   365
E value
                  7.0e-35
Match length
                  89
% identity
NCBI Description
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  28374
Contig ID
                  173326 1.R1040
5'-most EST
                  xzm700763704.h1
Method
                  BLASTX
NCBI GI
                  q4467124
BLAST score
                  505
E value
                  2.0e-51
Match length
                  116
% identity
NCBI Description
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  173342 1.R1040
5'-most EST
                  uC-gmropic101b04b1
Method
                  BLASTX
NCBI GI
                  q2388577
```

```
6.0e-28
E value
Match length
                   92
                   62
% identity
                   (AC000098) Similar to Arabidopsis putative ion-channel
NCBI Description
                   PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
Seq. No.
                   28376
                   173380 1.R1040
Contig ID
                   jex700\overline{9}08292.h1
5'-most EST
                   28377
Seq. No.
                   173381 1.R1040
Contig ID
5'-most EST
                   eep700869975.h1
Method
                   BLASTX
NCBI GI
                   g3004552
BLAST score
                   358
                   5.0e - 34
E value
Match length
                   127
% identity
                   57
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28378
Seq. No.
                   173430 1.R1040
Contig ID
                   hrw701058040.h1
5'-most EST
Seq. No.
                   28379
                   173436 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400055d05a1
Method
                   BLASTX
                   g1850546
NCBI GI
                   206
BLAST score
                   2.0e-16
E value
Match length
                   83
% identity
                   57
                   (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                   thaliana]
                   28380
Seq. No.
                   173438 1.R1040
Contig ID
5'-most EST
                   uC-gmropic101b08b1
                   28381
Seq. No.
Contig ID
                   173458 1.R1040
5'-most EST
                   eep700870137.hl
Seq. No.
                   28382
                   173466 1.R1040
Contig ID
5'-most EST
                   fua701036904.h1
Method
                   BLASTX
                   g3128187
NCBI GI
BLAST score
                   166
                   8.0e-12
E value
Match length
                   53
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
```

28383

Seq. No.

```
173499 1.R1040
Contig ID
                  eep700870218.hl
5'-most EST
                  28384
Seq. No.
Contig ID
                  173500 1.R1040
5'-most EST
                  uC-qmropic016e02b1
                  28385
Seq. No.
Contig ID
                  173526 1.R1040
5'-most EST
                  eep700870276.h1
Method
                  BLASTX
NCBI GI
                  q4490316
BLAST score
                  243
                   4.0e-21
E value
                  65
Match length
% identity
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                  28386
Seq. No.
                  173527 1.R1040
Contig ID
5'-most EST
                  zhf700958181.h1
                  28387
Seq. No.
                  173533 1.R1040
Contig ID
                  jC-gmro02910027h12a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3885334
                  430
BLAST score
E value
                  1.0e-42
Match length
                  110
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  28388
Seq. No.
                  173536 1.R1040
Contig ID
                  eep700\overline{8}70290.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244814
                  378
BLAST score
E value
                  2.0e-36
Match length
                  115
% identity
NCBI Description
                  (Z97336) protein kinase [Arabidopsis thaliana]
                  28389
Seq. No.
                  173555 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810034b08a2
Method
                  BLASTX
NCBI GI
                  g2143290
BLAST score
                  202
E value
                  2.0e-15
Match length
                  162
% identity
                  (Z95972) hypothetical protein Rv0669c [Mycobacterium
NCBI Description
                  tuberculosis]
```

```
Seq. No.
                 28390
Contig ID
                  173557 1.R1040
5'-most EST
                  g4260250
                  28391
Seq. No.
Contig ID
                  173593 1.R1040
5'-most EST
                  eep700870382.h1
Seq. No.
                  28392
                  173615 1.R1040
Contig ID
5'-most EST
                  eep700870429.h1
Seq. No.
                  28393
Contig ID
                  173622 1.R1040
5'-most EST
                  eep700870441.h1
Method
                  BLASTX
                  g112947
NCBI GI
BLAST score
                  258
                  2.0e-22
E value
Match length
                  102
% identity
                  43
NCBI Description
                  AAC-RICH MRNA CLONE AAC3 PROTEIN >qi 84121 pir S05357
                  hypothetical protein (clone AAC3) - slime mold
                  (Dictyostelium discoideum) (fragment)
                  >gi 7176 emb CAA34531 (X16524) coding region (AA 1 - 437)
                [Dictyostelium discoideum]
                  28394
Seq. No.
Contig ID
                  173632 1.R1040
5'-most EST
                  gsv701050008.hl
Method
                  BLASTX
NCBI GI
                  g2262177
BLAST score
                  530
E value
                  3.0e-54
Match length
                  138
% identity
                  70
NCBI Description
                  (AC002329) hypothetical protein similar to T18A10.3
                  [Arabidopsis thaliana]
Seq. No.
                  28395
Contig ID
                  173661 1.R1040
5'-most EST
                  zlv700807517.h1
Seq. No.
                  28396
Contig ID
                  173705 1.R1040
5'-most EST
                  uC-gmropic042a04b1
Seq. No.
                  28397
Contig ID
                  173728 1.R1040
5'-most EST
                  zlv700807612.h1
Method
                  BLASTX
NCBI GI
                  q3402758
BLAST score
                  428
E value
                  2.0e-45
Match length
                  152
% identity
NCBI Description (AL031187) serine/threonine kinase - like protein
```

....

NCBI Description

carotal

[Arabidopsis thaliana]

28398 Seq. No. 173787 1.R1040 Contig ID 5'-most EST qsf700698326.hl Method BLASTX q3785989 NCBI GI BLAST score 195 E value 3.0e-15 Match length 107 % identity 48 NCBI Description (AC005560) unknown protein [Arabidopsis thaliana] 28399 Seq. No. Contig ID 173806 1.R1040 5'-most EST gsf700698355.h1 Seq. No. 28400 Contig ID 173821 1.R1040 5'-most EST xpa700795033.hl Seq. No. 28401 Contig ID 173822 1.R1040 5'-most EST jC-gmro02910016g07d1 Method BLASTX NCBI GI g2262100 BLAST score 314 E value 8.0e-29 Match length 71 % identity NCBI Description (AC002343) unknown protein [Arabidopsis thaliana] Seq. No. 28402 Contig ID 173829 1.R1040 5'-most EST dpv701102034.h1 Method BLASTX NCBI GI g2129635 BLAST score 411 E value 5.0e-40 Match length 188 % identity 50 NCBI Description light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana] Seq. No. Contig ID 173864 1.R1040 5'-most EST fC-qmro700698445a1 Method BLASTX NCBI GI g2224911 BLAST score 225 E value 3.0e-18 Match length 145 % identity 39

(U93048) somatic embryogenesis receptor-like kinase [Daucus

E value

9.0e-26

```
Seq. No.
                   28404
Contig ID
                   173878 1.R1040
5'-most EST
                   gsf700698471.hl
                   28405
Seq. No.
Contig ID
                   173897 1.R1040
5'-most EST
                   leu701150681.hl
Method
                   BLASTX
NCBI GI
                   g3947733
BLAST score
                   168
                   3.0e-14
E value
Match length
                   93
                   47
% identity
NCBI Description
                   (AJ009719) NL25 [Solanum tuberosum]
Seq. No.
                   28406
Contig ID
                   173905 1.R1040
5'-most EST
                   zsg701124722.h1
                   28407
Seq. No.
Contig ID
                   173912 1.R1040
5'-most EST
                   uC-qmflminsoy061a05b1
Method
                  BLASTN
NCBI GI
                   g4159706
BLAST score
                   37
E value
                   4.0e-11
Match length
                   192 :--
% identity
                   85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   28408
Contig ID
                   174024 1.R1040
                   zhf700952960.h1
5'-most EST
Seq. No.
                   28409
Contig ID
                   174026 1.R1040
5'-most EST
                  uC-gmrominsoy198f01b1
Method
                  BLASTN
NCBI GI
                   g1370171
BLAST score
                   131
E value
                   2.0e-67
Match length
                   259
% identity
                  88
NCBI Description L.japonicus mRNA for small GTP-binding protein, RABIX
Seq. No.
                  28410
Contig ID
                  174088 1.R1040
5'-most EST
                  xpa700792630.h1
Seq. No.
                  28411
Contig ID
                  174089 1.R1040
5'-most EST
                  bth700844710.h1
Method
                  BLASTX
NCBI GI
                  g3164222
BLAST score
                  288
```

```
90
 Match length
% identity
                    61
 NCBI Description
                    (AB008518) RMA1 [Arabidopsis thaliana] >gi 4206205
                    (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                   thaliana]
                   28412
 Seq. No.
 Contig ID
                   174089 3.R1040
 5'-most EST
                   xpa700792631.h1
                   28413
 Seq. No.
                   174096 1.R1040
 Contig ID
 5'-most EST
                   uC-gmflminsoy097f12b1
Method
                   BLASTX
NCBI GI
                   g2909781
                   234
 BLAST score
                   1.0e-38
 E value
Match length
                   118
                   71
 % identity
NCBI Description
                    (AF020288) MgATP-energized glutathione S-conjugate pump
                    [Arabidopsis thaliana]
                   28414
Seq. No.
Contig ID
                   174107 1.R1040
 5'-most EST
                   g5606668
Method
                   BLASTX
NCBI GI
                   g2505877
BLAST score
                   323
E value
                   8.0e-30
Match length
                   195
 % identity
                   42
                   (Y12776) dehydrogenase [Arabidopsis thaliana]
NCBI Description
                   28415
Seq. No.
                   174146 1.R1040
Contig ID
 5'-most EST
                   xpa700797244.h1
                   28416
Seq. No.
                   174147 1.R1040 .
Contig ID
 5'-most EST
                   xpa700792742.h1
Seq. No.
                   28417
                   174192 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910049a02a1
Seq. No.
                   28418
Contig ID
                   174194 1.R1040
5'-most EST
                   jC-gmle01810094g03a1
Method
                   BLASTX
NCBI GI
                   g4092774
BLAST score
                   268
E value
                   2.0e-23
Match length
                   134
% identity
                   43
                   (AF105140) disease resistance gene homolog 9N [Brassica
NCBI Description
```

napus]

```
28419
Seq. No.
Contig ID
                   174205 1.R1040
5'-most EST
                   xpa700792836.h1
Method
                   BLASTX
                   g3461831
NCBI GI
BLAST score
                   244
                   9.0e-21
E value
Match length
                   61
% identity
                   75
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
                   28420
Seq. No.
                   174217 1.R1040
Contig ID
5'-most EST
                   bth700846982.h1
Method
                   BLASTX
NCBI GI
                   g2894603
BLAST score
                   339
E value
                   9.0e-32
Match length
                   103
% identity
                   41
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   28421
Contig ID
                   174223 1.R1040
5'-most EST
                   xpa700792871.h1
Seq. No.
                   28422
Contig ID
                   174225 1.R1040
5'-most EST
                   uC-gmronoir012d05b1
Seq. No.
                   28423
Contig ID
                   174232 1.R1040
5'-most EST
                   dpv701101304.h1
Seq. No.
                   28424
Contig ID
                   174241 1.R1040
5'-most EST
                   xpa700792912.h1
Method
                   BLASTN
NCBI GI
                   q516102
BLAST score
                   361
E value
                   0.0e + 00
Match length
                   492
% identity
NCBI Description
                  Soybean phytochrome B (phyB) gene exons 1-5, complete cds
                   28425
Seq. No.
Contig ID
                   174243 1.R1040
5'-most EST
                   pxt700945748.h1
Method
                   BLASTN
                   g3510247
NCBI GI
BLAST score
                   39
E value
                   1.0e-12
Match length
                   71
% identity
                   89
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F19D11 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

Contig ID

```
28426
Seq. No.
                   174246 1.R1040
Contig ID
5'-most EST
                   xpa700792922.hl
Seq. No.
                   28427
                   174252 1.R1040
Contig ID
5'-most EST
                   xpa700792933.h1
Seq. No.
                   28428
                   174266 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}05932.h1
                   28429
Seq. No.
Contig ID
                   174295 1.R1040
5'-most EST
                   uC-gmflminsoy020c09b1
                   28430
Seq. No.
                   174299 1.R1040
Contig ID
5'-most EST
                   sat701013788.hl
Method
                   BLASTX
NCBI GI
                   q3646451
BLAST score
                   154
E value
                   4.0e-10
Match length
                   130
% identity
NCBI Description
                  (AL031603) mRNA cap methyltransferase [Schizosaccharomyces
                   pombe]
Seq. No.
                   28431
                   174302 1.R1040
Contiq ID
5'-most EST
                   xpa700793016.hl
Seq. No.
                   28432
                   174337 1.R1040
Contig ID
5'-most EST
                   sat701009233.hl
Method
                   BLASTX
NCBI GI
                   g3822036
BLAST score
                   354
E value
                   4.0e-33
Match length
                   191
% identity
NCBI Description
                   (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
Seq. No.
                   28433
Contig ID
                   174356 1.R1040
5'-most EST
                   xpa700793402.hl
Method
                   BLASTN
NCBI GI
                   g3063438
BLAST score
                   71
E value
                   6.0e-32
Match length
                   183
% identity
NCBI Description
                  Complete sequence of Arabidopsis F22013, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   28434
```

174384 1.R1040

```
5'-most EST
                   kl1701212438.h1
Method
                   BLASTX
NCBI GI
                   g3075397
BLAST score
                   169
                   1.0e-11
E value
Match length
                   133
% identity
                   (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28435
                   174390 1.R1040
Contig ID
5'-most EST
                   hrw701063062.h1
                   28436
Seq. No.
Contig ID
                   174403 1.R1040
5'-most EST
                   xpa700793202.hl
Seq. No.
                   28437
Contig ID
                   174423 1.R1040
                   xpa700793236.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2511715
BLAST score
                   682
E value
                   6.0e-72
Match length
                   175
% identity
                   (AF019380) putative phosphatidylinositol-4-phosphate
NCBI Description
                   5-kinase [Arabidopsis thaliana]
Seq. No.
                   28438
Contig ID
                   174436 1.R1040
5'-most EST
                   xpa700793265.h1
                   28439
Seq. No.
Contig ID
                   174452 1.R1040
5'-most EST
                   xpa700793295.h1
Method
                   BLASTX
NCBI GI
                   q4097522
BLAST score
                   317
E value
                   5.0e-29
Match length
                   131
% identity
NCBI Description
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                   ananassal
                   28440
Seq. No.
                   174452 2.R1040
Contig ID
5'-most EST
                   jC-qmf102220091a11a1
Method
                   BLASTX
NCBI GI
                   q4097522
BLAST score
                   204
E value
                   5.0e-16
Match length
                   68
% identity
NCBI Description
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
```

ananassal

5'-most EST

```
28441
Seq. No.
                  174467 1.R1040 -
Contig ID
5'-most EST
                  jC-gmst02400011f04a1
Seq. No.
                  28442
                  174470 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810086a06a1
Method
                  BLASTX
NCBI GI
                  q2598573
BLAST score
                  161
E value
                  8.0e-11
Match length
                  89
% identity
NCBI Description (Y15292) MtN26 [Medicago truncatula]
Seq. No.
Contig ID
                  174474 1.R1040
5'-most EST
                  leu701148768.hl
Seq. No.
                  28444
Contig ID
                  174490 1.R1040
5'-most EST
                  xpa700794557.hl
                  28445
Seq. No.
Contig ID
                  174499 1.R1040
5'-most EST
                  uC-gmropic019g08b1
                  28446
Seq. No.
                  174501_1.R1040
Contig ID
5'-most EST
                  jC-gmle01810087a06a1
Method
                  BLASTX
NCBI GI
                  q2208988
BLAST score
                  392
E value
                  6.0e-38
Match length
                  91
% identity
NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]
                  28447
Seq. No.
Contig ID
                  174582 1.R1040
5'-most EST
                  xpa700793537.h1
Seq. No.
                  28448
Contig ID
                  174593 1.R1040
5'-most EST
                  xpa700793551.h1
                  28449
Seq. No.
Contig ID
                  174641 1.R1040
5'-most EST
                  xpa700793647.h1
                  28450
Seq. No.
                  174654 1.R1040
Contig ID
5'-most EST
                  pmv700892326.hl
Seq. No.
                  28451
                  174654 2.R1040
Contig ID
```

.:.

uC-gmflminsoy062e06b1

Contig ID

```
28452
Seq. No.
                  174688 1.R1040
Contig ID
5'-most EST
                  xpa700793734.h1
                  BLASTX
Method
                  q3869278
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
Match length
                  89
% identity
                  52
NCBI Description (AF058285) nicotinamidase/pyrazinamidase [Mycobacterium
                  28453
Seq. No.
Contig ID
                  174723 1.R1040
5'-most EST
                  kl1701205451.h1
Seq. No.
                  28454
                  174758 1.R1040
Contig ID
5'-most EST
                  q4313318
Method
                  BLASTX
NCBI GI
                  q2443329
BLAST score
                  580
E value
                  8.0e-60
Match length
                  221
% identity
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.
                  28455 -
Contig ID
                  174771 1.R1040
5'-most EST
                  asn701136955.hl
Seq. No.
                  28456
Contig ID
                  174786 1.R1040
5'-most EST
                  xpa700793966.hl
Method
                  BLASTX
NCBI GI
                  g1724100
BLAST score
                  175
E value
                  6.0e-13
Match length
                  76
% identity
NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
Seq. No.
Contig ID
                  174845 1.R1040
5'-most EST
                  dpv701097293.hl
Seq. No.
                  28458
Contig ID
                  174873 1.R1040
5'-most EST
                  xpa700794112.h1
Seq. No.
                  28459
Contig ID
                  174896 1.R1040
5'-most EST
                  xpa700794163.h1
Seq. No.
                  28460
```

174913 1.R1040

```
. 5'-most EST
                   xpa700794190.hl
 Method
                 BLASTX
                   g3288817
 NCBI GI
 BLAST score
                   142
                   9.0e-09
 E value
 Match length
                   82
 % identity
                   35
 NCBI Description
                   (AF058922) GLE1 [Homo sapiens]
                   >gi 4557627 ref NP 001490.1 pGLE1L GLE1-like, RNA export
                   28461
 Seq. No.
                   174932 1.R1040
 Contig ID
 5'-most EST
                   xpa700794222.h1
 Method
                   BLASTX
                   g4454468
 NCBI GI
 BLAST score
                   279
                   4.0e-25
 E value
 Match length
                   84
 % identity
                   58
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
 NCBI Description
                   thaliana]
                   28462
 Seq. No.
                   174937 1.R1040
 Contig ID
 5'-most EST
                   xpa700794227.hl
Method
                   BLASTX
 NCBI GI
                   g3885339
 BLAST score
                   157
                   1.0e-10
 E value
 Match length
                   44
 % identity
 NCBI Description (AC005623) putative bzip protein [Arabidopsis thaliana]
                   28463
 Seq. No.
                   174964 1.R1040
 Contig ID
 5'-most EST
                   jC-gmle01810085e08a1
 Method
                   BLASTX
 NCBI GI
                   g4432867
 BLAST score
                   166
 E value
                   2.0e-11
 Match length
                   41
 % identity
 NCBI Description
                   (AC006300) putative dnaJ-like protein [Arabidopsis
                   thaliana]
 Seq. No.
                   28464
 Contig ID
                   174981 1.R1040
 5'-most EST
                   zhf700962440.h1
 Seq. No.
                   28465
                                                                 -
 Contig ID
                   174993 1.R1040
 5'-most EST
                   crh700850729.h1
 Seq. No.
                   28466
                   174998 1.R1040
 Contig ID
```

xpa700794641.h1

5'-most EST

```
Seq. No.
                   28467
Contig ID
                   175057 1.R1040
5'-most EST
                   xpa700794496.hl
Seq. No.
                   28468
                   175077 1.R1040
Contig ID
5'-most EST
                   dpv701099318.h1
Method
                   BLASTX
NCBI GI
                   g2130024 -
BLAST score
                   332
                   5.0e-31
E value
Match length
                   111
% identity
                   58
NCBI Description
                   DNA-binding protein ABF2 - wild oat
                   >gi 1159879 emb CAA88331 (Z48431) DNA-binding protein
                   [Avena fatua]
                   28469
Seq. No.
                   175084 1.R1040
Contig ID
5'-most EST
                  bth700847836.h1
Seq. No.
                   28470
                   175086 1.R1040
Contig ID
5'-most EST
                  xpa700794548.h1
Seq. No.
                   28471
Contig ID
                  175093 1.R1040
5'-most EST
                  crh700854472.h1
Seq. No.
                   28472
Contig ID
                   175100 1.R1040
5'-most EST
                  dpv701103314.h1
Seq. No.
                  28473
                  175108 1.R1040
Contig ID
5'-most EST
                  hrw701059917.hl
Method
                  BLASTX
NCBI GI
                  g2134385
BLAST score
                   638
E value
                   1.0e-66
Match length
                  170
% identity
                   69
                  protein kinase - chicken >gi 571460 (U16656) protein kinase
NCBI Description
                   [Gallus gallus]
Seq. No.
                  28474
Contig ID
                  175127 1.R1040
5'-most EST
                  xpa700794634.h1
Method
                  BLASTX
NCBI GI
                  g2570342
BLAST score
                  355
E value
                  4.0e-34
Match length
                  91
% identity
NCBI Description
                   (U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis
```

thaliana]

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28475
Seq. No.
                   175129 1.R1040
Contig ID
5'-most EST
                   uC-gmropic098a10b1
                   28476
Seq. No.
                   175140 1.R1040
Contig ID
                   fde700873132.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3068717
BLAST score
                   424
                   5.0e-42
E value
                   98
Match length
                   79
% identity
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   28477
Contig ID
                   175147 1.R1040
5'-most EST
                   jC-qmst02400030h07a1
Method
                   BLASTX
NCBI GI
                   q1669591
BLAST score
                   520
E value
                   1.0e-52
Match length
                   155
                   63
% identity
NCBI Description
                   (D88742) O-methyltransferase [Glycyrrhiza echinata]
Seq. No.
Contig ID
                   175151 1.R1040
5'-most EST
                   zzp700831230.h1
                   28479
Seq. No.
Contig ID
                   175199 1.R1040
5'-most EST
                   xpa700794766.h1
Method
                   BLASTX
NCBI GI
                   g1388078
BLAST score
                   191
E value
                   9.0e-15
Match length
                   62
% identity
NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]
Seq. No.
                   28480
Contig ID
                   175230 1.R1040
5'-most EST
                   xpa700794824.hl
                   BLASTX
Method
NCBI GI
                   q2961348
BLAST score
                   271
E value
                   3.0e-24
Match length
                   83
% identity
                   (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
```

175270 1.R1040

xpa700795083.hl

5'-most EST

NCBI Description

```
1.
      Seq. No.
                         28482
      Contig ID
                         175271 1.R1040
      5'-most EST
                        xpa700794883.h1
                         28483
      Seq. No.
      Contig ID
                         175334 1.R1040
      5'-most EST
                        uC-gmrominsoy110a04b1
      Seq. No.
                         28484
                         175389 1.R1040
      Contig ID
      5'-most EST
                         jC-gmle01810087e06d1
                        28485
      Seq. No.
      Contig ID
                         175390 1.R1040
      5'-most EST
                        xpa700795801.h1
      Method
                         BLASTX
                         q3047116
      NCBI GI
      BLAST score
                         453
      E value
                         2.0e-45
      Match length
                         93
      % identity
                         (AF058919) No definition line found [Arabidopsis thaliana]
      NCBI Description
                         28486
      Seq. No.
                         175444 1.R1040
      Contig ID
                        bth700845016.h1
      5'-most EST
      Seq. No.
                         28487
                         175465 1.R1040
      Contig ID
      5'-most EST
                        jC-qmf102220127d05d1
      Seq. No.
                         28488
                        175465 2.R1040
      Contig ID
      5'-most EST
                        xpa700795266.h1
                         28489
      Seq. No.
      Contig ID
                        175483 1.R1040
      5'-most EST
                        uC-gmflminsoy049d09b1
      Method
                        BLASTX
                        g2443880
      NCBI GI
      BLAST score
                        159
                         1.0e-10
      E value
      Match length
                         44
      % identity
                        (AC002294) Hypothetical protein [Arabidopsis thaliana]
      NCBI Description
      Seq. No.
                        28490
      Contig ID
                        175509 1.R1040
                        r1r700898432.h1
      5'-most EST
     Method
                        BLASTX
     NCBI GI
                        g4432839
     BLAST score
                        357
      E value
                        5.0e - 34
     Match length
                        130
      % identity
```

(AC006283) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   28491
                   175586 1.R1040
Contig ID
5'-most EST
                   uC-gmropic099e01b1
Method
                   BLASTN
NCBI GI
                   q347452
BLAST score
                   60
E value
                   6.0e-25
Match length
                   300
% identity
NCBI Description
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,
                   partial cds
                   28492
Seq. No.
Contig ID
                   175687 1.R1040
5'-most EST
                   xpa700795752.h1
Seq. No.
                   28493
Contig ID
                   175690 1.R1040
5'-most EST
                   zsg701\overline{1}20031.h1
                   28494
Seq. No.
Contig ID
                   175711 1.R1040
5'-most EST
                   jC-qmf\overline{1}02220104q12d1
Method
                   BLASTX
NCBI GI
                   q393707
BLAST score
                   205
E value
                   3.0e-16
Match length
                   42
% identity
NCBI Description
                   (X67696) acetyl-CoA acyltransferase [Cucumis sativus]
Seq. No.
                   28495
Contig ID
                   175757 1.R1040
5'-most EST
                   xpa700795893.h1
Seq. No.
                   28496
                   175763 1.R1040
Contig ID
5'-most EST
                   xpa700795943.h1
Method
                   BLASTX
NCBI GI
                   g3688173
BLAST score
                   409
E value
                   4.0e-40
Match length
                   123
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   28497
                   175764 1.R1040
Contig ID
                   k11701\overline{2}05492.h1
5'-most EST
Seq. No.
                   28498
                   175779 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400028d08a1
Seq. No.
                   28499
                   175805 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir073g02b1
```

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```
Seq. No.
                   28500
Contig ID
                   175813 1.R1040
5'-most EST
                   xpa700796037.h1
Method
                   BLASTX
                   g3850584
NCBI GI
BLAST score
                   278
E value
                   7.0e-25
Match length
                   79
                   71
% identity
                   (AC005278) ESTs gb H37641 and gb_AA651422 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   28501
Seq. No.
                   175818 1.R1040
Contig ID
5'-most EST
                   bth700843582.h1
                   28502
Seq. No.
                   175830 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy145g03b1
                   28503
Seq. No.
                   175881 1.R1040
Contig ID
                   rca701\overline{0}02319.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4249384
BLAST score
                   330
E value
                   1.0e-30
Match length
                   124
% identity
                   (AC005966) Similar to gi_4056506 F3G5.25 nodulin-like
NCBI Description
                   protein from Arabidopsis thaliana BAC gb_AC005896.
                   [Arabidopsis thaliana]
                   28504
Seq. No.
                   175896 1.R1040
Contig ID
                   xpa700796213.h1
5'-most EST
Seq. No.
                   28505
                   175903 1.R1040
Contig ID
5'-most EST
                   epx701104094.h1
                   BLASTN
Method
NCBI GI
                   g1628472
BLAST score
                   190
E value
                   1.0e-103
Match length
                   258
                   93
% identity
                  Soybean mosiac virus mRNA for NIb and coat protein
NCBI Description
                   28506
Seq. No.
                   175907 1.R1040
Contig ID
5'-most EST
                   uC-gmropic021c01b1
                   28507
Seq. No.
                   175907 2.R1040
Contig ID
```

bth700847615.hl

5'-most EST

5'-most EST

```
Seq. No.
                   28508
Contig ID
                   175924_1.R1040
5'-most EST
                   uC-gmropic031f10b1
                   28509
Seq. No.
Contig ID
                   175942 1.R1040
5'-most EST
                   xpa700796325.h1
Method
                   BLASTX
NCBI GI
                   g4467148
                   237
BLAST score
E value
                   5.0e-20
Match length
                   112
% identity
                   53
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28510
                   175947 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy059f11b1
Method
                   BLASTX
NCBI GI
                   q3319682
BLAST score
                   625
E value
                   2.0e-65
Match length
                   147
% identity
                   23
NCBI Description (Y17720) SPINDLY protein [Petunia x hybrida]
Seq. No.
                   28511
Contig ID
                   175951 1.R1040
5'-most EST
                   sat701\overline{0}08991.h1
Method
                   BLASTN
NCBI GI
                   g2246441
BLAST score
                   97
                   2.0e-47
E value
Match length
                   221
% identity
NCBI Description
                  Pisum sativum farnesyltransferase alpha subunit mRNA,
                   complete cds
                   28512
Seq. No.
Contig ID
                   175974 1.R1040
5'-most EST
                   xpa700796432.h1
Method
                   BLASTX
NCBI GI
                   g3063445
BLAST score
                   308
                   5.0e-28
E value
Match length
                   174
% identity
NCBI Description
                  (AC003981) F22013.7 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   175980 1.R1040
5'-most EST
                  uC-gmflminsoy031g08b1
Seq. No.
                   28514
Contig ID
                   175983 1.R1040
```

xpa700796455.h1

Method

BLASTX

```
28515
Seq. No.
                  175989 1.R1040
Contig ID
5'-most EST
                  xpa700796471.hl
Method
                  BLASTX
NCBI GI
                  q2288887
BLAST score
                  257
                  1.0e-22
E value
Match length
                  74
% identity
NCBI Description
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                  thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                  [Arabidopsis thaliana]
Seq. No.
                  28516
Contig ID
                  176000 1.R1040
5'-most EST
                  xpa700796504.h1
                  28517
Seq. No.
Contig ID
                  176040 1.R1040
5'-most EST
                  xpa700796593.hl
Method
                  BLASTX
NCBI GI
                  q1928886
                  233
BLAST score
E value
                  1.0e-19
Match length
                  76
% identity
                  58
NCBI Description (U92010) lin-10 protein homolog [Rattus norvegicus]
Seq. No.
                  28518
                  176060 1.R1040
Contig ID
5'-most EST
                  xpa700796633.h1
                  28519
Seq. No.
Contig ID
                  176085 1.R1040
5'-most EST
                  jC-gmle01810018a06a2
Seq. No.
                  28520
Contig ID
                  176100 1.R1040
5'-most EST
                  uC-gmronoir006d12b1
Method
                  BLASTX
NCBI GI
                  g1498731
BLAST score
                  527
E value
                  2.0e-53
Match length
                  155
% identity
NCBI Description (U64806) pathogenesis-related protein PR1 [Brassica napus]
Seq. No.
                  176115 1.R1040
Contig ID
5'-most EST
                  gsv701047079.h1
                  28522
Seq. No.
                  176127 1.R1040
Contig ID
                  g5677573
5'-most EST
```



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NCBI GI
                   q3242708
BLAST score
                   404
E value
                   3.0e-39
Match length
                   196
% identity
NCBI Description
                   (AC003040) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   28523
Seq. No.
Contig ID
                   176133 1.R1040
5'-most EST
                   xpa700797096.hl
Method
                   BLASTX
NCBI GI
                   g3822223
BLAST score
                   543
E value
                   1.0e-55
Match length
                   141
% identity
                   69
NCBI Description
                   (AF077955) branched-chain alpha keto-acid dehydrogenase El
                   alpha subunit [Arabidopsis thaliana]
                   28524
Seq. No.
Contig ID
                   176158 1.R1040
                   xpa700\overline{7}96894.h1
5'-most EST
Seq. No.
                   28525
                   176166 1.R1040
Contig ID
5'-most EST
                   g4306800
Method
                   BLASTX
NCBI GI
                   g3258575
BLAST score
                   672
                   2.0e-70
E value
Match length
                   279
% identity
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28526
                   176215 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy165g09b1
Seq. No.
                   28527
                   176231 1.R1040
Contig ID
5'-most EST
                   xpa700797085.h1
Method
                   BLASTX
                   g4006896
NCBI GI
BLAST score
                   178
E value
                   8.0e-13
Match length
                   131
% identity
                   37
NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]
Seq. No.
                   28528
```

176287 1.R1040 Contig ID 5'-most EST $zsg701\overline{1}17806.h2$

Method BLASTX NCBI GI q434759 BLAST score 1130 1.0e-124 E value

BLAST score

158

```
266
Match length
% identity
                   78
                   (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                   [Homo sapiens]
Seq. No.
                   28529
                   176298 1.R1040
Contig ID
5'-most EST
                   xpa700797257.h1
                   BLASTX
Method
NCBI GI
                   g2104536
BLAST score
                   464
                   1.0e-46
E value
                   124
Match length
% identity
                   65
                   (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   28530
Seq. No.
Contig ID
                   176299 1.R1040
                   zzp700834854.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2789660
BLAST score
                   337
                   6.0e-40
E value
Match length
                   107
                   79
% identity
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
                   28531
Seq. No.
                   176380 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy002a07b1
                   28532
Seq. No.
                   176408 1.R1040
Contig ID
                   fua701037928.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4158219
BLAST score
                   687
E value
                   3.0e-98
                   271
Match length
% identity
                   65
NCBI Description (Y18623) amylogenin [Oryza sativa]
                   28533
Seq. No.
                   176427 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}14313.h1
                   28534
Seq. No.
                   176432 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}50659.h1
                   28535
Seq. No.
                   176512 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy027a11b1
Method
                   BLASTX
NCBI GI
                   g2346966
```

```
E value
                  2.0e-10
Match length
                   47
% identity
                   (AB004871) CPC [Arabidopsis thaliana]
NCBI Description
                  >gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
                  DNA binding protein CPC [Arabidopsis thaliana]
Seq. No.
                  28536
                  176528 1.R1040
Contig ID
                  jC-gmst02400004c12d1
5'-most EST
                  28537
Seq. No.
Contig ID
                  176570 1.R1040
                  xpa700797851.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3033391
BLAST score
                  284
                  7.0e-26
E value
                  78
Match length
                  72
% identity
                   (AC004238) putative amino acid transporter [Arabidopsis
NCBI Description
                  thaliana]
                  28538
Seq. No.
                  176584 1.R1040
Contig ID
5'-most EST
                  dpv701097015.hl
                  BLASTX
Method
NCBI GI
                  g3941524
                  Ž99
BLAST score
                  2.0e-27
E value
Match length
                  68
% identity
                  76
                   (AF062916) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  28539
Seq. No.
Contig ID
                  176611 1.R1040
5'-most EST
                  xpa700797933.h1
                  28540
Seq. No.
                  176614_1.R1040
Contig ID
5'-most EST
                  xpa700797938.hl
                  BLASTX
Method
NCBI GI
                  g2894600
BLAST score
                  162
E value
                  3.0e-11
Match length
                  81
% identity
NCBI Description (ALO21889) putative protein [Arabidopsis thaliana]
                  28541
Seq. No.
                  176739 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir062h08b1
Seq. No.
                  28542
                  176784 1.R1040
Contig -ID
```

xpa700798275.h1

5'-most EST

28543 Seq. No. Contig ID 176809 1.R1040 5'-most EST uC-gmflminsoy109g06b1 Seq. No. 28544 Contig ID 176813 1.R1040 5'-most EST rca700995923.hl Method BLASTX NCBI GI q3549665 BLAST score 522 E value 2.0e-53 Match length 122 % identity NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana] Seq. No. 28545 Contig ID 176834 1.R1040 5'-most EST rca700995956.hl Seq. No. 28546 176835 1.R1040 Contig ID 5'-most EST zhf700960168.hl Method BLASTX NCBI GI g2088650 BLAST score 238 E value 5.0e-20 Match length 78 % identity NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana] Seq. No. 28547 176845 1.R1040 Contig ID 5'-most EST $rca700\overline{9}95973.h1$ Seq. No. 28548 Contig ID 176861 1.R1040 5'-most EST $rca700\overline{9}98463.h1$ Method **BLASTX** NCBI GI g4206195 BLAST score 539 E value 2.0e-55 Match length 118 % identity 83 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana] Seq. No. 28549 176867 1.R1040 Contig ID

5'-most EST rca700996004.h1
Method BLASTX

NCBI GI g3402705
BLAST score 362
E value 2.0e-34
Match length 118

5'-most EST

```
% identity
NCBI Description
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
                   28550
Seq. No.
Contig ID
                   176869 1.R1040
5'-most EST
                   gsv701\overline{0}45327.h1
Method
                  BLASTX
NCBI GI
                  g3582340
BLAST score
                   240
                   3.0e-20
E value
Match length
                  81
% identity
                   60
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  28551
Seq. No.
                  176879 1.R1040
Contig ID
5'-most EST
                  rca700996463.hl
                  BLASTX
Method
NCBI GI
                  g4530327
BLAST score
                   418
                   2.0e-41
E value
Match length
                   95
% identity
                  84
NCBI Description
                   (AF110494) mitochondrial precursor protein import receptor
                  tom70 [Neurospora crassa]
                  28552
Seq. No.
                  176892 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy043g04b1
Method
                  BLASTX
                  g4335735
NCBI GI
BLAST score
                  435
E value
                   7.0e-60
Match length
                  228
% identity
                  58
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  28553
                  176913 1.R1040
Contig ID
5'-most EST
                  rca700996067.hl
Method
                  BLASTX
NCBI GI
                  g2760832
                  322
BLAST score
E value
                  8.0e-30
Match length
                  118
% identity
                  59
NCBI Description
                   (AC003105) similar to barley ids-4 gene product
                   [Arabidopsis thaliana]
                  28554
Seq. No.
                  176953 1.R1040
Contig ID
                  k11701204366.h2
5'-most EST
                  28555
Seq. No.
                  176960 1.R1040
Contig ID
```

zzp700830482.h1

28563

```
Seq. No.
                   28556
                   176974 1.R1040
Contig 'ID
                   rca700996145.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2226378
BLAST score
                   168
E value
                   4.0e-12
Match length
                   58
% identity
                  (AF006493) ACBP/ECHM [Cyprinus carpio]
NCBI Description
                   28557
Seq. No.
                   176977 1.R1040
Contig ID
                   rca700996150.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2827649
BLAST score
                   217
                   1.0e-17
E value
Match length
                   74
% identity
                   58
NCBI Description (AL021637) putative protein [Arabidopsis thaliana]
                   28558
Seq. No.
                   176988 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}06126.h1
                   28559
Seq. No.
Contig ID
                   177021 1.R1040
5'-most EST
                   rca700996209.hl
                   28560
Seq. No.
                   177071_1.R1040
Contig ID
5'-most EST
                   zsq701129370.hl
Method
                   BLASTX
NCBI GI
                   g543063
BLAST score
                   197
E value
                   2.0e-15
Match length
                   88
% identity
                   44
NCBI Description
                  zinc-finger protein, BR140 - human
Seq. No.
                   28561
                   177074 1.R1040
Contig ID
5'-most EST
                  rca700\overline{9}96279.h1
Method
                   BLASTX
NCBI GI
                   g1208497
BLAST score
                   150
E value
                   1.0e-09
                   132
Match length
% identity
                   36
NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]
Seq. No.
                   28562
                   177093 1.R1040
Contig ID
5'-most EST
                  rca700996307.hl
```

```
Contig ID
                   177100 1.R1040
5'-most EST
                   rca700\overline{9}96315.h1
                   28564
Seq. No.
Contig ID
                   177114 1.R1040
5'-most EST
                   rca700996332.hl
Method
                   BLASTX
                   g4580521
NCBI GI
BLAST score
                   309.
E value
                   6.0e-28
Match length
                   100
% identity
                   65
                   (AF036304) scarecrow-like 7 [Arabidopsis thaliana]
NCBI Description
                   28565
Seq. No.
                   177120 1.R1040
Contig ID
5'-most EST
                   rca700996340.hl
                   BLASTX
Method
NCBI GI
                   g2244865
BLAST score
                   562
                   3.0e-59
E value
                   199
Match length
                   63
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28566
Seq. No.
                   177128 1.R1040
Contig ID
5'-most EST
                   rca700996355.hl
Method
                   BLASTX
NCBI GI
                   g4510421
BLAST score
                   569
                   2.0e-58
E value
                   314
Match length
% identity
                   46
                  (AC006929) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28567
Seq. No.
                   177146 1.R1040
Contig ID
                   leu701\overline{1}56337.h1
5'-most EST
Seq. No.
                   28568
                   177150 1.R1040
Contig ID
5'-most EST
                   rca700996388.hl
Seq. No.
                   28569
Contig ID
                   177170 1.R1040
5'-most EST
                   uC-gmrominsoy061d12b1
Method
                   BLASTX
                   g4557060
NCBI GI
BLAST score
                   471
                   3.0e-47
E value
Match length
                   182
                   53
% identity
                   (AC007154) putative chromosome-associated polypeptide, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
```

28575

```
Contig ID
                  177201 1.R1040
5'-most EST
                  uC-gmronoir048b12b1
Method
                  BLASTX
NCBI GI
                  g2829888
BLAST score
                   418
                   5.0e-41
E value
Match length
                  162
% identity
                   56
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                  28571
Seq. No.
                  177221 1.R1040
Contig ID
                  rca700996515.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1363051
BLAST score
                  210
E value
                  5.0e-17
Match length
                  85
% identity
                  47
                  P58 protein - bovine >gi_468012 (U04631) PKR inhibitor P58
NCBI Description
                  [Bos taurus]
Seq. No.
                  28572
                  177227 1.R1040
Contig ID
                  fua701042066.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3334665
BLAST score
                  355
E value
                  5.0e-38
Match length
                  143
                  58
% identity
NCBI Description (Y10492) putative cytochrome P450 [Glycine max]
                  28573
Seq. No.
                  177295 1.R1040
Contig ID
5'-most EST
                  uC-gmropic062f09b1
Method
                  BLASTX
NCBI GI
                  g3831457
BLAST score
                  548
E value
                  6.0e-56
                  201
Match length
                  52
% identity
                   (AC005700) putative ion channel protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  28574
                  177309 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910074f01a1
Method
                  BLASTX
NCBI GI
                  g3341680
BLAST score
                  231
E value
                  6.0e-19
Match length
                  144
                  39
% identity
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
```

% identity

47

```
177315 1.R1040
Contig ID
5'-most EST
                   g43964\overline{1}9
                   BLASTX
Method
                   g2352084
NCBI GI
BLAST score
                   300
                   4.0e-27
E value
Match length
                   72
% identity
                   82
                  (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
                   28576
Seq. No.
                   177323 1.R1040
Contig ID
                   crh700850145.h1
5'-most EST
                   BLASTX
Method
                   g3402684
NCBI GI
BLAST score
                   241
                   9.0e-21
E value
Match length
                   65
% identity
                   69
NCBI Description
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   177327 1.R1040
Contig ID
5'-most EST
                   leu701149343.h1
                   28578
Seq. No.
                   177328 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910056d05a1
Seq. No.
                   28579
                   177339 1.R1040
Contig ID
                   rca701\overline{0}02590.h1
5'-most EST
Seq. No.
                   28580
Contig ID
                   177341 1.R1040
5'-most EST
                   q4397491
Method
                   BLASTX
NCBI GI
                   g2245100
BLAST score
                   189
E value
                   5.0e-14
Match length
                   152
% identity
                   39
NCBI Description (Z97343) DNA-binding protein homolog [Arabidopsis thaliana]
Seq. No.
                   28581
Contig ID
                   177354 1.R1040
5'-most EST
                   zhf700960441.h1
                   28582
Seq. No.
                   177381 1.R1040
Contig ID
5'-most EST
                   q5509673
Method
                   BLASTX
NCBI GI
                   q2829865
BLAST score
                   158
E value
                   2.0e-10
                   79
Match length
```

Contig ID

5'-most EST

```
NCBI Description
                   (AC002396) N-terminal region similar to DNA-J proteins
                   [Arabidopsis thaliana]
                   28583
Seq. No.
                   177399 1.R1040
Contig ID
5'-most EST
                   rca700\overline{9}96938.h1
Seq. No.
                   28584
                   177434 1.R1040
Contig ID
                   rca700996985.hl
                                                                  4.1
5'-most EST
                   28585
Seq. No.
                   177482 2.R1040
Contig ID
5'-most EST
                   pxt700944584.hl
Method
                   BLASTX
NCBI GI
                   g3176715
BLAST score
                   319
                   7.0e-30
E value
Match length
                   81
                   77
% identity
                   (AC002392) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   28586
Seq. No.
                   177500 1.R1040
Contig ID
5'-most EST
                   rca701002187.hl
Seq. No.
                   28587
                   177509 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}11222.h1
Method
                   BLASTX
NCBI GI
                   q4006868
BLAST score
                   135
E value
                   6.0e-11
Match length
                   104
% identity
                   39
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   28588
                   177510 1.R1040
Contig ID
5'-most EST
                   zhf700958041.h1
Method
                   BLASTN
NCBI GI
                   g1853969
BLAST score
                   303
E value
                   1.0e-169
Match length
                   774
% identity
                   86
NCBI Description Vigna unguiculata mRNA for CPRD46 protein, complete cds
Seq. No.
                   177557 1.R1040
Contig ID
5'-most EST
                   leu701155389.hl
                   28590
Seq. No.
```

177565 1.R1040

rca700998043.hl

5'-most EST

```
28591
Seq. No.
                   177566 1.R1040
Contig ID
                   rca700997214.h1
5'-most EST
                   28592
Seq. No.
                   177570 1.R1040
Contig ID
5'-most EST
                   g5606878
Method
                   BLASTX
NCBI GI
                   g4468817
BLAST score
                   241
E value
                   2.0e-20
Match length
                   115
% identity
                   45
NCBI Description
                   (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   177592 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810093c05a1
Seq. No.
                   28594
                   177598 1.R1040
Contig ID
5'-most EST
                   rca700\overline{9}97269.h1
Method
                   BLASTX
NCBI GI
                   g1929056
BLAST score
                   219
E value
                   3.0e-18
Match length
                   75
                   59
% identity
NCBI Description
                   (Y12090) putative 3,4-dihydroxy-2-butanone kinase
                   [Lycopersicon esculentum]
                   28595
Seq. No.
                   177607 1.R1040
Contig ID
5'-most EST
                   g56778<del>6</del>5
Seq. No.
                   28596
Contig ID
                   177623 1.R1040
5'-most EST
                   jC-gmro02910038a03a1
Method
                   BLASTX
NCBI GI
                   q4314363
BLAST score
                   376
E value
                   5.0e-36
Match length
                   179
% identity
                   42
NCBI Description
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28597
Contig ID
                   177631 1.R1040
5'-most EST
                   uC-gmropic091e09b1
                   28598
Seq. No.
                   177673 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}06354.h1
Seq. No.
                   28599
Contig ID
                   177684 1.R1040
```

 $rca700\overline{9}97413.h1$

```
Seq. No.
                   28600
                   177693 1.R1040
Contig ID
                   rca700997422.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1669341
BLAST score
                   533
E value
                   3.0e-54
Match length
                   193
% identity
                   53
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
Seq. No.
                   28601
                   177709 1.R1040
Contig ID
                   rca700997439.hl
5'-most EST
                   28602
Seq. No.
                   177728 1.R1040
Contig ID
                   rca700997479.hl
5'-most EST
                   28603
Seq. No.
                   177751 1.R1040
Contig ID
5'-most EST
                   rca701001310.hl
Method
                   BLASTX
NCBI GI
                   q4056502
BLAST score
                   323
E value
                   3.0e-30
Match length
                   97
                   68
% identity
                   (ACO05896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   28604
Seq. No.
                   177757 1.R1040
Contig ID
5'-most EST
                   rca700\overline{9}97518.h1
Seq. No.
                   28605
                   177761 1.R1040
Contig ID
5'-most EST
                   rca700997522.hl
                   BLASTX
Method
NCBI GI
                   q3201627
BLAST score
                   166
E value
                   1.0e-13
Match length
                   80
% identity
                   64
NCBI Description
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.
                   28606
Contig ID
                   177778 1.R1040
5'-most EST
                   rca701\overline{0}02305.h1
Method
                   BLASTX
NCBI GI
                   q3138972
BLAST score
                   351
                   1.0e-33
E value
                   90
Match length
                   73
% identity
```

NCBI Description (AF038505) dihydrolipoylacyltransferase subunit of the

branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No. 28607

Contig ID 177787 1.R1040 5'-most EST rca700997717.h1

Seq. No. 28608

Contig ID 177809_1.R1040 5'-most EST rca700997580.h1

Method BLASTX
NCBI GI g3600039
BLAST score 619
E value 1.0e-64
Match length 160
% identity 69

NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4

protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 28609

Contig ID 177824 1.R1040 5'-most EST gsv701044388.h1

Seq. No. 28610

Contig ID 177883_1.R1040 5'-most EST zhf700964771.h1

Method BLASTX
NCBI GI g3136056
BLAST score 253
E value 2.0e-21
Match length 238

% identity 28
NCBI Description (AL023592) RanBP7/importin-beta/Cse1p superfamily protein

[Schizosaccharomyces pombe]

Seq. No. 28611

Contig ID 177884_1.R1040

5'-most EST g4286329

Seq. No. 28612

Contig ID 177928_1.R1040 5'-most EST dpv701099792.h1

Seq. No. 28613

Contig ID 177938 1.R1040 5'-most EST leu701146354.h1

Seq. No. 28614

Contig ID 177941 1.R1040 5'-most EST fde700876196.h1

Seq. No. 28615

Contig ID 177960 1.R1040

5'-most EST jC-gmfl02220125e08a1

Seq. No. 28616

Contig ID 177986_1.R1040

```
5'-most EST
                   jC-gmle01810088b05a1
                   28617
Seq. No.
                   177995 1.R1040
Contig ID
5'-most EST
                   rca700\overline{9}97975.h1
                   28618
Seq. No.
                   178058 1.R1040
Contig ID
                   rca700997969.hl
5'-most EST
Seq. No.
                   28619
                   178064 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}08039.h1
Method
                   BLASTX
                   g3059095
NCBI GI
BLAST score
                   270
E value
                   9.0e-24
Match length
                   69
% identity
                   81
                   (AJ001091) magnesium chelatase subunit [Glycine max]
NCBI Description
                   28620
Seq. No.
                   178083 1.R1040
Contig ID
5'-most EST
                   gsv701052083.hl
                   28621
Seq. No.
Contig ID
                   178087 1.R1040
5'-most EST
                   rca700998035.hl
Method
                   BLASTX
                   g2935529
NCBI GI
BLAST score
                   139
                   5.0e-09
E value
Match length
                   31
% identity
                   77
                   (AF049069) No definition line found [Pinus radiata]
NCBI Description
                   28622
Seq. No.
                   178113 1.R1040
Contig ID
5'-most EST
                   rca701002365.hl
                   28623
Seq. No.
                   178121 1.R1040
Contig ID
5'-most EST
                   rca700998192.hl
Method
                   BLASTX
NCBI GI
                   g1351643
BLAST score
                   157
                   8.0e-11
E value
Match length
                   78
                   40
% identity
                   HYPOTHETICAL 43.0 KD PROTEIN C8A4.09C IN CHROMOSOME I
NCBI Description
                   >gi 2130450 pir S62525 hypothetical protein SPAC8A4.09c -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi 1052540 emb CAA91519 (Z66569) unknown
                   [Schizosaccharomyces pombe] >gi 4456834 emb CAB37424.1
                   (AL032824) hypothetical protein [Schizosaccharomyces pombe]
```

Seq. No.



```
Contig ID
                   178122 1.R1040
                   rca700998093.hl
5'-most EST
                   28625
Seq. No.
                   178122 2.R1040
Contig ID
                   fde700871420.hl
5'-most EST
                   28626
Seq. No.
                   178150 1.R1040
Contig ID
                   fde700874357.hl
5'-most EST
                   BLASTX
Method
                   g2500139
NCBI GI
                   597
BLAST score
                   4.0e-62
E value
                   154
Match length
% identity
                   71
                   PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
NCBI Description
                   >gi 1653916 dbj BAA18826_ (D90917) peptide chain release
                   factor [Synechocystis sp.]
                   28627
Seq. No.
                   178158 1.R1040
Contig ID
                   rca700\overline{9}98149.h1
5'-most EST
Method
                   BLASTX
                   g4455359
NCBI GI
BLAST score
                   171
                   2.0e-12
E value
Match length
                   96
% identity
                   36
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   28628
Seq. No.
                   178196 1.R1040
Contig ID
5'-most EST
                   uC-qmronoir047c08b1
                   28629
Seq. No.
                   178216 1.R1040
Contig ID
5'-most EST
                   g4283398
                   BLASTX
Method
                   g4006878
NCBI GI
BLAST score
                   255
                   7.0e-22
E value
Match length
                   123
% identity
                   (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   28630
Seq. No.
                   178242 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910072f04a1
Seq. No.
                   28631
                   178248 1.R1040
Contig ID
                   rca700998277.hl
5'-most EST
                   28632
Seq. No.
                   178342 1.R1040
Contig ID
```

fua701037580.h1

5'-most EST

```
Method
                  BLASTX
NCBI GI
                  q2827552
BLAST score
                  202
E value
                   2.0e-28
Match length
                  76
                   75
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                  28633
Seq. No.
                  178365 1.R1040
Contig ID
                   fC-gmse700655491d4
5'-most EST
                  28634
Seq. No.
                  178381 1.R1040
Contig ID
5'-most EST
                  rca700998483.hl
                  28635
Seq. No.
                  178425 1.R1040
Contig ID
                  uC-gmrominsoy139c02b1
5'-most EST
                  28636
Seq. No.
                  178428 1.R1040
Contig ID
                  asn701133668.h2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3850588
                  147
BLAST score
E value
                   4.0e-09
Match length
                  315
                  27
% identity
                   (AC005278) Contains similarity to gb_AB011110 KIAA0538
NCBI Description
                  protein from Homo sapiens brain and to phospholipid-binding
                  domain C2 PF 00168. ESTs gb_AA585988 and gb_T04384 come
                  from this gene. [Arabidopsis thaliana]
                  28637
Seq. No.
                  178465 1.R1040
Contig ID
                   zhf700964765.h1
5'-most EST
                  28638
Seq. No.
                  178470 1.R1040
Contig ID
                  g5677023
5'-most EST
                  28639
Seq. No.
                  178500 1.R1040
Contig ID
                  uC-gmflminsoy022b11b1
5'-most EST
                  28640
Seq. No.
                  178504 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810067g05a1
                  28641
Seq. No.
                  178525 1.R1040
Contig ID
5'-most EST
                   zhf700961951.hl
                  28642
Seq. No.
                  178532 1.R1040.
Contig ID
```

rca700998705.hl

5'-most EST

```
Method
                  BLASTX
                  g4106683
NCBI GI
BLAST score
                  171
                   5.0e-12
E value
Match length
                  111
% identity
                   32
                   (AL035065) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   28643
Seq. No.
                   178540 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220100b01a1
                  28644
Seq. No.
                   178552 1.R1040
Contig ID
                   jC-gmro02910037h10a1
5'-most EST
                  28645
Seq. No.
                  178579 1.R1040
Contig ID
5'-most EST
                   zsg701117701.h2
                  BLASTX
Method
                   g1255448
NCBI GI
BLAST score
                   441
E value
                   1.0e-43
Match length
                   124
% identity
                   69
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   28646
                   178579 2.R1040
Contig ID
                   uC-gmrominsoy117g11b1
5'-most EST
Method
                   BLASTX
                   q1255448
NCBI GI
BLAST score
                   158
                   1.0e-14
E value
Match length
                   83
% identity
                   48
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   28647
                   178592 1.R1040
Contig ID
                   zhf700963061.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   188
E value
                   2.0e-14
Match length
                   66
% identity
                   55
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   28648
Contig ID
                   178613 1.R1040
                   rca700998818.hl
5'-most EST
Seq. No.
                   28649
```

5'-most EST rca700998922.h1 28650 Seq. No. Contig ID 178648 1.R1040 $k11701\overline{2}10150.h1$ 5'-most EST 28651 Seq. No. 178688 1.R1040 Contig ID 5'-most EST rca700998964.hl 28652 Seq. No. 178742 1.R1040 Contig ID 5'-most EST uC-gmrominsoy250f08b1 BLASTN Method g2055227 NCBI GI BLAST score 46 1.0e-16 E value 66 Match length 92 % identity Glycine max mRNA for SRC1, complete cds NCBI Description Seq. No. 28653 178799 1.R1040 Contig ID $rca700\overline{9}99148.h1$ 5'-most EST 28654 Seq. No. Contig ID 178831 1.R1040 5'-most EST fC-gmse700660737g3 28655 Seq. No. 178843 1.R1040 Contig ID rca700999269.hl 5'-most EST 28656 Seq. No. 178862 1.R1040 Contig ID rca700999302.hl 5'-most EST 28657 Seq. No. 178874 1.R1040 Contig ID zhf700952248.h1 5'-most EST 28658 Seq. No. 178932 1.R1040 Contig ID rca700999506.hl 5'-most EST 28659 Seq. No. 178950 1.R1040 Contig ID $jC-gmf\overline{1}02220077g11d1$ 5'-most EST 28660 Seq. No. 178969 1.R1040 Contig ID zhf700962302.h1 5'-most EST 28661 Seq. No. 179028 1.R1040 Contig ID zsq701124449.h1 5'-most EST

BLASTX

Method

Contig ID 5'-most EST

```
NCBI GI
                   q3402684
BLAST score
                   535
E value
                   1.0e-54
Match length
                   138
% identity
                   74
NCBI Description
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   179074 1.R1040
5'-most EST
                   zsg701\overline{1}22609.h1
                   28663
Seq. No.
Contig ID
                   179083 1.R1040
5'-most EST
                   jC-qmle01810085d07d1
Method
                   BLASTX
NCBI GI
                   q3080421
BLAST score
                   177
                   1.0e-12
E value
Match length
                   83
% identity
                   41
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   28664
Seq. No.
Contig ID
                   179117 1.R1040
                   fde700876425.h1
5'-most EST
                   28665
Seq. No.
                   179118 1.R1040
Contig ID
                   rca700\overline{9}99823.h1
5'-most EST
Seq. No.
                   28666
                   179141 1.R1040
Contig ID
                   leu701157279.hl
5'-most EST
Method
                   BLASTX
                   g4056507
NCBI GI
BLAST score
                   229
E value
                   9.0e-19
                   91
Match length
% identity
                   51
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   28667
Seq. No.
                   179143 1.R1040
Contig ID
                   jC-gmr002910062a03d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2673918
BLAST score
                   212
E value
                   7.0e-17
                   57
Match length
                   70
% identity
                   (AC002561) unknwon protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28668
                   179198 1.R1040
```

uC-gmrominsoy219b02b1

BLAST score

416

```
28669
Seq. No.
                   179216 1.R1040
Contig ID
5'-most EST
                   zhf700954425.hl
                   28670
Seq. No.
                   179239 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}00716.h1
                   28671
Seq. No.
                   179265 1.R1040
Contig ID
                   zsg701126938.hl
5'-most EST
                   BLASTX
Method
                   g1276977
NCBI GI
BLAST score
                   660
                   3.0e-69
E value
Match length
                   152
% identity
                   84
                   (U47143) nonsymbiotic hemoglobin [Glycine max]
NCBI Description
                   28672
Seq. No.
                   179274 1.R1040
Contig ID
5'-most EST
                   zhf700958082.h1
                   28673
Seq. No.
                   179300 1.R1040
Contig ID
5'-most EST
                   al1700863273.h1
Method
                   BLASTN
NCBI GI
                   g2253091
BLAST score
                   44
                   1.0e-15
E value
                   104
Match length
                   86
% identity
                   Spinacia oleracea ORF, clone SAM2B4.1T7
NCBI Description
                   28674
Seq. No.
                   179301 1.R1040
Contig ID
5'-most EST
                   g5126612
Method
                   BLASTX
NCBI GI
                   g3096949
BLAST score
                   239
                   2.0e-20
E value
                   98
Match length
                   47
% identity
NCBI Description
                   (Y16328) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   28675
Seq. No.
                   179349 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}00362.h1
Seq. No.
                   28676
                   179357 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}00382.h1
                   BLASTX
Method
                   q3550661
NCBI GI
```

Method

BLASTX

```
1.0e-40
E value
                   101
Match length
% identity
                   44
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
                   tuberosum]
                   28677
Seq. No.
                   179361 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810094h09d1
Method
                   BLASTX
                   g4006861
NCBI GI
BLAST score
                   362
E value
                   2.0e-34
Match length
                   115
% identity
                   57
                   (Z99707) tubulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   179419 1.R1040
Contig ID
                   rca701\overline{0}00472.h1
5'-most EST
                   28679
Seq. No.
                   179420 1.R1040
Contig ID
5'-most EST
                   q5509254
                   28680
Seq. No.
                   179438 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}00509.h1
                   28681
Seq. No.
                   179447 1.R1040
Contig ID
                   fde700\overline{8}73138.h1
5'-most EST
                   28682
Seq. No.
                   179515 1.R1040
Contig ID
5'-most EST
                   rca701000646.h1
Method
                   BLASTX
NCBI GI
                   q1352269
BLAST score
                   179
                   4.0e-13
E value
Match length
                   135
% identity
                   29
                   DIAPHANOUS PROTEIN >qi 575927 (U11288) diaphanous protein
NCBI Description
                   [Drosophila melanogaster]
                   28683
Seq. No.
Contig ID
                   179516 1.R1040
5'-most EST
                   rca701000648.hl
Seq. No.
                   28684
                   179534 1.R1040
Contig ID
5'-most EST
                   rca701002356.h1
Seq. No.
                   28685
                   179563 1.R1040
Contig ID
5'-most EST
                   uC-gmropic110d12b1
```

5'-most EST

```
NCBI GI
                    g2832717
BLAST score
                    672
E value
                    7.0e-71
                    139
Match length
                    89
% identity
                    (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
Seq. No.
                    179589 1.R1040
Contig ID
5'-most EST
                    rca701000848.hl
Seq. No.
                    28687
                    179595 1.R1040
Contig ID
5'-most EST
                    uC-gmropic037b06b1
Seq. No.
                    179606 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}01387.h1
Method
                    BLASTX
NCBI GI
                    q4102839
BLAST score
                    749
                    9.0e-80
E value
Match length
                    172
% identity
                    76
                    (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                    28689
Seq. No.
                    179609 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}00785.h1
Seq. No.
                    28690
                    179610 1.R1040
Contig ID
5'-most EST
                    g5605841
                    28691
Seq. No.
Contig ID
                    179612 1.R1040
5'-most EST
                    hrw701\overline{0}62674.h1
                    28692
Seq. No.
                    179613 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}03330.h1
                    28693
Seq. No.
                    179626 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}04934.h1
Seq. No.
                    28694
                    179632 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}00817.h1
                    28695
Seq. No.
                    179642 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}00831.h1
                    28696
Seq. No.
                    179666 1.R1040
Contig ID
```

rca701000858.hl

```
28697
Seq. No.
                    179728 1.R1040
Contig ID
.5'-most EST
                    rca701\overline{0}00962.h1
                    28698
Seq. No.
                   179734 1.R1040
Contig ID
                   rca701\overline{0}00972.h1
5'-most EST
Method
                   BLASTX
                   g3582333
NCBI GI
BLAST score
                    274
E value
                    4.0e-24
Match length
                   146
                    40
% identity
                    (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28699
Seq. No.
                   179738 1.R1040
Contig ID
5'-most EST
                   uC-gmropic092f12b1
Method
                   BLASTX
NCBI GI
                   g1657621
BLAST score
                   362
                    1.0e-34
E value
                    97
Match length
                    66
% identity
NCBI Description
                    (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                   28700
Seq. No.
                   179742 1.R1040
Contig ID
                   rca701000981.hl
5'-most EST
                   BLASTX
Method
                   g3005576
NCBI GI
                   298
BLAST score
E value
                    6.0e-27
Match length
                   103
                   55
% identity
NCBI Description
                    (AF047718) putative high affinity nitrate transporter;
                   GmNRT2 [Glycine max]
                   28701
Seq. No.
                   179757 1.R1040
Contig ID
5'-most EST
                   rca701001007.hl
Method
                   BLASTX
NCBI GI
                   g3218550
BLAST score
                   147
                   2.0e-09
E value
                   74
Match length
% identity
                   41
                    (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
NCBI Description
                   28702
Seq. No.
                   179769 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}01068.h1
                   28703
Seq. No.
```

```
5'-most EST
                      jC-qmst02400055g12a1
Method
                      BLASTX
NCBI GI
                      g132127
BLAST score
                      155
E value
                      4.0e-10
Match length
                      140
% identity
                      31
                     RIBOKINASE >gi_66667_pir__KIECRB ribokinase (EC 2.7.1.15) - Escherichia coli >gi_2981974_pdb_1RKD__ E. Coli Ribokinase
NCBI Description
                     Complexed With Ribose And Adp >gi_147516 (M13169) ribokinase [Escherichia coli] >gi_290602 (L10328) ribokinase [Escherichia coli] >gi_1790193 (AE000452)
                      ribokinase [Escherichia coli]
Seq. No.
                      28704
                      179805 1.R1040
Contig ID
5'-most EST
                      uC-qmronoir060e06b1
                      BLASTX
Method
NCBI GI
                      q2791896
BLAST score
                      914
                      4.0e-99
E value
Match length
                      186
% identity
                      (Y08997) 146kDa nuclear protein [Xenopus laevis]
NCBI Description
                      28705
Seq. No.
                      179824 1.R1040
Contig ID
5'-most EST
                      rca701\overline{0}01087.h1
                      28706
Seq. No.
Contig ID
                      179858 1.R1040
                      rca701\overline{0}01127.h1
5'-most EST
                      28707
Seq. No.
                      179858 2.R1040
Contig ID
5'-most EST
                      jC-gmle01810022a08d1
                      28708
Seq. No.
                      179876 1.R1040
Contig ID
5'-most EST
                      rca701\overline{0}01211.h1
                      28709
Seq. No.
                      179884 1.R1040
Contig ID
5'-most EST
                      rca701\overline{0}01160.h1
Method
                      BLASTX
NCBI GI
                      q416730
BLAST score
                      876
E value
                      2.0e-94
Match length
                      213
% identity
                      BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE)
NCBI Description
                      (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE)
                      >gi_285064_pir__S27881 beta-alanine synthase - rat
                      >gi 203106 (M97662) beta-alanine synthase [Rattus
                      norvegicus]
```

Seq. No.

Method

BLASTX

```
Contig ID
                    179889 1.R1040
5'-most EST
                    rca701\overline{0}01167.h1
Seq. No.
                    28711
                   179912 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}01195.h1
                   BLASTX
Method
NCBI GI
                   g228403
BLAST score
                    277
È value
                    6.0e-25
Match length
                   83
% identity
                    65
                   glycolate oxidase [Lens culinaris]
NCBI Description
                   28712
Seq. No.
                   179913 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}01675.h1
Method
                   BLASTN
                   g12137
NCBI GI
BLAST score
                   90
E value
                   5.0e-43
Match length
                   196 .
                   89
% identity
                   Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit
NCBI Description
Seq. No.
                   28713
                   179957 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}01268.h1
Method
                   BLASTX
NCBI GI
                   g4098582
BLAST score
                   162
E value
                   4.0e-11
Match length
                   116
                   39
% identity
                   (U79567) RBM1 [Sminthopsis macroura]
NCBI Description
Seq. No.
                   28714
Contig ID
                   179983 1.R1040
5'-most EST
                   rca701001303.hl
                   28715
Seq. No.
Contig ID
                   179999 1.R1040
5'-most EST
                   rca701001322.hl
                   28716
Seq. No.
                   180001 1.R1040
Contig ID
5'-most EST
                   rca701001395.hl
                   28717
Seq. No.
                   180010 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy043b11b1
                   28718
Seq. No.
                   180025 1.R1040
Contig ID
                   rca701\overline{0}01353.h1
5'-most EST
```

```
NCBI GI
                   q2224695
                   171
BLAST score
                   4.0e-12
E value
Match length
                   65
% identity
                   51
                   (AB002375) KIAA0377 [Homo sapiens]
NCBI Description
                   28719
Seq. No.
                   180032 1.R1040
Contig ID
5'-most EST
                   g4396732
                   28720
Seq. No.
                   180037 1.R1040
Contig ID
                   rca701\overline{0}01368.h1
5'-most EST
                   28721
Seq. No.
                   180047 1.R1040
Contig ID
                   rca701001380.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2499570
BLAST score
                   268
                   2.0e-23
E value
                   74
Match length
                   69
% identity
                   PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE
NCBI Description
                   (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN
                   L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN
                   CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941)
                   L-isoaspartyl methyltransferase [Triticum aestivum]
                   28722
Seq. No.
                   180076 1.R1040
Contig ID
                   rca701\overline{0}01423.h1
5'-most EST
                   28723
Seq. No.
                   180082 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910010g02d1
Method
                   BLASTX
                   g4455366
NCBI GI
                   204
BLAST score
                   1.0e-15
E value
Match length
                   52
                   75
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   28724
Seq. No.
                   180111 1.R1040
Contig ID
5'-most EST
                   zhf700958630.h1
                   28725
Seq. No.
                   180162 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}01548.h1
                   BLASTX
Method
                   g2582351
NCBI GI
                   374
BLAST score
E value
                   9.0e-36
```

Match length

```
% identity:
NCBI Description
                   (AF018639) unknown [Dictyostelium discoideum]
                   28726
Seq. No.
                   180165 1.R1040
Contig ID
                   uC-gmflminsoy012h02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4415920
BLAST score
                   325
                   9.0e-30
E value
Match length
                   277
% identity
                   33
NCBI Description
                   (AC006282) putative glucosyl transferase [Arabidopsis
                   thaliana]
                   28727
Seq. No.
                   180180 1.R1040
Contig ID
                   jC-gmf\overline{1}02220108e05a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3819099
BLAST score
                   257
                   4.0e-22
E value
                   142
Match length
                   37
% identity
                   (AJ009825) copper amine oxidase [Cicer arietinum]
NCBI Description
Seq. No.
                   28728
                   180190 1.R1040
Contig ID
                   jC-gmf\overline{1}02220057a10d1
5'-most EST
                   BLASTX
Method
                   g1871187
NCBI GI
BLAST score
                   253
                   1.0e-42
E value
                   130
Match length
                   71
% identity
                   (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28729
                   180202_1.R1040
Contig ID
5'-most EST
                   rca701001603.hl
                   BLASTX
Method
NCBI GI
                   g2244835
BLAST score
                   837
                   5.0e-90
E value
Match length
                   188
                   79
% identity
                   (Z97337) protein kinase homolog [Arabidopsis thaliana]
NCBI Description
                   28730
Seq. No.
                   180216 1.R1040
Contig ID
                   rca701001618.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1407705
BLAST score
                   533
                   2.0e-54
E value
                   140
Match length
```

% identity

```
(U60202) lipoxygenase [Solanum tuberosum]
NCBI Description
                  28731
Seq. No.
                  180229 1.R1040
Contig ID
5'-most EST
                  zhf700954791.hl
                  BLASTX
Method
NCBI GI
                  q2760832
BLAST score
                  138
E value
                  2.0e-15
                  76
Match length
% identity
                  55
                  (AC003105) similar to barley ids-4 gene product
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  28732
                  180248 1.R1040
Contig ID
                  jC-gmle01810024g07a1
5'-most EST
Method
                  BLASTX
                  g730751
NCBI GI
BLAST score
                  200
E value
                  2.0e-15
Match length
                  149
                  36
% identity
                  DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)
NCBI Description
                  >gi_401776 (L14754) DNA-binding protein [Homo sapiens]
                  >gi 4504623 ref_NP_002171.1_pIGHMBP2__ immunoglobulin mu
                  binding protein
                  28733
Seq. No.
                  180284 1.R1040
Contig ID
                  jC-gmle01810024b08a1
5'-most EST
                  28734
Seq. No.
                  180293_1.R1040
Contig ID
                  jC-gmle01810048c05a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2281088
BLAST score
                  416
                  1.0e-40
E value
                  205
Match length
                  43
% identity
                  (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                  [Arabidopsis thaliana]
                  28735
Seq. No.
                  180315 1.R1040
Contig ID
                  uC-gmrominsoy033a05b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4220480
BLAST score
                  501
E value
                  2.0e-50
Match length
                  246
                  45
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  28736
Seq. No.
```

```
5'-most EST
                    jC-gmle01810014e10d1
Seq. No.
                    28737
                    180419 1.R1040
Contig ID
5'-most EST
                    asn701\overline{1}34847.h2
                    28738
Seq. No.
                    180443 1.R1040
Contig ID
5'-most EST
                    r1r700\overline{9}01202.h1
Seq. No.
                    28739
                    180462_1.R1040
Contig ID
                    jC-gmro02910022g06a1
5'-most EST
Method
                    BLASTX
                    g1483230
NCBI GI
BLAST score
                    440
                    2.0e-43
E value
Match length
                    143
% identity
                    64
NCBI Description
                    (X99654) MADS4 protein [Betula pendula]
                    28740
Seq. No.
Contig ID
                    180471_1.R1040
5'-most EST
                    q43966\overline{2}8
Method
                    BLASTX
NCBI GI
                    q4204288
BLAST score
                    470
E value
                    8.0e-47
Match length
                    153
                    58
% identity
                    (AC003027) lcl prt seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                    28741
Seq. No.
                    180480 1.R1040
Contig ID
5'-most EST
                    zhf700\overline{9}64493.h1
Seq. No.
                    28742
                    180504 1.R1040
Contig ID
5'-most EST
                    uC-gmropic047a12b1
                    28743
Seq. No.
                    180511 1.R1040
Contig ID
5'-most EST
                    rca701\overline{0}02449.h1
                    28744
Seq. No.
Contig ID
                    180520 1.R1040
5'-most EST
                    dpv701\overline{0}98607.h1
Seq. No.
                    28745
                    180523 1.R1040
Contig ID
5'-most EST
                    g5126709
                    28746
Seq. No.
Contig ID
                    180523 2.R1040
                    rca701\overline{0}02214.h1
5'-most EST
                    BLASTX
Method
```



```
g4164473
NCBI GI
                   185
BLAST score
                   1.0e-13
E value
                    65
Match length
% identity
                    65
                    (AF061157) negatively light-regulated protein [Vernicia
NCBI Description
                    fordii]
                   28747
Seq. No.
                    180553 1.R1040
Contig ID
                    rca701\overline{0}02275.h1
5'-most EST
                   28748
Seq. No.
                    180576 1.R1040
Contig ID
                    fde700875914.h1
5'-most EST
                    28749
Seq. No.
                    180581 1.R1040
Contig ID
                   jC-gmf102220052d02a1
5'-most EST
                   28750
Seq. No.
                    180584 1.R1040
Contig ID
                    rca701002324.h1
5'-most EST
                    BLASTX
Method
                    g2262111
NCBI GI
                    358
·BLAST score
                    6.0e-34
E value
Match length
                    136
% identity
                    54
                    (ACO02343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                    thaliana]
                    28751
Seq. No.
                    180631 1.R1040
Contig ID
                    fua701040090.h1
5'-most EST
                    28752
Seq. No.
                    180649 1.R1040
Contig ID
5'-most EST
                    uC-gmropic067g02b1
                    BLASTX
Method
NCBI GI
                    q3395432
                    812
BLAST score
                    7.0e-87
E value
Match length
                    220
% identity
                    66
                    (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                    28753
Seq. No.
                    180662 1.R1040
Contig ID
                    rca701\overline{0}02520.h1
5'-most EST
                    28754
Seq. No.
```

Contig ID 180690_1.R1040 5'-most EST rca701002466.h1

Method BLASTX NCBI GI g1076685 BLAST score 210

NCBI GI

```
E value
                   4.0e-17
Match length
                   79
                   62
% identity
                   SPF1 protein - sweet potato >gi_484261_dbj BAA06278
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
                   28755
Seq. No.
                   180691 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810052g02a1
                   BLASTX
Method
                   g4206197
NCBI GI
BLAST score
                   176
E value
                   2.0e-12
Match length
                   227
% identity
                   6
                   (AF071527) putative pre-mRNA splicing factor [Arabidopsis
NCBI Description
                   thaliana]
                   28756
Seq. No.
Contig ID
                   180714 1.R1040
                   g4405586
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3395432
BLAST score
                   509
                   8.0e-52
E value
Match length
                   126
                   82
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28757
Seq. No.
Contig ID
                   180733 1.R1040
5'-most EST
                   leu701146108.hl
                   28758
Seq. No.
                   180733 2.R1040.
Contig ID
5'-most EST
                   kl1701214442.h1
                   28759
Seq. No.
                   180738 1.R1040
Contig ID
5'-most EST
                   rca701\overline{0}02651.h1
Seq. No.
                   28760
                   180745 1.R1040
Contig ID
                   jC-gmle01810086g01d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1220453
BLAST score
                   246
E value
                   8.0e-21
Match length
                   66
% identity
                   (M79328) alpha-amylase [Solanum tuberosum]
NCBI Description
             19
                   28761
Seq. No.
                   180760 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910075h08a1
Method
                   BLASTX
```

q4539525

Method

BLASTX

```
232
BLAST score
                   5.0e-19
E value
Match length
                   165
                   33
% identity
NCBI Description
                   (AJ012370) NAALADase II protein [Homo sapiens]
                   28762
Seq. No.
                   180775 1.R1040
Contig ID
5'-most EST
                   uC-gmropic107h03b1
                   28763
Seq. No.
Contig ID
                   180780 1.R1040
5'-most EST
                   rca701\overline{0}02592.h1
                  BLASTX
Method
                   g4415942
NCBI GI
BLAST score
                   341
                   3.0e-32
E value
                   106
Match length
                   65
% identity
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28764
Seq. No.
                   180784_1.R1040
Contig ID
                   uC-gmropic027g02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2190544
BLAST score
                   299
E value
                   1.0e-48
                   119
Match length
% identity
                   (AC001229) Similar to Saccharomyces hypothetical protein
NCBI Description
                   P9642.2 (gb U40828). [Arabidopsis thaliana]
                   28765
Seq. No.
                   180815 1.R1040
Contig ID
                   rca701002662.hl
5'-most EST
Seq. No.
                   28766
Contig ID
                   180821 1.R1040
5'-most EST
                   jC-qmst02400015b12d1
Method
                   BLASTX
NCBI GI
                   q2833380
BLAST score
                   343
                   2.0e-32
E value
Match length
                   98
% identity
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL
NCBI Description
                   PYROPHOSPHATE SYNTHETASE 2) (PRS II)
                   >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase
                   (EC 2.7.6.1) II - Arabidopsis thaliana (fragment)
                   >gi_1064885_emb_CAA63552_ (X92974) phosphoribosyl
                  pyrophosphate synthetase II [Arabidopsis thaliana]
Seq. No.
                  28767
Contig ID
                  180834 1.R1040
5'-most EST
                   jex700\overline{9}04870.h1
```

NCBI Description

```
g2252840
NCBI GI
                  157
BLAST score
E value
                  8.0e-11
Match length
                  83
                   39
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                  28768
Seq. No.
                   180844 1.R1040
Contig ID
5'-most EST
                   fde700870511.hl
                  28769
Seq. No.
                  180850 1.R1040
Contig ID
5'-most EST
                   fC-qmst700889683f3
Method
                   BLASTX
                   q128195
NCBI GI
BLAST score
                   187
E value
                   1.0e-13
Match length
                   110
% identity
                   38
                  NITRATE REDUCTASE (NR) >gi_66203_pir__RDTONH nitrate
NCBI Description
                   reductase (NADH) (EC 1.6.6.1) - tomato
                   >gi 19283_emb_CAA32218_ (X14060) nitrate reductase
                   [Lycopersicon esculentum]
Seq. No.
                   28770
                   180866 1.R1040
Contig ID
                   fde700870539.h1
5'-most EST
                   28771
Seq. No.
                   180872 1.R1040
Contig ID
                   fde700872774.h1
5'-most EST
                   28772
Seq. No.
                   180886 1.R1040
Contig ID
5'-most EST
                   fde700870562.hl
                   28773
Seq. No.
                   180912 1.R1040
Contig ID
                   fde700870606.h1
5'-most EST
                   28774-
Seq. No.
                   180917 1.R1040
Contig ID
                   fde700870769.h1
5'-most EST
                   28775
Seq. No.
Contig ID
                   180978 1.R1040
                   fde700870695.hl
5'-most EST
Method
                   BLASTX
                   g1800147
NCBI GI
BLAST score
                   277
                   2.0e-24
E value
Match length
                   71
                   76
% identity
```

(U83655) membrane associated protein [Arabidopsis thaliana]

```
28776
Seq. No.
                   180982 1.R1040
Contig ID
5'-most EST
                   fC-qmst700889363h1
Method
                   BLASTX
NCBI GI
                   g1345955
BLAST score
                   723
E value
                   3.0e-76
Match length
                   391
% identity
                   41
NCBI Description
                   GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                   (FALDH) >gi 496118 (L33464) alcohol dehydrogenase 3
                   [Methylobacter marinus]
                   28777
Seq. No.
                   180990 1.R1040
Contig ID
                   fde700870714.h1
5'-most EST
                   BLASTN
Method
                   q416037
NCBI GI
BLAST score
                   120
E value
                   4.0e-61
                   165
Match length
                   16
% identity
NCBI Description O.sativa rubl mRNA for polyubiquitin
                   28778
Seq. No.
                   180994 1.R1040
Contig ID
                   dpv701\overline{1}01807.h1
5'-most EST
                   28779
Seq. No.
                   180996 1.R1040
Contig ID
5'-most EST
                   fde700873111.h1
                   28780
Seq. No.
                   181007 1.R1040
Contig ID
                   jC-gmf102220141d11a1
5'-most EST
Seq. No.
                   28781
                   181044 1.R1040
Contig ID
                   fde700876004.hl
5'-most EST
                   28782
Seq. No.
                   181056 1.R1040
Contig ID
5'-most EST
                   fde700870809.hl
                   28783
Seq. No.
                   181075_1.R1040
Contig ID
5'-most EST
                   fC-gmst700889690a3
Method
                   BLASTX
                   g2388985
NCBI GI
BLAST score
                   272
                   5.0e-24
E value
                   90
Match length
                   57
% identity
                   (Z98980) transcription factor [Schizosaccharomyces pombe]
NCBI Description
                   28784
Seq. No.
```

Match length

217

```
fde700870845.hl
5'-most EST
Seq. No.
                   28785
                   181094 1.R1040
Contig ID
                   fde700875879.h1
5'-most EST
Seq. No.
                   28786
Contig ID
                   181110 1.R1040
5'-most EST
                   fde700870873.h1
Seq. No.
                   28787
                   181117 1.R1040
Contig ID
5'-most EST
                   kl1701205580.h1
Seq. No.
                   28788
                   181117 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir038a08b1
                   28789
Seq. No.
Contig ID
                   181121 1.R1040
5'-most EST
                   fjg700968353.hl
                   28790
Seq. No.
                   181127 1.R1040
Contig ID
                   fde700871025.h1
5'-most EST
                   28791
Seq. No.
                   181144_1.R1040
Contig ID
                   hrw701\overline{0}61362.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2792155
BLAST score
                   562
E value
                   1.0e-57
Match length
                   179
% identity
                   60
NCBI Description
                   (AJ223291) chalcone reductase [Sesbania rostrata]
Seq. No.
                   28792
                   181148 1.R1040
Contig ID
                   fde700\overline{8}70931.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4375833
BLAST score
                   969
E value
                   1.0e-105
Match length
                   318
% identity
NCBI Description
                   (AL021713) receptor serine/threonine kinase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   28793
                   181150 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97108.h1
Method
                   BLASTX
NCBI GI
                   g3142301
BLAST score
                   606
E value
                   7.0e-63
```

```
% identity
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb_M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb_Q05946.
                  ESTs gb N65081 gb Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                  gb_H3630
                  28794
Seq. No.
Contig ID
                  181156 1.R1040
                  fde700870946.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2642448
                  282
BLAST score
                  1.0e-25
E value
Match length
                  79
% identity
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3169187 (AC004401) hypothetical protein [Arabidopsis
                  thaliana]
                  28795
Seq. No.
                  181158_1.R1040
Contig ID
                  uC-gmrominsoy080e12b1
5'-most EST
                  BLASTN
Method
                  g2264321
NCBI GI
BLAST score
                  46
E value
                  1.0e-16
                  94
Match length
                  42
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
                  28796
Seq. No.
                  181204_1.R1040
Contig ID
                  fde700871020.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3550554
BLAST score
                  373
                  3.0e-36
E value
                  84
Match length
                  82
% identity
                   (Y17469) sarco/endoplasmic reticulum Ca2+ -ATPase
NCBI Description
                   [Paramecium tetraurelia]
                  28797
Seq. No.
                  181232 1.R1040
Contig ID
                  uC-gmropic026c02b1
5'-most EST
                  BLASTX
Method
                  g2262105
NCBI GI
BLAST score
                  323
                  7.0e-30
E value
                  96
Match length
                  64
% identity
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                  28798
Seq. No.
```

```
5'-most EST
                   fde700871115.h1
Seq. No.
                   28799
                   181302 1.R1040
Contig ID
                   fde700871158.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832629
BLAST score
                   176
E value
                   1.0e-12
Match length
                   115
% identity
                   37
                   (ALO21711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   28800
                   181320 1.R1040
Contig ID
5'-most EST
                   q56771\overline{3}7
                   BLASTN
Method
NCBI GI
                   q3046710
BLAST score
                   320
                   1.0e-180
E value
Match length
                   468
% identity
                   92
NCBI Description
                   Cicer arietinum mRNA for replication factor C/activator 1
                   subunit, partial
                   28801
Seq. No.
                   181375 1.R1040
Contig ID
                   fde700871370.hl
5'-most EST
                   28802
Seq. No.
                   181378 1.R1040
Contig ID
                   fde700\overline{8}71384.h1
5'-most EST
                   28803
Seq. No.
                   181380 1.R1040
Contig ID
5'-most EST
                   fde700871475.h1
                   28804
Seq. No.
                   181406 1.R1040
Contig ID
                   fde700875863.h1
5'-most EST
                   BLASTX
Method
                   g421842
NCBI GI
BLAST score
                   263
                   6.0e-31
E value
Match length
                   86
                   81
% identity
                   potassium channel protein - Arabidopsis thaliana >gi_166774
NCBI Description
                   (M86990) potassium channel protein [Arabidopsis thaliana]
                   >gi 1065906 (U25088) potassium channel protein [Arabidopsis
                   thaliana]
                   28805
Seq. No.
                   181414 1.R1040
Contig ID
                   fde700872880.hl
5'-most EST
```

Seq. No.

NCBI Description

```
181441 1.R1040
Contig ID
5'-most EST
                   fde700871614.h1
Seq. No.
                   28807
                   181446 1.R1040
Contig ID
5'-most EST
                   fde700873667.h1
                   28808
Seq. No.
Contig ID
                   181448 1.R1040
5'-most EST
                   jex700\overline{9}09437.h1
                   28809
Seq. No.
                   181457 1.R1040
Contig ID
                   zzp700\overline{8}31121.h1
5'-most EST
Method
                   BLASTX
                   g1706884
NCBI GI
BLAST score
                   365
E value
                   2.0e-34
Match length
                   276
                   34
% identity
NCBI Description
                   FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR
                   (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS)
                   28810
Seq. No.
Contig ID
                   181461 1.R1040
                   fde700\overline{8}75886.h1
5'-most EST
                   28811
Seq. No.
                   181486 1.R1040
Contig ID
5'-most EST
                   fde700875642.hl
                   BLASTX
Method
                   g4567263
NCBI GI
BLAST score
                   366
                   2.0e-35
E value
Match length
                   84
% identity
NCBI Description
                   (AC006841) putative cell division inhibitor [Arabidopsis
                   thaliana]
                   28812
Seq. No.
                   181510 1.R1040
Contig ID
5'-most EST
                   bth700845762.h1
                                                                            3.
                   28813
Seq. No.
                   181514 1.R1040
Contig ID
5'-most EST
                   hrw701063367.hl
                   28814
Seq. No.
                   181541_1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}36708.h1
                   BLASTX
Method
                   g4490317
NCBI GI
BLAST score
                   380
E value
                   2.0e-36
Match length
                   188
                   43
% identity
```

(AL035678) putative protein [Arabidopsis thaliana]

Seq. No. Contig ID

```
28815
Seq. No.
                  181610 1.R1040
Contig ID
                  fde700871835.hl
5'-most EST
                  28816
Seq. No.
                  181620 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220055g03a1
Method
                  BLASTX
NCBI GI
                  g2565297
BLAST score
                  332
                   6.0e-31
E value
                  158
Match length
% identity
                  50
                   (AF024590) RNA polymerase sigma subunit 1 [Arabidopsis
NCBI Description
                  thaliana]
                  28817
Seq. No.
                  181635 1.R1040
Contig ID
                  fde700871879.h1
5'-most EST
Seq. No.
                  28818
                  181645 1.R1040
Contig ID
5'-most EST
                  pxt700942623.h1
Seq. No.
                  28819
                  181649 1.R1040
Contig ID
                  fde700874147.hl
5'-most EST
                  28820
Seq. No.
                  181672 1.R1040
Contig ID
5'-most EST
                  pmv700888202.h1
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  32
E value
                  1.0e-08
Match length
                  76
                  86
% identity
NCBI Description
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  28821
                  181688 1.R1040
Contig ID
5'-most EST
                  q4296088
Method
                  BLASTX
NCBI GI
                  q3065814
BLAST score
                  213
E value
                  7.0e-17
Match length
                  169
% identity
NCBI Description
                   (AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus
                  norvegicus] >gi_3168585_dbj_BAA28609_ (AB001321)
                  sodium-dependent dicarboxylate transporter [Rattus
                  norvegicus]
```

181706 1.R1040

```
5'-most EST
                  fde700872031.hl
Seq. No.
                  28823
                  181714 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy111g01b1
Method
                  BLASTX
NCBI GI
                  q3236247
BLAST score
                   386
E value
                   7.0e-49
Match length
                  155
% identity
                   69
NCBI Description
                   (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
                  28824
Seq. No.
Contig ID
                  181721 1.R1040
5'-most EST
                   fde700872030.hl
                  28825
Seq. No.
                  181743 1.R1040
Contig ID
5'-most EST
                   fde700872078.hl
                  28826
Seq. No.
Contig ID
                  181778 1.R1040
5'-most EST
                   zhf700958516.h1
Method
                  BLASTX
NCBI GI
                  g3402717
BLAST score
                  162
                   9.0e-15
E value
Match length
                   63
% identity
NCBI Description
                   (AC004261) putative heat shock protein [Arabidopsis
                  thaliana]
                  28827
Seq. No.
                  181790 1.R1040
Contig ID
5'-most EST
                   fde700876485.hl
Seq. No.
                  28828
Contig ID
                  181798 1.R1040
5'-most EST
                   jC-gmro02910060f04a1
Method
                  BLASTX
NCBI GI
                  g4467148
                  588
BLAST score
E value
                  7.0e-61
Match length
                  178
% identity
                  72
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  28829
Seq. No.
Contig ID
                  181807 1.R1040
5'-most EST
                  jC-gmle01810019b10a2
                  BLASTX
Method
NCBI GI
                  g3914136
BLAST score
                  282
E value
                  8.0e-25
Match length
                  87
```

% identity

5'-most EST

```
NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   >gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                   [Cicer arietinum]
Seq. No.
                   28830
                   181815 1.R1040
Contig ID
5'-most EST
                   zsg701130235.hl
                  BLASTX
Method
NCBI GI
                   q1723832
BLAST score
                   154
E value
                   5.0e-10
Match length
                  71
                   44
% identity
                  HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION
NCBI Description
                  >gi_2132531_pir__S64058 probable membrane protein YGL054c -
                  yeast (Saccharomyces cerevisiae) >gi 1322550 emb CAA96756
                   (Z72576) ORF YGL054c [Saccharomyces cerevisiae]
                  28831
Seq. No.
                   181817 1.R1040
Contig ID
                   fde700876653.h1
5'-most EST
                  28832
Seq. No.
Contig ID
                  181846 1.R1040
5'-most EST
                   fde700872278.h1
                  BLASTX
Method
                  g3176726
NCBI GI
BLAST score
                   474
E value
                   2.0e-47
Match length
                  181
                   51
% identity
NCBI Description
                   (AC002392) putative serine proteinase [Arabidopsis
                  thaliana]
                   28833
Seq. No.
                  181858 1.R1040
Contig ID
5'-most EST
                   fde700872310.h1
                                                     The car
                  28834
Seq. No.
                  181861 2.R1040
Contig ID
5'-most EST
                   fde700872465.h1
Seq. No.
                  28835
                  181865 1.R1040
Contig ID
                   fde700\overline{8}73959.h1
5'-most EST
                  BLASTX
Method
                  g2605714
NCBI GI
BLAST score
                  140
E value
                  8.0e-09
Match length
                  59
% identity
                  46
NCBI Description
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
                  28836
Seq. No.
                  181887 1.R1040
Contig ID
```

fde700872369.hl

```
28837
Seq. No.
                  181896 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy048d07b1
                  28838
Seq. No.
                  181915 1.R1040
Contig ID
5'-most EST
                   fde700876846.h1
Method
                  BLASTX
NCBI GI
                  q1652649
BLAST score
                   478
                  7.0e-48
E value
Match length
                   161
                   55
% identity
                   (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                  28839
Seq. No.
                   181927 1.R1040
Contig ID
                   jC-gmle01810011e07a1
5'-most EST
Method
                  BLASTX
                   g728905
NCBI GI
BLAST score
                   159
E value
                   2.0e-10
Match length
                  155
% identity
                   27
                  PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC
NCBI Description
                  RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable
                  ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)
                  >gi 171114 (L01795) ATPase [Saccharomyces cerevisiae]
                   >gi 595560 (U12980) Drs2p: Membrane spanning
                   Ca-ATPase(P-type), member of the cation transport(E1-E2)
                  ATPase [Saccharomyces cerevisiae]
                   28840
Seq. No.
                   181953 1.R1040
Contig ID
5'-most EST
                   kl1701209449.hl
Method
                  BLASTX
                   g4559396
NCBI GI
BLAST score
                   259
E value
                   8.0e-23
Match length
                   66
% identity
                   71
                   (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28841
Seq. No.
                   181971 1.R1040
Contig ID
                   crh700850692.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4490304
BLAST score
                   521
                   3.0e-53
E value
Match length
                   121
                   82
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   28842
Seq. No.
```

```
5'-most EST
                  fde700872574.h1
Seq. No.
                  28843
                  182038 1.R1040
Contig ID
                  dpv701102023.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g289124
BLAST score
                  202
E value
                  1.0e-110
Match length
                  270
% identity
                  94
                  Medicago sativa MAP kinase MsERK1 mRNA, complete cds
NCBI Description
Seq. No.
                  182050 1.R1040
Contig ID
5'-most EST
                  fde700872717.h1
Method
                  BLASTN
NCBI GI
                  g1134881
BLAST score
                  118
E value
                  7.0e-60
Match length
                  262
                  86
% identity
NCBI Description P.sativum mRNA for cysteine protease
                  28845
Seq. No.
Contig ID
                  182065 1.R1040
5'-most EST
                  sat701015446.h1
Method
                  BLASTX
NCBI GI
                  q2129820
BLAST score
                  190
E value
                  9.0e-15
Match length
                  82
                  49
% identity
                  chitinase (EC 3.2.1.14) class II - peanut
NCBI Description
                  >gi_1237025_emb_CAA57773_ (X82329) chitinase (class II)
                   [Arachis hypogaea]
                  28846
Seq. No.
                  182066 1.R1040
Contig ID
5'-most EST
                  fde700872743.hl
                  28847
Seq. No.
                  182067 1.R1040
Contig ID
5'-most EST
                  fde700875456.hl
Seq. No.
                  28848
Contig ID
                  182077 1.R1040
5'-most EST
                  fde700872757.h1
                  28849
Seq. No.
                  182078_1.R1040
Contig ID
5'-most EST
                  jC-gmro02910008g10a1
Method
                  BLASTX
                  g3877656
NCBI GI
BLAST score
                  324
                  8.0e-30
E value
```

Match length

```
% identity
NCBI Description
                   (Z72511) similar to nucleotide translocator [Caenorhabditis
                   elegans]
                   28850
Seq. No.
                   182078 2.R1040
Contig ID
5'-most EST
                   fde700872758.h1
Method
                   BLASTN
NCBI GI
                   q3510339
BLAST score
                   36
E value
                   6.0e-11
                   96
Match length
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   28851
Seq. No.
                   182078 3.R1040
Contig ID
                   leu701156558.hl
5'-most EST
                   BLASTN
Method
                   g3510339
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
Match length
                   96
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   28852
Seq. No.
                   182079 1.R1040
Contig ID
                   fde700875724.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4063746
BLAST score
                   221
                   4.0e-18
E value
                   85
Match length
                   57
% identity
NCBI Description
                   (AC005851) nodulin-like protein [Arabidopsis thaliana]
                   28853
Seq. No.
                   182131 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy195e05b1
Method
                   BLASTX
NCBI GI
                   g2765817
BLAST score
                   493
                   1.0e-49
E value
                   214
Match length
                   47
% identity
NCBI Description
                   (Z95352) AtMlo-hl [Arabidopsis thaliana]
                   >gi 3892049 gb AAC78258.1 AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                   28854
Seq. No.
                   182141 1.R1040
Contig ID
                   g50580<del>5</del>7
5'-most EST
```

Seq. No.

Match length

162

```
182209 1.R1040
Contig ID
5'-most EST
                   fde700873982.hl
Method
                   BLASTX
NCBI GI
                   g4558556
BLAST score
                   230
                   5.0e-19
E value
Match length
                   107
                   44
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   28856
Seq. No.
                   182214 1.R1040
Contig ID
5'-most EST
                   uC-gmropic032b02b1
                   28857
Seq. No.
                   182217 1.R1040
Contig ID
                   pmv700892710.h1
5'-most EST
Seq. No.
                   28858
                   182218 1.R1040
Contig ID
                   k11701\overline{2}06235.h1
5'-most EST
                   28859
Seq. No.
                   182228 1.R1040
Contig ID
5'-most EST
                   bth700848581.hl
Method
                   BLASTX
NCBI GI
                   g4049399
BLAST score
                   167
E value
                   5.0e-12
Match length
                   66
% identity
                   39
                   (Y09581) FRO2 [Arabidopsis thaliana]
NCBI Description
                   28860
Seq. No.
                   182240 1.R1040
Contig ID
5'-most EST
                   fde700873913.hl
                   28861
Seq. No.
Contig ID
                   182249 1.R1040
                   fde700873010.hl
5'-most EST
Method
                   BLASTX
                   g2979546
NCBI GI
BLAST score
                   142
E value
                   4.0e-09
Match length
                   44
                   61
% identity
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28862
Seq. No.
                   182257_1.R1040
Contig ID
                   fC-gmle700873022a1
5'-most EST
Method
                   BLASTX
                   g113626
NCBI GI
                   590
BLAST score
E value
                   4.0e-61
```

```
% identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE >gi 68202 pir ADBY2
NCBI Description
                    fructose-bisphosphate aldolase (EC 4.1.2.13) II - yeast (Saccharomyces cerevisiae) >gi_3696_emb_CAA33111_ (X15003) fructose-bisphosphate aldolase [Saccharomyces cerevisiae]
                    >gi 433637 emb CAA53412 (X75781) yeast
                    fructose-bisphate-aldolase [Saccharomyces cerevisiae]
                    >gi_486081_emb_CAA81897_ (Z28060) ORF YKL060c
                    [Saccharomyces cerevisiae] >gi_1587557_prf__2206495F
                    fructosebisphosphate aldolase [Saccharomyces cerevisiae]
                    28863
Seq. No.
                    182281 1.R1040
Contig ID
                    jex700\overline{9}09558.h1
5'-most EST
Method
                    BLASTX
                    q473874
NCBI GI
                    379
BLAST score
                    8.0e-37
E value
Match length
                    93
                    41
% identity
                    (U08285) a membrane-associated salt-inducible protein
NCBI Description
                    [Nicotiana tabacum]
                    28864
Seq. No.
                    182283 1.R1040
Contig ID
5'-most EST
                    fde700873065.hl
Method
                    BLASTX
                    q4406820
NCBI GI
BLAST score
                    285
E value
                    4.0e-34
Match length
                    108
% identity
                    76
                    (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                    thaliana]
                    28865
Seq. No.
Contig ID
                    182308 1.R1040
5'-most EST
                    fde700874276.hl
                    BLASTX
Method
                    g4106690
NCBI GI
BLAST score
                    151
                    4.0e-10
E value
Match length
                    46
% identity
                    (AL035065) putative urea active transporter
NCBI Description
                    [Schizosaccharomyces pombe]
                    28866
Seq. No.
                    182340 1.R1040
Contig ID
5'-most EST
                    leu701155963.h1
                    28867
Seq. No.
                    182350 1.R1040
Contig ID
5'-most EST
                    fde700873155.hl
                    28868
Seq. No.
```

```
5'-most EST
                    all700863165.hl
 Method
                    BLASTX
 NCBI GI
                    q3183377
 BLAST score
                    238
 E value
                    9.0e-20
 Match length
                    148
 % identity
                    22
 NCBI Description
                    HYPOTHETICAL 79.3 KD PROTEIN C24C9.05C IN CHROMOSOME I
                    >gi 2330788 emb CAB11262 (Z98601) hypothetical protein.
                    [Schizosaccharomyces pombe]
 Seq. No.
                    28869
                    182390 1.R1040
 Contig ID
 5'-most EST
                    uC-qmflminsoy063a03b1
                    28870
 Seq. No.
                    182441 1.R1040
 Contig ID
 5'-most EST
                    uC-gmflminsoy084d03b1
 Method
                    BLASTX
 NCBI GI
                    g3292826
BLAST score
                    182
                    1.0e-13
 E value
 Match length
                    88
 % identity
                    42
                    (AL031018) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    28871
 Seq. No.
                    182455 1.R1040
 Contig ID
 5'-most EST
                    fde700873293.hl
 Seq. No.
                    28872
                    182458 1.R1040
 Contig ID
 5'-most EST
                    g5510075
 Method
                    BLASTX
                    g1171577
 NCBI GI
 BLAST score
                    273
 E value
                    9.0e-34
                    149 ...
 Match length
 % identity
                    58
                    (X95343) hypersensitivity-related gene [Nicotiana tabacum]
 NCBI Description
                    28873
 Seq. No.
                    182465 1.R1040
 Contig ID
                    uC-gmrominsoy273g01b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g4544383
 BLAST score
                    414
 E value
                    1.0e-40
 Match length
                    110
 % identity
                    (AC007047) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    28874
                    182482 1.R1040
 Contig ID
 5'-most EST
                    fde700873332.h1
```

Seq. No.

```
Contig ID
                   182489 1.R1040
5'-most EST
                   fde700873647.h1
Seq. No.
                   28876
                   182497 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}09071.h1
Method
                   BLASTN
                   g1354856
NCBI GI
BLAST score
                   396
                   0.0e+00
E value
Match length
                   707
% identity
                   89
                   Phaseolus vulgaris bZIP transcriptional repressor ROM1
NCBI Description
                   mRNA, complete cds
                   28877
Seq. No.
                   182516 1.R1040
Contig ID
                   zhf700965290.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245065
BLAST score
                   175
E value
                   5.0e-13
Match length
                   43
                   13
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   28878
                   182525 1.R1040
Contig ID
                   fC-gmle700873411a1
5'-most EST
                   BLASTX
Method
                   g4512667
NCBI GI
BLAST score
                   248
                   3.0e-37
E value
Match length
                   118
% identity
                   65
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28879
                   182528 1.R1040
Contig ID
5'-most EST
                   bth700845409.h1
                   BLASTX
Method
                   g2792155
NCBI GI
BLAST score
                   504
                   5.0e-51
E value
                   183
Match length
                   56
% identity
                   (AJ223291) chalcone reductase [Sesbania rostrata]
NCBI Description
                   28880
Seq. No.
                   182536 1.R1040
Contig ID
                   crh700\overline{8}51111.h1
5'-most EST
Method
                   BLASTN
                   g516102
NCBI GI
BLAST score
                   268
                   1.0e-149
E value
                   414
Match length
```

95

% identity.

NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 28881

Contig ID 182540_1.R1040 5'-most EST fC-gmle700873428r1

Method BLASTX
NCBI GI g1168409
BLAST score 147
E value 2.0e-09
Match length 95
% identity 43

NCBI Description PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE 2

>gi_709990_dbj_BAA03299_ (D14399) hypothetical protein
[Bacillus subtilis] >gi_2636513_emb_CAB16003_ (Z99124)
fructose-1,6-bisphosphate aldolase [Bacillus subtilis]

Seq. No. 28882

Contig ID 182542 1.R1040 5'-most EST fde700873430.h1

Method BLASTN
NCBI GI g10789
BLAST score 136
E value 1.0e-70
Match length 247
% identity 21

NCBI Description T.pyriformis TU20 gene for ubiquitin

Seq. No. 28883

Contig ID 182556 1.R1040

5'-most EST jC-gmst02400047g05d1

Method BLASTX
NCBI GI g4115382
BLAST score 407
E value 9.0e-40
Match length 101

Match length 101 % identity 75

NCBI Description (AC005967) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28884

Contig ID 182562_1.R1040 5'-most EST fde700873462.h1 Method BLASTX

NCBI GI g3164140
BLAST score 283
E value 1.0e-25
Match length 78
% identity 64

NCBI Description (D78605) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No. 28885

Contig ID 182597 1.R1040 5'-most EST fde700874048.h1

Seq. No. 28886

Contig ID 182612 1.R1040 5'-most EST fde700873542.h1

5'-most EST

```
BLASTX
Method
                   g2735017
NCBI GI
                   394
BLAST score
E value
                   2.0e-38
Match length
                   96
                   79
% identity
                   (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
                   28887
Seq. No.
                   182617 1.R1040
Contig ID
5'-most EST
                   fde700874501.h1
                   28888
Seq. No.
                   182630 1.R1040
Contig ID
5'-most EST
                   fde700873984.h1
                   28889
Seq. No.
                   182636_1.R1040
Contig ID
                   uC-gmflminsoy071a12b2
5'-most EST
                   28890
Seq. No.
                   182649 1.R1040
Contig ID
                   \mathtt{sat701}\overline{\mathtt{0}}\mathtt{15457.h1}
5'-most EST
                   BLASTN
Method
                   g857396
NCBI GI
BLAST score
                   134
E value
                   2.0e-69
                   250
Match length
                   89
% identity
                   Glycine max mRNA for mitotic cyclin a2-type, complete cds
NCBI Description
Seq. No.
                   28891
Contig ID
                   182665_1.R1040
5'-most EST
                   pxt700941060.hl
                   BLASTX
Method
NCBI GI
                   g3355478
BLAST score
                   141
E value
                   5.0e-09
                   74
Match length
% identity
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28892
Seq. No.
                   182687 1.R1040
Contig ID
                   fde700873651.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006851
BLAST score
                   204
                   2.0e-31
E value
Match length
                   116
% identity
                   68
                   (Z99707) cytochrome P450-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   28893
Seq. No.
                   182688 1.R1040
Contig ID
```

fde700873652.hl

```
Seq. No.
                   28894
                   182738 1.R1040
Contig ID
                   fde700874019.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q20880
BLAST score
                   32
E value
                   1.0e-08
Match length
                   36
                   97
% identity
NCBI Description
                   Pea mRNA for plastid ribosomal protein CL9
                   28895
Seq. No.
                   182746 1.R1040
Contig ID
5'-most EST
                   fde700873732.hl
                   28896
Seq. No.
                   182752 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400008h09a1
Method
                   BLASTX
                   g3152592
NCBI GI
BLAST score
                   330
E value
                   1.0e-30
Match length
                   110
% identity
                   58
NCBI Description
                   (ACO02986) Contains similarity to 8A-2V protein gb Y10496
                   from Mus musculus. [Arabidopsis thaliana]
                   28897
Seq. No.
                   182753 1.R1040
Contig ID
5'-most EST
                   fde700873744.hl
                   28898
Seq. No.
                   182764 1.R1040
Contig ID
                   pmv700892512.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129698
BLAST score
                   454
E value
                   3.0e-45
Match length
                   132
                   67
% identity
NCBI Description
                   protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi 1054633 emb CAA63387 (X92728) protein kinase
                   [Arabidopsis thaliana]
                   28899
Seq. No.
Contig ID
                   182797 1.R1040
5'-most EST
                   zhf700960172.h1
                   28900
Seq. No.
                   182808 1.R1040
Contig ID
                   jex700\overline{9}05406.h1
5'-most EST
                   28901
Seq. No.
                   182840 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073f03a1
```

BLASTX

Method

Method

BLASTX

```
....
NCBI GI
                   g3292824
                                    - المعروب
BLAST score
                   237
                   9.0e-20
E value
                   65
Match length
% identity
NCBI Description
                   (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   28902
                   182840 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810016e06a1
Method
                   BLASTX
NCBI GI
                   q3292824
BLAST score
                   182
E value
                   2.0e-13
                   57 😘
Match length
                   61
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   28903
                   182851 1.R1040
Contig ID
5'-most EST
                   fde700873885.h1
                   28904
Seq. No.
                   182860 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220138b08d1
                   28905
Seq. No.
                   182882 1.R1040
Contig ID
                   fde700873968.hl
5'-most EST
                   28906
Seq. No.
                   182894 1.R1040
Contig ID
                   fde700873956.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4521152
BLAST score
                   100
E value
                   4.0e-49
Match length
                   272
% identity
                   84
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   28907
Seq. No.
                   182919 1.R1040
Contig ID
                   fde700873986.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3953463
BLAST score
                   204
E value
                   6.0e-16
Match length
                   47
% identity
                   79
NCBI Description
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
                   28908
Seq. No.
                   182920 1.R1040
Contig ID
                   jC-qmle01810051d08a1
5'-most EST
```

```
NCBI GI
                   q4490317
BLAST score
                   228
E value
                   1.0e-18
                   100
Match length
% identity
                   44
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   182945 1.R1040
Contig ID
5'-most EST
                   fde700874024.hl
                   28910
Seq. No.
                   182948 1.R1040
Contig ID
5'-most EST
                   dpv701099247.hl
Method
                   BLASTN
NCBI GI
                   g2342717
BLAST score
                   52
E value
                   2.0e-20
Match length
                   80
% identity
                   91
                   Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   28911
                   183009 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810025e05a1
                   28912
Seq. No.
                   183014 1.R1040
Contig ID
                   jsh701\overline{0}69970.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1279640
BLAST score
                   449
E value
                   1.0e-44
Match length
                   126
                   66
% identity
NCBI Description
                   (X92204) NAM [Petunia x hybrida]
                   28913
Seq. No.
                   183027 1.R1040
Contig ID
5'-most EST
                   fde700874161.hl
                   28914
Seq. No.
                   183032 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}07729.h1
Seq. No.
                   28915
Contig ID
                   183069 1.R1040
5'-most EST
                   zsg701\overline{1}18022.h2
                   28916
Seq. No.
                   183074 1.R1040
Contig ID
5'-most EST
                   fua701037884.hl
Method
                   BLASTX
                   g2827637
NCBI GI
BLAST score
                   141
```

1.0e-08

E value

Method

NCBI GI

BLASTX q4454469

```
Match length 77
% identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                   28917
Seq. No.
                   183097 1.R1040
Contig ID
                   k11701\overline{2}05752.h1
5'-most EST
Seq. No.
                   28918
                   183132 1.R1040
Contig ID
                   k11701\overline{2}02418.h1
5'-most EST
                   28919
Seq. No.
                   183161 1.R1040
Contig ID
5'-most EST
                   fde700874663.hl
                   28920
Seq. No.
                   183169 1.R1040
Contig ID
                   fde700874373.hl
5'-most EST
                   28921
Seq. No.
                   183202 1.R1040
Contig ID
5'-most EST
                   fde700874417.h1
                   28922
Seq. No.
                   183216 1.R1040
Contig ID
                                                             fde700874745.h1
5'-most EST
                   28923
Seq. No.
Contig ID
                   183247_1.R1040
5'-most EST
                   jC-gmro02910057c12a1
Method
                   BLASTX
                   g3377803
NCBI GI
                   477
BLAST score
E value
                   5.0e-48
Match length
                   133
% identity
                   71
                   (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
                   28924
Seq. No.
Contig ID
                   183256 1.R1040
                   jC-gmle01810012g08d1
5'-most EST
Method
                   BLASTX
                   g3367522
NCBI GI
BLAST score
                   412
E value
                   3.0e-40
Match length
                   106
                   69
% identity
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   28925
Seq. No.
                   183282 1.R1040
Contig ID
                   uC-gmrominsoy241f03b1
5'-most EST
```

BLAST score

318

```
BLAST score
                   451
                   8.0e-45
E value
Match length
                   161
% identity
                   54
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   28926
                   183311 1.R1040
Contig ID
5'-most EST
                   zhf700963066.h1
                   BLASTX
Method
NCBI GI
                   q4140326
BLAST score
                   212
                   5.0e-27
E value
Match length
                   126
% identity
                   50
                   (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to
NCBI Description
                  many (archae) bacterial, worm and yeast hypothetical
                  proteins) [Homo sapiens]
Seq. No.
                   28927
                   183325 1.R1040
Contig ID
                   zhf700960204.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q282881
                   202
BLAST score
E value
                  1.0e-15
Match length
                   134
% identity
NCBI Description
                   receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi 166846 (M84658) receptor-like protein kinase
                   [Arabidopsis thaliana]
                   28928
Seq. No.
                   183331 1.R1040
Contig ID
5'-most EST
                  pxt700941705.hl
Seq. No.
                   28929
                   183334 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810075c07a1
Method
                   BLASTX
                   g4455367
NCBI GI
BLAST score
                   169
E value
                   8.0e-12
Match length
                   144
                   35
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   28930
Seq. No.
                   183350 1.R1040
Contig ID
                   fde700874675.hl
5'-most EST
Seq. No.
                  28931
                  183356 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy245b09b1
Method
                  BLASTX
                  g4371292
NCBI GI
```

```
5.0e-29
E value
Match length
                   138
% identity
                   46
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   28932
Seq. No.
                   183358 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}59607.h1
Method
                   BLASTX
NCBI GI
                   q4102839
BLAST score
                   138
E value
                   1.0e-08
Match length
                   50
                   54
% identity
NCBI Description
                   (AF016713) LeOPT1 [Lycopersicon esculentum]
                   28933
Seq. No.
                   183359 1.R1040
Contig ID
5'-most EST
                   fde700875018.hl
                   28934
Seq. No.
                   183363 1.R1040
Contig ID
5'-most EST
                   fde700874836.h1
                   28935
Seq. No.
                                               -14.
Contig ID
                   183377 1.R1040
                   fde700\overline{8}74667.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2465923
BLAST score
                   596
E value
                   1.0e-61
Match length
                   186
% identity
                   61
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   28936
                   183386_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy067f06b1
Method
                   BLASTX
                   q1438875
NCBI GI
BLAST score
                   183
                   1.0e-13
E value
Match length
                   40
% identity
                   80
NCBI Description
                   (U31462) violaxanthin de-epoxidase precursor [Lactuca
                   sativa]
                   28937
Seq. No.
                   183394 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810042b03d1
                   28938
Seq. No.
                   183440 1.R1040
Contig ID
5'-most EST
                   fde700\overline{8}74742.h1
```

28939

Seq. No.

Contig ID 5'-most EST

```
183479 1.R1040
 Contig ID
 5'-most EST
                    uC-qmronoir060d04b1
 Seq. No.
                    28940
                    183489 1.R1040
 Contig ID
                    fde700874808.hl
 5'-most EST
                    28941
 Seq. No.
                    183510 1.R1040
 Contig ID
 5'-most EST
                    fde700874837.hl
 Seq. No.
                    28942
                    183513_1.R1040
 Contig ID
 5'-most EST
                    ary700764453.hl
 Method
                    BLASTX
 NCBI GI
                    g629669
 BLAST score
                    182
 E value
                    2.0e-13
 Match length
                    62
 % identity
                    50
                    hypothetical protein - tomato
 NCBI Description
 Seq. No.
                    28943
                    183520 1.R1040
 Contig ID
5'-most EST
                    fde700874852.h1
                                          71.
                    28944
 Seq. No.
                    183535 1.R1040
 Contig ID
 5'-most EST
                    fde700874875.hl
 Seq. No.
                    28945
                    183542_1.R1040
 Contig ID
                    jC-gmro02910051e10a1
 5'-most EST
 Method
                    BLASTX
                    g2444174
 NCBI GI
 BLAST score
                    852
 E value
                    9.0e-92
Match length
                    195
                    82
% identity
                    (U94781) unconventional myosin [Helianthus annuus]
 NCBI Description
                    28946
 Seq. No.
                    183596 1.R1040
 Contig ID
 5'-most EST
                    awf700836895.hl
 Method
                    BLASTX
 NCBI GI
                    g2129656
 BLAST score
                    292
 E value
                    2.0e-39
Match length
                    140
 % identity
                    61
                    OBP33pep protein - Arabidopsis thaliana (fragment)
 NCBI Description
                    >gi_1022801 (U37699) OBP33pep [Arabidopsis thaliana]
                    28947
 Seq. No.
```

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183598 1.R1040

fde700874962.h1

```
28948
Seq. No.
                     183615 1.R1040
Contig ID
                     leu701155293.hl
5'-most EST
                     28949
Seq. No.
                     183624 1.R1040
Contig ID
                     fua701037786.hl
5'-most EST
Seq. No.
                     28950
                     183631 1.R1040
Contig ID
5'-most EST
                     jC-gmle01810094e07a1
Method
                     BLASTN
NCBI GI
                     q868002
BLAST score
                     122
E value
                     4.0e-62
Match length
                     338
                     84
% identity
NCBI Description
                    Pumpkin mRNA for aconitase, complete cds
Seq. No.
                     183638 1.R1040
Contig ID
5'-most EST
                     fde700875021.h1
Seq. No.
                     28952
                     183646 1.R1040
Contig ID
5'-most EST
                     fde700875129.hl
                     BLASTN
Method
NCBI GI
                     a1235600
BLAST score
                     154
                     2.0e-81
E value
Match length
                     234
% identity
                    S.macrospora EF1-alpha gene
NCBI Description
                     28953
Seq. No.
Contig ID
                     183651 1.R1040
5'-most EST
                     fde700875216.hl
                     28954
Seq. No.
                     183665 1.R1040
Contig ID
5'-most EST
                     sat701\overline{0}11418.h1
                     28955
Seq. No.
                     183677 1.R1040
Contig ID
5'-most EST
                     zhf700958916.hl
Method
                     BLASTX
NCBI GI
                     q1076365
BLAST score
                     170
E value
                     8.0e-12
Match length
                     184
                     29
% identity
NCBI Description
                    pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis
                    thaliana >gi_2129666_pir__JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275 (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649)
```

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ATPME1 precursor [Arabidopsis thaliana]

```
28956
Seq. No.
                   183684 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810062d09a1
                   28957
Seq. No.
                   183714 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220070d06a1
Seq. No.
                   28958
                   183842 1.R1040
Contig ID
                   fde700875315.h1
5'-most EST
                   28959
Seq. No.
                   183845 1.R1040
Contig ID
5'-most EST
                   fde700875318.hl
                   BLASTX
Method
NCBI GI
                   g2947063
BLAST score
                   231
E value
                   4.0e-19
Match length
                   144
% identity
                   38
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   28960
Seq. No.
                   183856 1.R1040
Contig ID
                   fde700875338.h1
5'-most EST
                   28961
Seq. No.
                   183890 1.R1040
Contig ID
5'-most EST
                   fde700875379.h1
                   28962
Seq. No.
                   183919 1.R1040
Contig ID
                   k11701\overline{2}05968.h1
5'-most EST
Seq. No.
                   28963
                   183975 1.R1040
Contig ID
                   fde700875494.h1
5'-most EST
Method
                   BLASTX
                   g1653767
NCBI GI
BLAST score
                   330
E value
                   7.0e-31
Match length
                   121
                   53
% identity
                   (D90916) oligopeptidase A [Synechocystis sp.]
NCBI Description
                   28964
Seq. No.
                   183992 1.R1040
Contig ID
5'-most EST
                   g5677624
Seq. No.
                   28965
                   184065 1.R1040
Contig ID
                   fde700875620.h1
5'-most EST
                   28966
Seq. No.
                   184078 1.R1040
Contig ID
```

```
fde700875640.h1
5'-most EST
                  28967
Seq. No.
                  184084 1.R1040
Contig ID
                  leu701149946.hl
5'-most EST
                  28968
Seq. No.
                  184089 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910012g06d1
                  28969
Seq. No.
                  184089 2.R1040
Contig ID
                  asn701142114.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244936
BLAST score
                  142
                   5.0e-09
E value
Match length
                  42
% identity
                   (Z97339) similarity to chloroplast outer envelope protein
NCBI Description
                  OEP8 [Arabidopsis thaliana]
Seq. No.
                  28970
                   184119 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810014e03d1
                  28971
Seq. No.
                   184136 1.R1040
Contig ID
                   fde700875730.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2160173
BLAST score
                   263
                   3.0e-23
E value
Match length
                   86
% identity
NCBI Description
                   (AC000132) Similar to N. tabacum salt-inducible protein
                   (gb_U08285). [Arabidopsis thaliana]
                   28972
Seq. No.
                   184150 1.R1040
Contig ID
5'-most EST
                  pxt700941132.hl
                   28973
Seq. No.
                   184152 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400026a02a1
Seq. No.
                   28974
                   184165 1.R1040
Contig ID
5'-most EST
                   fde700875776.h1
                   28975
Seq. No.
                   184193 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy162f07b1
                   BLASTX
Method
                   q1946371
NCBI GI
BLAST score
                   227
                   1.0e-18
E value
```

NCBI Description

```
73
Match length
% identity
                   56
NCBI Description
                   (U93215) regulatory protein Viviparous-1 isolog
                   [Arabidopsis thaliana]
                   28976
Seq. No.
                   184206 1.R1040
Contig ID
5'-most EST
                   fde700875834.hl
Method
                   BLASTX
NCBI GI
                   g2245115
BLAST score
                   352
                   3.0e - 33
E value
                   113
Match length
% identity
                   64
                   (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   28977
Seq. No.
                   184207 1.R1040
Contig ID
                   fde700875836.h1
5'-most EST
                   28978
Seq. No.
                   184272_1.R1040
Contig ID
                   jC-gmle01810080g05d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3242704
BLAST score
                   406
E value
                   2.0e-39
Match length
                   134
                   56
% identity
                   (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28979
Seq. No.
                   184280_1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}18495.h1
                   28980
Seq. No.
Contig ID
                   184304 1.R1040
                   fde700\overline{8}75979.h1
5'-most EST
                   28981
Seq. No.
                   184347 1.R1040
Contig ID
5'-most EST
                   fde700876044.h1
                   28982
Seq. No.
                   184382 1.R1040
Contig ID
5'-most EST
                   hrw701058203.hl
                   28983
Seq. No.
                   184402 1.R1040
Contig ID
5'-most EST
                   g55091\overline{3}1
Method
                   BLASTX
                   g401213
NCBI GI
                   352
BLAST score
                   3.0e-33
E value
                   118
Match length
                   58
% identity
                   ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792
```

(M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 28984

Contig ID 184404_1.R1040

5'-most EST jC-gmle01810086g04a1

Method BLASTX
NCBI GI 94572676
BLAST score 387
E value 2.0e-37
Match length 129
% identity 60

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 28985

Contig ID 184414_1.R1040 5'-most EST fde700876809.h1

Seq. No. 28986

Contig ID 184420_1.R1040 5'-most EST fde700876155.h1

Seq. No. 28987

Contig ID 184421_1.R1040 5'-most EST fde700877225.h1

Seq. No. 28988

Contig ID 184422_1.R1040 5'-most EST epx701105813.h1

Seq. No. 28989

Contig ID 184441 1.R1040 5'-most EST zhf700955464.h1

Seq. No. 28990

Contig ID 184445 1.R1040

5'-most EST $jC-gmf\overline{102220056a10a1}$

Method BLASTN
NCBI GI g3243214
BLAST score 41
E value 1.0e-13
Match length 163
% identity 87

NCBI Description Arabidopsis thaliana BAC T19B17 from chromsome IV, near

19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 28991

Contig ID 184488_1.R1040 5'-most EST fde700876250.h1

Seq. No. 28992

Contig ID 184516_1.R1040 5'-most EST fde700877171.h1

Method BLASTX NCBI GI g1652609

Method

BLASTX

```
BLAST score
                   150
E value
                   5.0e-10
Match length
                   78
% identity
                   36
NCBI Description
                   (D90906) 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase
                   [Synechocystis sp.]
                   28993
Seq. No.
Contig ID
                   184528_1.R1040
5'-most EST
                   jC-gmle01810040d01a1
Method
                   BLASTX
NCBI GI
                   q4455278
BLAST score
                   115
                   2.0e-13
E value
Match length
                   156
% identity
                   25
                   (AL035527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28994
Seq. No.
                   184530 1.R1040
Contig ID
                   fde700877123.hl
5'-most EST
                   28995
Seq. No.
                   184545 1.R1040
Contig ID
                   fde700876343.h1
5'-most EST
                   28996
Seq. No.
                   184597 1.R1040
Contig ID
                   fde700\overline{8}76433.h1
5'-most EST
                   28997
Seq. No.
                   184604 1.R1040
Contig ID
5'-most EST
                   fde700876445.h1
                   BLASTX
Method
NCBI GI
                   g1279911
BLAST score
                   441
E value
                   3:0e-44
Match length
                   84
                   98
% identity
                   (U52963) mitogen-activated protein kinase [Nectria
NCBI Description
                   haematococca var. brevicona]
                   28998
Seq. No.
                   184612 1.R1040
Contig ID
5'-most EST
                   fde700876454.h1
                   BLASTX
Method
NCBI GI
                   g3522948
BLAST score
                   357
                   8.0e-34
E value
Match length
                   143
                   54
% identity
                   (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   28999
Seq. No.
                   184628 1.R1040
Contig ID
5'-most EST
                   q5342489
```

```
NCBI GI
                    q2137562
BLAST score
                    130
                    2.0e-17
E value
Match length
                    181
                    35
% identity
                    mouse Dhm1 protein - mouse >gi_1060921_dbj BAA07524
NCBI Description
                    (D38517) Dhml protein [Mus musculus]
Seq. No.
                    29000
                    184629 1.R1040
Contig ID
                    fde700876476.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    g133961
BLAST score
                    311
E value
                    6.0e-29
Match length
                    83
                    70
% identity
                    40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPRESSOR PROTEIN
NCBI Description
                    SUP44) (RP12) (S2E) >gi_70888_pir__R3BYS2 ribosomal protein
                    S2.e - yeast (Saccharomyces cerevisiae) >gi 172793 (M59375)
                    ribosomal protein S4 [Saccharomyces cerevisiae]
                    >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w
[Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_
                    (X94106) SUP44 [Saccharomyces cerevisiae]
Seq. No.
                    29001
                    184665 1.R1040
Contig ID
5'-most EST
                    a56063\overline{0}2
                    BLASTX
Method
                    q1705651
NCBI GI
BLAST score
                    444
                    6.0e-44
E value
                    141
Match length
% identity
                    61
                    20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)
NCBI Description
                    (CBP20) >gi_984139_emb_CAA58962_ (X84157) subunit of the dimeric cap binding complex CBC [Homo sapiens]
                    >gi 1582342 prf 2118330A cap-binding protein [Homo
                    sapiens]
                    29002
Seq. No.
                    184684 1.R1040
Contig ID
5'-most EST
                    jC-gmst02400049d06a1
                    29003
Seq. No.
                    184705 1.R1040
Contig ID
5'-most EST
                    fde700876592.hl
Seq. No.
                    29004
                    184708 1.R1040
Contig ID
                    fde700877110.hl
5'-most EST
Method
                    BLASTX
                    q3876337
NCBI GI
BLAST score
                    270
                    4.0e-24
E value
                    72
Match length
                    69
% identity
```

```
(Z79754) similar to nucleoside diphosphate kinase; cDNA EST
NCBI Description
                   CEMSG50F comes from this gene; cDNA EST EMBL:D71761 comes
                   from this gene; cDNA EST EMBL: D72901 comes from this gene;
                   cDNA EST EMBL: D72956 comes from this gene; cDNA ES
Seq. No.
                   29005
                   184713 1.R1040
Contig ID
5'-most EST
                   fde700876604.hl
                   29006
Seq. No.
                  184749 1.R1040
Contig ID
5'-most EST
                   sat701012630.hl
Method
                  BLASTX
NCBI GI
                   q2160692
BLAST score
                   863
E value
                   4.0e-93
Match length
                   193
% identity
NCBI Description
                   (U73527) B' regulatory subunit of PP2A [Arabidopsis
                   thaliana]
                   29007
Seq. No.
Contig ID
                   184792 1.R1040
5'-most EST
                   fde700876732.hl
Method
                  BLASTX
NCBI GI
                  q3025189 ·
BLAST score
                   178
                   3.0e-13
E value
Match length
                   69
% identity
                   57
NCBI Description
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                  >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
                   29008
Seq. No.
Contig ID
                  184804 1.R1040
5'-most EST
                   zsg701119021.hl
Method
                  BLASTX
NCBI GI
                  q2344854
BLAST score
                  161
E value
                  1.0e-10
Match length
                  128
% identity
                  36
                                                                               ٠٠.
                  (Z98756) endopeptidase IV [Mycobacterium leprae]
NCBI Description
                  29009
Seq. No.
Contig ID
                  184808_1.R1040
5'-most EST
                   zsg701118427.h1
Method
                  BLASTX
NCBI GI
                  g2842482
                  183
BLAST score
E value
                  1.0e-13
Match length
                  73
% identity
NCBI Description
                   (AL021749) protein phosphatase 2C-like protein [Arabidopsis
```

thaliana]

```
29010
Seq. No.
                   184816 1.R1040
Contig ID
                   zhf700955674.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2262116
BLAST score
                   247
E value
                   4.0e-21
Match length
                   122
                   43
% identity
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                   29011
Seq. No.
                   184840 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09913.h1
                   29012
Seq. No.
                   184850 1.R1040
Contig ID
5'-most EST
                   fde700877149.hl
                   29013
Seq. No.
                   184856 1.R1040
Contig ID
                   fde700876844.hl
5'-most EST
                   BLASTX
Method
                   g1076334
NCBI GI
                   175
BLAST score
                   6.0e-13
E value
Match length
                   82
% identity
                   48
                   hypothetical protein HYP1 - Arabidopsis thaliana
NCBI Description
                   >gi 499168 emb CAA56145 (X79707) HYP1 [Arabidopsis
                   thaliana]
                   29014
Seq. No.
                   184860 1.R1040
Contig ID
                   fua701041059.hl
5'-most EST
                   29015
Seq. No.
                   184869 1.R1040
Contig ID
                   fde700876880.hl
5'-most EST
                   29016
Seq. No.
                   184876 1.R1040
Contig ID
5'-most EST
                   sat701011851.hl
                   29017
Seq. No.
                   184877 1.R1040
Contig ID
                   dpv701\overline{1}02090.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3355477
                   425
BLAST score
E value
                   3.0e-42
Match length
                   91
                   50
% identity
                   (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
```

thaliana]

29018

Seq. No.

```
184878 1.R1040
Contig ID
                   fde700877003.h1
5'-most EST
                   29019
Seq. No.
                   184902 1.R1040
Contig ID
                   uC-qmflminsoy018h06b1
5'-most EST
Seq. No.
Contig ID
                   184915_1.R1040
5'-most EST
                   uC-gmrominsoy030h02b1
Method
                   BLASTN
NCBI GI
                   q4220643
BLAST score
                   39
                   2.0e-12
E value
Match length
                   200
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD22, complete sequence [Arabidopsis thaliana]
                   29021
Seq. No.
                   184919 1.R1040
Contig ID
                   zzp700836090.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3063455
BLAST score
                   426
E value
                   5.0e-42
                   98
Match length
                   76
% identity
                   (AC003981) F22013.17 [Arabidopsis thaliana]
NCBI Description
                   29022
Seq. No.
                   184969 1.R1040
Contig ID
5'-most EST
                   g5057575
                   29023
Seq. No.
                   185038_1.R1040
Contig ID
5'-most EST
                   fde700877132.h1
Method
                   BLASTX
NCBI GI
                   g1001541
BLAST score
                   160
E value
                   4.0e-11
Match length
                   74
                   41
% identity
                   (D64000) ABC transporter [Synechocystis sp.]
NCBI Description
                   29024
Seq. No.
                   185045 1.R1040
Contig ID
5'-most EST
                   fC-gmst700894694a3
Method
                   BLASTX
NCBI GI
                   g4204303
BLAST score
                   319
                   1.0e-29
E value
Match length
                   73
% identity
                   79
                   (AC003027) lcl prt seq No definition line found
NCBI Description
```

[Arabidopsis thaliana]

NCBI GI

BLAST score

```
29025
Seq. No.
                   185098 1.R1040
Contig ID
5'-most EST
                   hrw701057980.hl
Method
                   BLASTX
NCBI GI
                   g2880047
BLAST score
                   481
E value
                   2.0e-48
Match length
                   132
% identity
                   70
NCBI Description
                   (AC002340) hypothetical protein [Arabidopsis thaliana]
                   29026
Seq. No.
Contig ID
                   185110 1.R1040
5'-most EST
                   jC-gmle01810024e05a1
Method
                   BLASTX
NCBI GI
                   q3928543
BLAST score
                   196
E value
                   8.0e-15
Match length
                   139
% identity
NCBI Description
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   29027
                   185147 1.R1040
Contig ID
5'-most EST
                   fde700877282.h1
Method
                   BLASTX
NCBI GI
                   q3341693
BLAST score
                   163
E value
                   2.0e-11
Match length
                   74
% identity
                   45
NCBI Description
                   (AC003672) unknown protein [Arabidopsis thaliana]
                   29028
Seq. No.
Contig ID
                   185191 1.R1040
5'-most EST
                   leu701156146.hl
                   29029
Seq. No.
Contig ID
                   185202 2.R1040
5'-most EST
                   qsv701\overline{0}47468.h1
Method
                   BLASTX
NCBI GI
                   g3024871
BLAST score
                   357
E value
                   4.0e-34
Match length
                   111
% identity
                   57
NCBI Description
                   HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                   >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                   sp.]
                   29030
Seq. No.
Contig ID
                   185205 1.R1040
5'-most EST
                   xzm700763756.h1
Method
                   BLASTX
```

q1707642

348

```
7.0e-33
E value
Match length
                   141
                   52
% identity
                   (Y07748) TMK [Oryza sativa]
NCBI Description
                   29031
Seq. No.
                   185233 1.R1040
Contig ID
                   qsv701\overline{0}53512.h1
5'-most EST
Seq. No.
                   29032
                   185236 1.R1040
Contig ID
                   xzm700763802.h1
5'-most EST
Seq. No.
                   29033
                   185246 1.R1040
Contig ID
                   uC-gmropic112d05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g961450
BLAST score
                   153
E value
                   5.0e-10
Match length
                   69
                   39
% identity
                   (D63879) KIAA0156 gene product is related to Xenopus
NCBI Description
                   nucleolin. [Homo sapiens]
Seq. No.
                   29034
                   185258 1.R1040
Contig ID
5'-most EST
                   fC-qmle7000763827f1
Method
                   BLASTX
NCBI GI
                   g3192042
BLAST score
                   404
E value
                   1.0e-39
Match length
                   117
% identity
NCBI Description
                   (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
                   29035
Seq. No.
                   185315 1.R1040
Contig ID
                   xzm700763896.h1
5'-most EST
                   29036
Seq. No.
                   185318 1.R1040
Contig ID
5'-most EST
                   fC-gmro7000763905f1
                   BLASTX
Method
NCBI GI
                   q3892866
BLAST score
                   173
E value
                   5.0e-12
Match length
                   146
% identity
                   (X56958) ankyrin (brank-2) [Homo sapiens]
NCBI Description
                   29037
Seq. No.
                   185346 1.R1040
Contig ID
                   k11701\overline{2}04634.h1
5'-most EST
                   BLASTX
Method
```

g4539347

104

NCBI GI BLAST score

Contig ID

```
4.0e-11
E value
Match length
                   94
                   43
% identity
                   (AL035539) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
                   29038
Seq. No.
                   185351 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910069d03a1
Method
                   BLASTX
                   q2213602
NCBI GI
                   293
BLAST score
                   2.0e-26
E value
Match length
                   125
                   50
% identity
                   (AC000348) T7N9.22 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29039
                   185366 1.R1040
Contig ID
                   pmv700894654.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3695060
BLAST score
                   162
E value
                   4.0e-86
Match length
                   286
% identity
                   90-
                   Lotus japonicus rac GTPase activating protein 2 mRNA,
NCBI Description
                   partial cds
Seq. No.
                   29040
                   185376 1.R1040
Contig ID
5'-most EST
                   sat701006641.hl
Method
                   BLASTX
NCBI GI
                   g2129956
BLAST score
                   255
E value
                   3.0e-22
Match length
                   74
                   68
% identity
NCBI Description
                   photoassimilate-responsive protein PAR-1c precursor -
                   common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y
                   expressed in sugar-accumulating plants [Nicotiana tabacum]
Seq. No.
                   29041
                   185394 1.R1040
Contig ID
5'-most EST
                   yza700764023.hl
Method
                   BLASTX
NCBI GI
                   q3873408
BLAST score
                   214
E value
                   5.0e-17
Match length
                   138
% identity
                   (L76926) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29042
```

185407 1.R1040

E value

1.0e-49

```
5'-most EST
                   epx701103845.hl.
Method
                   BLASTX
NCBI GI
                   q3063706
BLAST score
                   345
E value
                   2.0e-32
Match length
                   173
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
                   29043
Seq. No.
Contig ID
                   185410 1.R1040
                   pxt700941214.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1491617
BLAST score
                   749
                   1.0e-79
E value
                   193
Match length
                   75
% identity
                  (X99952) peroxidase [Arabidopsis thaliana]
NCBI Description
                   29044
Seq. No.
                   185424_1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}17471.h1
Method
                   BLASTX
NCBI GI
                   g2979555
BLAST score
                   227
E value
                   7.0e-19
                   97
Match length
% identity
                   45
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29045
                   185450 1.R1040
Contig ID
5'-most EST
                   fua701039269.hl
Method
                   BLASTX
NCBI GI
                   g3236246
BLAST score
                   526
                   9.0e-54
E value
                   106
Match length
                   87
% identity
NCBI Description
                   (AC004684) putative expansin protein [Arabidopsis thaliana]
                   29046
Seq. No.
                   185461 1.R1040
Contig ID
5'-most EST
                   zzp700829558.hl
                   29047
Seq. No.
Contig ID
                   185465 1.R1040
5'-most EST
                   zzp700832744.h1
                   29048
Seq. No.
                   185471 1.R1040
Contig ID
                   pmv700889702.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244898
BLAST score
                   492
```

```
146
Match length
% identity
                   63
NCBI Description
                   (Z97338) strong similarity to protein phosphatase 2A
                  regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                  185480 1.R1040
Contig ID
5'-most EST
                  asn701139454.h1
                  29050
Seq. No.
                  185483 1.R1040
Contig ID
5'-most EST
                  zhf700963571.hl
Seq. No.
                  29051
                  185486 1.R1040
Contig ID
                  zzp700829606.hl
5'-most EST
                  BLASTX
Method
                  q2493318
NCBI GI
BLAST score
                  265
E value
                  2.0e-23
                  76
Match length
                  74
% identity
NCBI Description
                  BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963_
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
                  29052
Seq. No.
                  185527 1.R1040
Contig ID
5'-most EST
                  jex700905589.h1
                  29053
Seq. No.
                  185547 1.R1040
Contig ID
5'-most EST
                  zzp700832556.h1
Method
                  BLASTX
                  q1076715
NCBI GI
BLAST score
                  172
E value
                  1.0e-12
March length 57
dentity 53
NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589
                   (L19119) A22 [Hordeum vulgare]
                  29054
Seq. No.
                  185557 1.R1040
Contig ID
5'-most EST
                  jex700\overline{9}03613.h1
Method
                  BLASTX
NCBI GI
                  g1710663
BLAST score
                  392
E value
                  2.0e-38
Match length
                  90
                  77
% identity
                  PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE
NCBI Description
                   (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558_
                   (Z69727) putative DNA-directed RNA polymerase III 130 kd
                  subunit [Schizosaccharomyces pombe]
```

29055

Seq. No.

```
185558 1.R1040
Contig ID
5'-most EST
                  dpv701\overline{1}02174.h1
                  29056
Seq. No.
                  185581_1.R1040
Contig ID
5'-most EST
                  jC-qmf102220073a03a1
Method
                  BLASTX
NCBI GI
                  g2760839
BLAST score
                  241
E value
                   3.0e-20
Match length
                  93
                   53
% identity
NCBI Description
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
Seq. No.
                  29057
                  185604 1.R1040
Contig ID
5'-most EST
                  uC-qmrominsoy177a06b1
                  29058
Seq. No.
Contig ID
                  185612 1.R1040
5'-most EST
                   zzp700829884.h1
Seq. No.
                  29059
Contig ID
                  185627 1.R1040
5'-most EST
                  zzp700834172.hl
                  29060
Seq. No.
                  185660 1.R1040
Contig ID
                  uC-gmrominsoy073c05b1
5'-most EST
Seq. No.
                  29061
                  185661 1.R1040
Contig ID
5'-most EST
                  zzp700833292.h1
Method
                  BLASTX
                  g2317717
NCBI GI
BLAST score
                  250
E value
                  8.0e-22
Match length
                  75
                                              % identity
                  56
NCBI Description
                  (AF012943) RblA [Dictyostelium discoideum]
                  29062
Seq. No.
                  185667 1.R1040
Contig ID
5'-most EST
                  zzp700829991.hl
                  29063
Seq. No.
Contig ID
                  185678_1.R1040
5'-most EST
                  jC-gmro02910048g11d1
Method
                  BLASTX
NCBI GI
                  q3243234
BLAST score
                  162
                  4.0e-11
E value
Match length
                  38
% identity
                  79
NCBI Description
                   (AF071477) isoflavone reductase related protein [Pyrus
```

communis]

5'-most EST

```
Seq. No.
                   29064
                   185679 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}70177.h1
Method
                   BLASTX
NCBI GI
                   q349379
BLAST score
                   404
E value
                   8.0e-40
Match length
                   87
% identity
                   91
NCBI Description
                   (L22847) HAHB-1 [Helianthus annuus]
Seq. No.
                   185683 1.R1040
Contig ID
5'-most EST
                   sat701009239.hl
                   29066
Seq. No.
                   185684 1.R1040
Contig ID
5'-most EST
                   asn701132976.hl
Seq. No.
                   29067
                   185694 1.R1040 -
Contig ID
5'-most EST
                   zzp700830049.h1
Method
                   BLASTX
                   q3688177
NCBI GI
BLAST score
                   479
E value
                   6.0e-48
Match length
                   128
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   29068
                   185754 1.R1040
Contig ID
5'-most EST
                   zzp700830288.h1
                   BLASTX
Method
NCBI GI
                   q4097522
BLAST score
                   586
E value
                   2.0e-60
                   142
Match length
% identity
NCBI Description
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                   ananassa]
Seq. No.
                   29069
                   185765 1.R1040
Contig ID
5'-most EST
                   zzp700830201.h1
Seq. No.
                   29070
                   185786 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910052f11a1
Seq. No.
                   29071
                   185800 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400044h01a1
                   29072
Seq. No.
                   185812 1.R1040
Contig ID
```

zzp700830276.h1

Contig ID

```
29073
Seq. No.
                   185824 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}07490.h2
Method
                   BLASTX
                   g3548806
NCBI GI
                   260
BLAST score
E value
                   3.0e-22
Match length
                   123
% identity
                   39
NCBI Description
                   (AC005313) unknown protein [Arabidopsis thaliana]
                   29074
Seq. No.
                   185884 1.R1040
Contig ID
5'-most EST
                   hrw701060967.hl
                   29075
Seq. No.
                   185901 1.R1040
Contig ID
5'-most EST
                   zzp700830441.h1
                   BLASTX
Method
                   g4309698
NCBI GI
BLAST score
                   244
                   8.0e-21
E value
                   101
Match length
                   55
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   29076
Seq. No.
                   185911 1.R1040
Contig ID
                   zsg701123782.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539301
BLAST score
                   275
                   4.0e-24
E value
Match length
                   111
                   51
% identity
NCBI Description
                   (AL049480) putative mitochondrial protein [Arabidopsis]
                   thaliana]
                   29077
Seq. No.
                   185920 1.R1040
Contig ID
5'-most EST
                   zzp700830472.h1
                   BLASTX
Method
                   g4558678
NCBI GI
BLAST score
                   181
                   8.0e-13
E value
Match length
                   86
                   42
% identity
NCBI Description
                   (AC006586) unknown protein [Arabidopsis thaliana]
                   29078
Seq. No.
                   185928 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68871.h1
                   29079
Seq. No.
```

185971 1.R1040

5'-most EST

```
5'-most EST
                  zzp700830562.h1
                  29080
Seq. No.
                  185976 1.R1040
Contig ID
                  zzp700830758.hl
5'-most EST
                  BLASTX
Method
                  q4567265
NCBI GI
BLAST score
                  141
E value
                  6.0e-20
                  77
Match length
% identity
                   (AC006841) putative kinesin protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  185983 1.R1040
Contig ID
                  fua701039571.hl
5'-most EST
                  29082
Seq. No.
                  185994 1.R1040
Contig ID
5'-most EST
                  uC-gmropic035h11b1
Seq. No.
                  185994 2.R1040
Contig ID
5'-most EST
                  zzp700830606.h1
Seq. No.
                  29084
                  186007 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy246d04b1
Method
                  BLASTX
NCBI GI
                  q3135273
BLAST score
                  308
E value
                   4.0e-28
Match length
                  120
                  53
% identity
NCBI Description
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
                  >gi 4191773 (AC005917) putative WD-40 repeat protein
                   [Arabidopsis thaliana]
Seq. No.
                  29085
                  186011 1.R1040
Contig ID
5'-most EST
                  uC-qmropic102h03b1
Method
                  BLASTX
NCBI GI
                  q3319349
BLAST score
                  246
                   6.0e-21
E value
Match length
                  119
% identity
                   43
                   (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  29086
                  186029 1.R1040
Contig ID
5'-most EST
                   zzp700830656.h1
                  29087
Seq. No.
                  186035 1.R1040
Contig ID
```

zzp700830663.h1

```
29088
Seq. No.
                   186043 1.R1040
Contig ID
5'-most EST
                   q5126618
Method
                   BLASTX
NCBI GI
                   g2832661
BLAST score
                   179
E value
                   5.0e-13
Match length
                   73
% identity
NCBI Description
                   (AL021710) pherophorin - like protein [Arabidopsis
                   thaliana]
                   29089
Seq. No.
                   186051 1.R1040
Contig ID
5'-most EST
                   leu701151237.h1
                   29090
Seq. No.
                   186061 1.R1040
Contig ID
5'-most EST
                   sat701009937.h2
Method
                   BLASTX
NCBI GI
                   g571484
BLAST score
                   378
E value
                   1.0e-36
Match length
                   91
% identity
                   81
                   (U16727) peroxidase precursor [Medicago truncatula] .
NCBI Description
                   29091
Seq. No.
                   186079 1.R1040
Contig ID
5'-most EST
                   zzp700830727.hl
                   29092
Seq. No.
                   186090 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}04872.h1
                   29093
Seq. No.
Contig ID
                   186116_1.R1040
5'-most EST
                   zhf700959735.hl
Method
                   BLASTX
                   g3746060
NCBI GI
BLAST score
                   290
                   5.0e-26
E value
Match length
                   60
% identity
                   (AC005311) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29094
Contig ID
                   186134 1.R1040
5'-most EST
                   zzp700830813.h1
Method
                   BLASTX
                   g2344894
NCBI GI
BLAST score
                   453
E value
                   2.0e-45
Match length
                   98
% identity
                   27
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]
```

```
29095
Seq. No.
                   186146 1.R1040
Contig ID
5'-most EST
                   zzp700830930.h1
Method
                   BLASTX
                   g3004556
NCBI GI
                   390
BLAST score
E value
                   3.0e-38
Match length
                   84
% identity
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   186174 1.R1040
Contig ID
5'-most EST
                   zzp700830882.h1
Method
                   BLASTX
                   g4314391
NCBI GI
BLAST score
                   270
                   5.0e-28
E value
                   88
Match length
% identity
                   71
                   (AC006232) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29097
Seq. No.
                   186180_1.R1040
Contig ID
5'-most EST
                   uC-gmropic120c12b1
                   BLASTN
Method
                   g4220633
NCBI GI
BLAST score
                   52
E value
                   3.0e-20
                   200
Match length
                   81
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K7J8, complete sequence [Arabidopsis thaliana]
                   29098
Seq. No.
                   186181 1.R1040
Contig ID
                   zzp700\overline{8}30892.h1
5'-most EST
                   29099
Seq. No.
                   186194 1.R1040
Contig ID
                   zzp700830922.h1
5'-most EST
                   BLASTX
Method
                   g3080448
NCBI GI
BLAST score
                   212
                   2.0e-17
E value
                  . 61
Match length
                   64
% identity
NCBI Description
                   (AL022605) putative protein [Arabidopsis thaliana]
                   29100
Seq. No.
                   186196 1.R1040
Contig ID
                   zzp700830925.hl
5'-most EST
                   29101
Seq. No.
                   186201 1.R1040
Contig ID
```

zhf700953126.h1

5'-most EST

NCBI GI

```
29102
Seq. No.
                   186206 1.R1040
Contig ID
                   zzp700830940.h1
5'-most EST
Method
                   BLASTX
                   g2827638
NCBI GI
BLAST score
                   166
                   8.0e-12
E value
                   93
Match length
                   43
% identity
                   (AL021636) Cytochrome P450-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   29103
Seq. No.
                   186233 1.R1040
Contig ID
5'-most EST
                   zzp700830985.hl
                   29104
Seq. No.
                   186234 1.R1040
Contig ID
                   zzp700830986.h1
5'-most EST
                   29105
Seq. No.
                   186278 1.R1040
Contig ID
                   gsv701045850.hl
5'-most EST
                   29106
Seq. No.
                   186283 1.R1040
Contig ID
5'-most EST
                   zzp700831073.hl
                   29107
Seq. No.
                   186329 1.R1040
Contig ID
                   jex700\overline{9}09430.h1
5'-most EST
                   29108
Seq. No.
                   186331 1.R1040
Contig ID
                   zzp700831134.hl
5'-most EST
                   29109
Seq. No.
                   186332_1.R1040
Contig ID .
5'-most EST
                   jC-gmro02910001b06d1
Method
                   BLASTX
                   g1652082
NCBI GI
                   199
BLAST score
E value
                   2.0e-15
Match length
                   67
                   58
% identity
                   (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase
NCBI Description
                   [Synechocystis sp.]
                   29110
Seq. No.
                   186382 1.R1040
Contig ID
                   zzp700\overline{8}31205.h1
5'-most EST
                   29111
Seq. No.
                   186398 1.R1040
Contig ID
5'-most EST
                   zzp700831222.h1
Method
                   BLASTX
```

g2736286

```
BLAST score
                   412
                   2.0e-40
E value
Match length
                   84
                   90
% identity
                   (AF031079) isopentenyl diphosphate isomerase I [Camptotheca
NCBI Description
                   acuminata]
Seq. No.
                   29112
                   186407 1.R1040
Contig ID
5'-most EST
                   awf700838333.hl
Method
                   BLASTX
NCBI GI
                   q3411152
BLAST score
                   352
E value
                   3.0e-33
                   95
Match length
% identity
                   69
NCBI Description
                   (AF066050) thymidine kinase [Oryza sativa]
                   29113
Seq. No.
                   186432 1.R1040
Contig ID
5'-most EST
                   zzp700831275.h1
Seq. No.
                   29114
Contig ID
                   186475 1.R1040 ·
                   sat701005501.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3738297
BLAST score
                   143
E value
                   5.0e-09
Match length
                   72
% identity
                   12
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29115
Seq. No.
                   186486 1.R1040
Contig ID
5'-most EST
                   pxt700943302.h1
Method
                   BLASTN
                   g1370200
NCBI GI
BLAST score
                   55
                   3.0e-22
E value
Match length
                   79
% identity
                  L.japonicus mRNA for small GTP-binding protein, RAC2
NCBI Description
                   29116
Seq. No.
                   186503 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}65671.h1
Seq. No.
                   29117
                   186517 1.R1040
Contig ID
                   zzp700831429.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252827
BLAST score
                   403
E value
                   1.0e-39
Match length
                   100
```

75

% identity

Contig ID

```
NCBI Description
                   (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                   29118
                   186518 1.R1040
Contig ID
5'-most EST
                   zzp700831430.h1
Method
                   BLASTN
NCBI GI
                   q4159704
BLAST score
                   35
E value
                   6.0e-10
Match length
                   71
% identity
                   87
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MCB17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   29119
                   186539 1.R1040
Contig ID
5'-most EST
                   zzp700831477.h1
                   29120
Seq. No.
Contig ID
                   186548 1.R1040
5'-most EST
                   zzp700831491.hl
Method
                   BLASTX
NCBI GI
                   g3947735
BLAST score
                   379
E value
                   2.0e-36
                                     Match length
                   119
% identity
                   61
                   (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
                   29121
Seq. No.
Contig ID
                   186556 1.R1040
                   hrw701\overline{0}60646.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252631
BLAST score
                   312
E value
                   1.0e-28
Match length
                   115
% identity
                   61
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29122
Seq. No.
Contig ID
                   186574 1.R1040
                   zzp700831529.h1
5'-most EST
Method
                   BLASTX
                   g4539321
NCBI GI
BLAST score
                   271
E value
                   8.0e-24
Match length
                   69
% identity
                   70
                   (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29123
Contig ID
                   186584 1.R1040
5'-most EST
                   zzp700831550.h1
                   29124
Seq. No.
```

186656_1.R1040

```
5'-most EST
                  uC-gmropic101e02b1
Method
                  BLASTX
                   g4510401
NCBI GI
                   371
BLAST score
                   1.0e-35
E value
                  85
Match length
                   72
% identity
                   (AC006587) putative general negative regulator of
NCBI Description
                   transcription [Arabidopsis thaliana]
                   29125
Seq. No.
                   186658 1.R1040
Contig ID
                   jC-qmst02400033f02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2529677
BLAST score
                   216
                   2.0e-17
E value
Match length
                   120
% identity
                   (AC002535) kinesin-like protein, heavy chain [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29126
                   186662 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy083d10b1
                   29127
Seq. No.
                   186662 2.R1040
Contig ID
5'-most EST
                   leu701147412.h1
Seq. No.
                   29128
                   186677 1.R1040
Contig ID
5'-most EST
                   gsv701049260.hl
                   29129
Seq. No.
Contig ID
                   186697 1.R1040
5'-most EST
                   zzp700831730.hl
                   29130
Seq. No.
                   186734 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}02390.h1
                   29131
Seq. No.
                   186756 1.R1040
Contig ID
                   zzp700831811.h1
5'-most EST
                   29132
Seq. No.
                   186789 1.R1040
Contig ID
5'-most EST
                   zzp700831860.hl
                   BLASTN
Method
                   g2828183
NCBI GI
                   46
BLAST score
E value
                   8.0e-17
                   82
Match length
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MPL12, complete sequence [Arabidopsis thaliana]

NCBI Description

```
Seq. No.
                   29133
                   186835 1.R1040
Contig ID
                   k11701213194.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3047075
BLAST score
                   214
E value
                   1.0e-17
Match length
                   72
% identity
                   53
                   (AF058914) contains similarity to SRF-type transcription
NCBI Description
                   factors DNA-binding and dimerization domains (PFam:
                   transcript fact.hmm, score 58.97) [Arabidopsis thaliana]
                   29134
Seq. No.
                   186836 1.R1040
Contig ID
                   fjg700\overline{9}68457.h1
5'-most EST
Seq. No.
                   29135
                   186859 1.R1040
Contig ID
5'-most EST
                   zzp700833807.h1
Seq. No.
                   29136
                   186871 1.R1040
Contig ID
5'-most EST
                   qsv701051432.hl
Seq. No.
                   29137
                   186874 1.R1040
Contig ID
5'-most EST
                   q42846\overline{3}8
Method
                   BLASTX
NCBI GI
                   q4107099
BLAST score
                   393
E value
                   4.0e-38
Match length
                   136
                   57
% identity
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
                                           ; 5
72
                   29138
Seq. No.
                   186887 1.R1040
Contig ID
5'-most EST
                   dpv701102773.h1
                   29139
Seq. No.
                   186901_1.R1040
Contig ID
5'-most EST
                   uC-gmropic064h06b1
Seq. No.
                   29140
Contig ID
                   186931 1.R1040
5'-most EST
                   zzp700832477.h1
Method
                   BLASTX
NCBI GI
                   q2244866
BLAST score
                   193
E value
                   4.0e-15
Match length
                   81
% identity
```

(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.

29151

```
Seq. No.
                   29141
                   186976 1.R1040
Contig ID
                   leu701156322.h1
5'-most EST
Seq. No.
                   29142
Contig ID
                   187004 1.R1040
5'-most EST
                   zzp700832146.h1
Seq. No.
                   29143
                   187007 1.R1040
Contig ID
                   sat701009295.hl
5'-most EST
Seq. No.
                   29144
                   187013 1.R1040
Contig ID
5'-most EST
                   zzp700832162.hl
                   29145
Seq. No.
                   187021 1.R1040
Contig ID
5'-most EST
                   pmv700892075.hl
Seq. No.
                   29146
                   187041_1.R1040
Contig ID
5'-most EST
                   uC-gmropic041d04b1
Method
                   BLASTX
                  g4335751 🛒 .
NCBI GI
BLAST score
                   480
E value
                   2.0e-48
Match length
                   102
% identity
                   83
NCBI Description
                   (AC006284) putative methyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   29147
Contig ID
                   187079 1.R1040
5'-most EST
                   zzp700832247.h1
                   29148
Seq. No.
                   187092 1.R1040
Contig ID
5'-most EST
                   iC-qmf102220072h05a1
Method
                   BLASTN
NCBI GI
                   q914860
BLAST score
                   178
E value
                   2.0e-95
Match length
                   404
% identity
NCBI Description
                  M. varia mRNA for mitotic cyclin
Seq. No.
                   29149
                   187100 1.R1040
Contig ID
5'-most EST
                  bth700849008.h1
Seq. No.
                   29150
                   187105 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy123e01b1
```

```
187108 1.R1040
Contig ID
                   fua701040291.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q416922
BLAST score
                   337
                   1.0e-31
E value
Match length
                   81
% identity
                   78
NCBI Description
                   DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
                   (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir JQ1599 dUTP
                   pyrophosphatase (EC 3.6.1.23) - tomato
                   >gi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase,
                   dUTPase, PT8 (EC 3.6.1.23) [tomatoes, Tint Tim cultivar
                   LA154, Peptide, 169 aa] [Lycopersicon esculentum]
Seq. No.
                   29152
                   187133 1.R1040
Contig ID
5'-most EST
                   .g5688128
Seq. No.
                   29153
                   187134 1.R1040
Contig ID
5'-most EST
                   zzp700832368.hl
Method
                   BLASTX
NCBI GI
                   g1091678
BLAST score
                   144
E value
                   3.0e-09
Match length
                   100
% identity
                   33
NCBI Description
                   activator-like transposable element [Pennisetum glaucum]
Seq. No.
                   29154
                   187135 1.R1040
Contig ID
5'-most EST
                   g4313562
Method
                   BLASTN
NCBI GI
                   g4115370
BLAST score
                   55
E value
                   9.0e-22
Match length
                  127
% identity
                   86
                   Arabidopsis thaliana chromosome II BAC F27D4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   29155
Seq. No.
                   187155 1.R1040
Contig ID
                   k11701\overline{2}06753.h1
5'-most EST
Seq. No.
                   29156
                   187161 1.R1040
Contig ID
5'-most EST
                   zzp700832411.h1
Method
                   BLASTX
NCBI GI
                   q4580462
BLAST score
                   231
E value
                   3.0e-19
Match length
                   127
% identity
                   46
```

NCBI Description (AC006081) hypothetical protein [Arabidopsis thaliana]

Contig ID 5'-most EST

```
29157
Seq. No.
                   187176 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810090c06d1
Method
                   BLASTX
NCBI GI
                   g2388585
BLAST score
                   262
E value
                   1.0e-22
Match length
                   109
% identity
                   56
NCBI Description
                   (AC000098) Similar to Caenorhabditis unknown protein
                   T03F1.1 (gb_U88169). [Arabidopsis thaliana]
                   29158
Seq. No.
Contig ID
                  187188 1.R1040
5'-most EST
                   jC-gmst02400047e04d1
                   BLASTX
Method
NCBI GI
                   q4539324
BLAST score
                   294
E value
                   1.0e-26
Match length
                   140
                   50
% identity
NCBI Description
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
                   29159
Seq. No.
                   187282 1.R1040
Contiq ID
5'-most EST
                   zzp700832571.hl
                   29160
Seq. No.
                   187287_1.R1040
Contig ID
                   fC-gmro700877049d1
5'-most EST
Method
                   BLASTN
                   g1806139
NCBI GI
BLAST score
                   43
E value
                   9.0e-15
                  151
Match length
% identity
                   89
NCBI Description
                  M.sativa mRNA for cdc2 kinase homologue, cdc2MsC
                   29161
Seq. No.
                   187329 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy140d09b1
                   29162
Seq. No.
                   187335_1.R1040
Contig ID
                  bth700849582.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1922242
BLAST score
                   249
E value
                   2.0e-21
Match length
                  66
% identity
                   76
                  (Y10084) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

4498

29163

187351 1.R1040

zzp700833703.h1



Contig ID 187355 1.R1040 5'-most EST dpv701103408.h1

Seq. No. 29165

Contig ID 187392 1.R1040 5'-most EST zhf700953442.h1

Seq. No. 29166

Contig ID 187411_1.R1040 5'-most EST pmv700892727.h1

Seq. No. 29167

Contig ID 187468_1.R1040

5'-most EST g4290412

Seq. No. 29168

Contig ID 187485_1.R1040 5'-most EST zzp700832828.h1

Seq. No. 29169

Contig ID 187501 1.R1040

5'-most EST jC-gmro02910061d07a1

Seq. No. 29170

Contig ID 187515_1.R1040 5'-most EST zzp700832864.h1

Method BLASTX
NCBI GI g3021270
BLAST score 371
E value 2.0e-35
Match length 122
% identity 59

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No. 29171

Contig ID 187527_1.R1040 5'-most EST zzp700832881.h1

Method BLASTX
NCBI GI g3608495
BLAST score 339
E value 4.0e-32
Match length 82
% identity 82

NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis

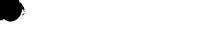
thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid

division protein FtsZ [Arabidopsis thaliana]

Seq. No. 29172

Contig ID 187535_1.R1040 5'-most EST zzp700832890.h1

Method BLASTX
NCBI GI g3335341
BLAST score 204
E value 3.0e-16
Match length 84



% identity NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana] 29173 Seq. No. 187537 1.R1040 Contig ID $asn701\overline{1}35218.h1$ 5'-most EST Seq. No. 29174 187547 1.R1040 Contig ID 5'-most EST uC-gmrominsoy171e09b1 Seq. No. 187594 1.R1040 Contig ID 5'-most EST zzp700833073.h1

29176 Seq. No. 187598 1.R1040 Contig ID 5'-most EST uC-gmrominsoy117g12b1 Method BLASTX NCBI GI g4337174

BLAST score 246 5.0e-21 E value Match length 117 % identity

(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P NCBI Description

homolog (pepP) from Haemophilus influenzae genome

gb_U32764. [Arabidopsis thaliana]

29177 Seq. No. 187602 1.R1040 Contig ID 5'-most EST fua701037621.hl

29178 Seq. No. 187621_1.R1040 Contig ID 5'-most EST uC-gmropic004a03b1

Seq. No. 29179 187622 1.R1040 Contig ID 5'-most EST zzp700833005.h1

29180 Seq. No. 187631 1.R1040 Contig ID sat701014046.hl 5'-most EST

29181 Seq. No. Contig ID 187656 1.R1040 5'-most EST zzp700833048.hl

29182 Seq. No. Contig ID 187712_1.R1040 $hrw701\overline{0}58357.h1$ 5'-most EST

Method BLASTX NCBI GI g3236235 BLAST score 357 3.0e-34 E value Match length 77 % identity 81

NCBI GI

```
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
                   >qi 4056501 (AC005896) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   29183
                   187724 1.R1040
Contig ID
5'-most EST
                   zzp700833130.h1
Seq. No.
                   29184
                   187737 1.R1040
Contig ID
5'-most EST
                   bth700844156.h1
Method
                   BLASTX
NCBI GI
                   q1168719
BLAST score
                   313
E value
                   2.0e-28
Match length
                   108
                   57
% identity
NCBI Description
                   C6.1A PROTEIN >gi_2135176_pir___I38167 gene C6.1A protein -
                   human >gi 36088 emb CAA45917 (X64643) C6.1A [Homo sapiens]
Seq. No.
                   29185
                   187761 1.R1040
Contig ID
                   uC-gmrominsoy057d02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4206210
BLAST score
                   554
E value
                   2.0e-56
Match length
                   232
% identity
                   50
                   (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >gi_4263043_gb_AAD15312_ (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
Seq. No.
                   29186
                   187842_1.R1040
Contig ID
5'-most EST
                   uC-gmropic022c04b1
                   29187
Seq. No.
Contig ID
                   187845_1.R1040
5'-most EST
                   uC-gmrominsoy128h04b1
Method
                   BLASTX
NCBI GI
                   g3250697
BLAST score
                   601
                   2.0e-62
E value
Match length
                  136
% identity
NCBI Description
                   (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  29188
                  187845 2.R1040
Contig ID
5'-most EST
                   fua701039548.hl
Seq. No.
                  29189
Contig ID
                  187849 1.R1040
                  zzp700833293.hl
5'-most EST
Method
                  BLASTN
```

g4580454

```
BLAST score
                   36
E value
                   6.0e-11
Match length
                   88
% identity
                   85
                   Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
                   29190
Seq. No.
Contig ID
                   187853 1.R1040
5'-most EST
                   zhf700960325.h1
Method
                   BLASTX
NCBI GI
                   g3157942
BLAST score
                   149
                   6.0e-10
E value
Match length
                   73
                   49
% identity
                   (AC002131) Similar to style development-specific protein
NCBI Description
                   9612 precursor gb_X55193 and pectate lyase P59 precursor
                   gb_X15499 from Lycopersicon esculentum. [Arabidopsis
                   thaliana]
                   29191
Seq. No.
Contig ID
                   187858 1.R1040
5'-most EST
                   zzp700833309.hl
                   29192
Seq. No.
                   187870 1.R1040
Contig ID
5'-most EST
                   zhf700952319.hl
                   29193
Seq. No.
Contig ID
                   187870 2.R1040
                   jex700\overline{9}08277.h1
5'-most EST
                   29194
Seq. No.
                   187878 1.R1040
Contig ID
5'-most EST
                   zzp700833333.hl
Seq. No.
                   29195
                   187882_1.R1040
Contig ID
5'-most EST
                   zzp700833337.hl
Method
                   BLASTX
NCBI GI
                   q3608263
BLAST score
                   322
E value
                   6.0e-30
Match length
                   82
% identity
NCBI Description
                   (AB017565) Dof zinc finger protein [Arabidopsis thaliana]
                   29196
Seq. No.
                   187898 1.R1040
Contig ID
5'-most EST
                   zzp700833362.hl
                   29197
Seq. No.
                   187904 1.R1040
Contig ID
                   zzp700833369.h1
5'-most EST
```

29198

Seq. No.

5'-most EST

```
187917 1.R1040
Contig ID
5'-most EST
                   zzp700833386.hl
Seq. No.
                   29199
                   187922_1.R1040
Contig ID
5'-most EST
                   uC-gmropic101d01b1
Method
                   BLASTX
NCBI GI
                   q3063449
BLAST score
                   511
E value
                   7.0e-52
Match length
                   137
                   70
% identity
                   (AC003981) F22013.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29200
                   187929 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}03791.h1
                   29201
Seq. No.
Contig ID
                   187955 1.R1040
                   zzp700836295.h1
5'-most EST
Method
                   BLASTN
                   g4432829
NCBI GI
BLAST score
                   33
E value
                   4.0e-09
Match length
                   41
% identity
                   95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T1B3 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   29202
                   187970 1.R1040
Contig ID
5'-most EST
                   zhf700954165.hl
                   BLASTX
Method
                   g3128192
NCBI GI
BLAST score
                   794
E value
                   5.0e-85
Match length
                   190
                   78
% identity
NCBI Description
                   (AC004521) axi 1-like protein [Arabidopsis thaliana]
                   29203
Seq. No.
Contig ID
                   187997 1.R1040
5'-most EST
                   uC-gmrominsoy224g06b1
Seq. No.
                   29204
Contig ID
                   188021 1.R1040
5'-most EST
                   uC-gmropic089h09b1
                   29205
Seq. No.
                   188026 1.R1040
Contig ID
5'-most EST
                   sat701008619.hl
Seq. No.
                   29206
                   188093 1.R1040
Contig ID
```

fC-qmse7000764839f1

```
29207
Seq. No.
                   188105 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400060e10d1
                   29208
Seq. No.
                   188118 1.R1040
Contig ID
                   zzp700833677.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4567279
BLAST score
                   353
E value
                   3.0e-33
Match length
                   142
% identity
                   52
NCBI Description
                   (AC006841) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   29209
                   188119 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}53208.h1
Seq. No.
                   29210
                   188126 1.R1040
Contig ID
5'-most EST
                   pxt700945449.h1
Seq. No.
                   29211
                   188128 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}48757.h1
Method
                   BLASTX
NCBI GI
                   q4538961
BLAST score
                   937
E value
                   1.0e-101
Match length
                   205
% identity
NCBI Description
                   (AL049488) isoleucine-tRNA ligase-like protein (Arabidopsis
                   thaliana]
Seq. No.
                   29212
                   188156 1.R1040
Contig ID
5'-most EST
                   bth700848590.hl
Method
                   BLASTX
NCBI GI
                   q4262224
BLAST score
                   159
E value
                   3.0e-14
Match length
                   67
% identity
                   64
NCBI Description
                   (AC006200) putative amino acid or GABA permease
                   [Arabidopsis thaliana]
Seq. No.
                   29213
                   188172 1.R1040
Contig ID
5'-most EST
                   zzp700833757.hl
Seq. No.
                   29214
                   188183 1.R1040
Contig ID
5'-most EST
                   zzp700833768.hl
```

Match length

```
188190 1.R1040
Contig ID
5'-most EST
                   zzp700833776.h1
Method
                   BLASTX
NCBI GI
                   g3043612
BLAST score
                   275
                   2.0e-24
E value
                   131
Match length
% identity
                   40
                   (AB011116) KIAA0544 protein [Homo sapiens]
NCBI Description
Seq. No.
                   29216
                   188204 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy158c08b1
                   29217
Seq. No.
                   188204 3.R1040
Contig ID
                   pmv700890839.h1
5'-most EST
Seq. No.
                   29218
                   188211 1.R1040
Contig ID
5'-most EST
                   zzp700833804.hl
                   BLASTX
Method
NCBI GI
                   q3377941
BLAST score
                   194
E value
                   8.0e-15
Match length
                   82
% identity
NCBI Description
                   (AL021960) putative protein (fragment) [Arabidopsis
                   thaliana]
Seq. No.
                   29219
                   188231 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}50952.h1
                   BLASTX
Method
NCBI GI
                   q4455371
BLAST score
                   324
E value . .
                   2.0e-30
Match length
                   90
                   70
% identity
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   188240 1.R1040
Contig ID
5'-most EST
                   zzp700833839.h1
                   29221
Seq. No.
                   188247 1.R1040
Contig ID
5'-most EST
                   jsh701064965.hl
                   29222
Seq. No.
                   188248 1.R1040
Contig ID
5'-most EST
                   zzp700833848.h1
Method
                   BLASTX
NCBI GI
                   g3482979
BLAST score
                   332
E value
                   6.0e-31
```

Method

BLASTX

```
% identity
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4567258 gb AAD23672.1 AC007070 21 (AC007070)
                   hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29223
                   188249 1.R1040
Contig ID
5'-most EST
                   bth700848866.h1
Method
                   BLASTX
NCBI GI
                   q1076486
BLAST score
                   231
                   1.0e-19
E value
                   74
Match length
% identity
                   64
                   cim1 protein - soybean >qi 555616 (U03860) cytokinin
NCBI Description
                   induced message [Glycine max]
Seq. No.
                   29224
Contig ID
                   188280 1.R1040
5'-most EST
                   jC-qmle01810045f07a1
Method
                   BLASTX
NCBI GI
                   q3152566
BLAST score
                   147
E value
                   2.0e-09
Match length
                   109
% identity
NCBI Description
                   (AC002986) Similar to hypothetical protein YLR002c,
                   gb Z7314 from S. cerevisiae. [Arabidopsis thaliana]
                   29225
Seq. No.
                   188281 1.R1040
Contig ID
5'-most EST
                   zzp700833886.hl
                   29226
Seq. No.
                   188285 1.R1040
Contig ID
5'-most EST
                   zhf700957450.h1
Method
                   BLASTN
NCBI GI
                   q3894098
BLAST score
                   213
E value
                   1.0e-116
Match length
                   388
% identity
                   Pisum sativum mRNA for protein encoded by MCM3 gene,
NCBI Description
                   partial
                   29227
Seq. No.
Contig ID
                   188296 1.R1040
5'-most EST
                   pmv700891237.hl
Seq. No.
                   29228
Contig ID
                   188329 1.R1040
5'-most EST
                   k11701\overline{2}13764.h1
                   29229
Seq. No.
                   188334 1.R1040
Contig ID
5'-most EST
                   zzp700833950.h1
```

Contig ID

```
q129021
NCBI GI
BLAST score
                   266
E value
                   2.0e-23
Match length
                   109
% identity
                   51
NCBI Description
                   SPOOB-ASSOCIATED GTP-BINDING PROTEIN >gi_98326_pir__B32804
                   GTP-binding protein, spo0B 3'-region - Bacillus subtilis
                   >gi_508979 (M24537) GTP-binding protein [Bacillus subtilis]
                   >gi_2635257_emb_CAB14752_ (Z99118) GTPase activity
                   [Bacillus subtilis]
Seq. No.
                   29230
                   188350 1.R1040
Contig ID
5'-most EST
                   zzp700833967.hl
Method
                   BLASTX
NCBI GI
                   g2642433
BLAST score
                   230
E value
                   2.0e-19
Match length
                   83
% identity
NCBI Description
                   (AC002391) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   29231
                   188397 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}04442.h1
Method
                   BLASTX
NCBI GI
                   a3941448
BLAST score
                   423
E value
                   5.0e-42
Match length
                   87
% identity
NCBI Description
                   (AF062878) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   29232
Contig ID
                   188403 1.R1040
5'-most EST
                   fua701\overline{0}37879.h1
Method
                   BLASTN
NCBI GI
                   a2739003
BLAST score
                   132
E value
                   4.0e-68
Match length
                   272
% identity
                   Glycine max cytochrome P450 monooxygenase CYP82Clp
NCBI Description
                   (CYP82C1) mRNA, complete cds
Seq. No.
                   29233
                   188407 1.R1040
Contig ID
5'-most EST
                   zzp700834038.hl
                   29234
Seq. No.
Contig ID
                   188414 1.R1040
5'-most EST
                   zzp700834045.hl
                   29235
Seq. No.
```

188430_1.R1040

```
jex700907604.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3881761
BLAST score
                    158
                    2.0e-10
E value
                    123
Match length
% identity
                    35
NCBI Description
                    (237093) alternative splicing in ZK669.1a; cDNA EST
                    EMBL: D36754 comes from this gene [Caenorhabditis elegans]
                    >gi_3881779_emb_CAA86848_ (Z46812) alternative splicing in ZK669.1a; cDNA EST EMBL:D36754 comes from this gene
                    [Caenorhabditis elegans]
Seq. No.
                    29236
                    188447 1.R1040
Contig ID
5'-most EST
                    fC-gmse700646582g1
Seq. No.
                    188469 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}56189.h1
                    29238
Seq. No.
Contig ID
                    188509 1.R1040
5'-most EST
                    zzp700834153.hl
Seq. No.
                    29239
                    188517 1.R1040
Contig ID
5'-most EST
                    uC-qmrominsoy035f10b1
                    29240
Seq. No.
Contig ID
                    188542 1.R1040
5'-most EST
                    zhf700954428.hl
Method
                    BLASTX
NCBI GI
                    g4510339
BLAST score
                    251
                                                                    100
E value
                    1.0e-21
Match length
                    75
% identity
                    (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    29241
                    188548 1.R1040
Contig ID
5'-most EST
                    pxt700946279.hl
Seq. No.
                    29242
Contig ID
                    188568_1.R1040
5'-most EST
                    uC-gmflminsoy075h06b1
Method
                    BLASTX
NCBI GI
                    q2224695
BLAST score
                    552
                    9.0e-57
E value
Match length
                    150
% identity
                    (AB002375) KIAA0377 [Homo sapiens]
NCBI Description
```

```
Contig ID
                  188579 1.R1040
5'-most EST
                  uC-gmrominsoy260h06b1
Method
                  BLASTX
NCBI GI
                  g3360291
BLAST score
                  314
E value
                  8.0e-29
Match length
                  77
% identity
                  44 '
                   (AF023165) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  2 [Zea mays]
                  29244
Seq. No.
                  188584 1.R1040
Contig ID
5'-most EST
                  zzp700834242.hl
Seq. No.
                  29245
                  188606 1.R1040
Contig ID
5'-most EST
                  zzp700834266.h1
Method
                  BLASTX
NCBI GI
                  g4039155
BLAST score
                  202
E value
                  2.0e-15
Match length
                  121
% identity
                  31
NCBI Description
                   (AF104258) putative copper-inducible 35.6 kDa protein
                   [Festuca rubra]
                  29246
Seq. No.
                  188614 1.R1040
Contig ID
5'-most EST
                  zzp700834277.h1
                  29247
Seq. No.
                  188625 1.R1040
Contig ID
5'-most EST
                  zzp700834289.h1
Method
                  BLASTX
NCBI GI
                  g1491931
BLAST score
                  572
E value
                   4.0e-59
                  147
Match length
% identity
                  76
NCBI Description
                   (U52078) kinesin-like protein [Nicotiana tabacum]
                  29248
Seq. No.
                  188640 1.R1040
Contig ID
5'-most EST
                  zzp700834310.hl
Seq. No.
                  29249
                  188658 1.R1040
Contig ID
5'-most EST
                  fua701037533.h1
Method
                  BLASTX
NCBI GI
                  q2262099
BLAST score
                  173
E value
                  1.0e-12
Match length
                  82
% identity
                  44
```

NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]

```
Seq. No.
                   29250
Contig ID
                   188663 1.R1040
5'-most EST
                   uC-qmflminsoy022f09b1
Method
                   BLASTX
                   g4049353
NCBI GI
BLAST score
                   340
E value
                   3.0e-37
Match length
                   162
% identity
                   47
NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   188676 1.R1040
Contig ID
5'-most EST
                   kl1701206281.h1
                   29252
Seq. No.
                   188695 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}02629.h1
Seq. No.
                   29253
                   188750 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}70358.h1
Seq. No.
                   29254
                   188751 1.R1040
Contig ID
                   dpv701\overline{1}01342.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3724087
BLAST score
                   392
                   5.0e-38
E value
Match length
                   115
% identity
                   66
NCBI Description
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
                   [Catharanthus roseus]
Seq. No.
                   29255
Contig ID
                   188751_2.R1040
5'-most EST
                   jC-gmro02910006h07a1
Method
                   BLASTX
                   g3724087
NCBI GI
BLAST score
                   235
E value
                   1.0e-19
Match length
                   89
% identity
NCBI Description
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
                   [Catharanthus roseus]
Seq. No.
                   29256
Contig ID
                   188761 1.R1040
5'-most EST
                   epx701106429.hl
                   29257
Seq. No.
Contig ID
                   188793 1.R1040
5'-most EST
                   zzp700834573.hl
Method
                   BLASTX
                   q2347188
NCBI GI
                   187
BLAST score
```

Method

BLASTX

```
2.0e-14
E value
Match length
                   53
% identity
                   (AC002338) laccase isolog [Arabidopsis thaliana]
NCBI Description
                  >gi 3150401 (AC004165) putative laccase [Arabidopsis
                  thaliana]
Seq. No.
                   29258
                   188798 1.R1040
Contig ID
5'-most EST
                   uC-gmropic109g12b1
Method
                  BLASTX
NCBI GI
                   q3790593
BLAST score
                   286
E value
                   2.0e-25
Match length
                   92
% identity
                   59
                   (AF079185) RING-H2 finger protein RHYla [Arabidopsis
NCBI Description
                   thaliana]
                   29259
Seq. No.
                   188804 1.R1040
Contig ID
5'-most EST
                   zzp700834584.h1
Seq. No.
                   29260
Contig ID
                   188817_1.R1040
5'-most EST
                   uC-gmropic116h02b1
Method
                  BLASTX
NCBI GI
                   q3080439
BLAST score
                   200
E value
                   1.0e-15
Match length
                   75
% identity
NCBI Description
                   (AL022605) putative protein [Arabidopsis thaliana]
                   29261
Seq. No.
Contig ID
                   188843 1.R1040
5'-most EST
                   zzp700834638.h1
                                            Method
                  BLASTX
NCBI GI
                  q2632252
BLAST score
                  260
E value
                   1.0e-22
Match length
                   125
% identity
NCBI Description
                   (Y12464) serine/threonine kinase [Sorghum bicolor]
                   29262
Seq. No.
Contig ID
                   188896 1.R1040
5'-most EST
                  pmv700889915.h1
                  29263
Seq. No.
Contig ID
                  188898 1.R1040
5'-most EST
                   zsq701\overline{1}20708.h1
                  29264
Seq. No.
                  188899 1.R1040
Contig ID
5'-most EST
                  k11701\overline{2}05278.h1
```

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```
NCBI GI
                      g1871158
BLAST score ·
                      170
E value
                      3.0e-12
                      62
Match length
% identity
                      50
                      (U52364) SMCY [Equus caballus]
NCBI Description
                      29265
Seq. No.
                      188951 1.R1040
Contig ID
5'-most EST
                      zzp700834840.h1
Seq. No.
                      188952 1.R1040
Contig ID
5'-most EST
                      jC-gmf102220070g01d1
Method
                      BLASTX
NCBI GI
                      q3913437
BLAST score
                      479
E value
                      4.0e-48
Match length
                      111
% identity
                      PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                      \label{eq:helicase} \begin{array}{lll} \texttt{HELICASE} > & \texttt{gi\_1402875\_emb\_CAA66825\_} & \texttt{(X98130)} & \texttt{RNA helicase} \\ \texttt{[Arabidopsis thaliana]} > & \texttt{gi\_1495271\_emb\_CAA66613\_} & \texttt{(X97970)} \\ \end{array}
                      RNA helicase [Arabidopsis thaliana]
                      29267
Seq. No.
                      189011 1.R1040
Contig ID
5'-most EST
                      jC-gmle01810094a04d1
                      29268
Seq. No.
Contig ID
                      189012 1.R1040
                      uC-gmrominsoy283h11b1
5'-most EST
Method
                      BLASTX
                      g3249105
NCBI GI
BLAST score
                      191
E value
                      2.0e-27
Match length
                      108
% identity
                      (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                      (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
                      29269
Seq. No.
                      189019 1.R1040
Contig ID
                      sat701\overline{0}03223.h1
5'-most EST
Method
                      BLASTX
                      g3834318
NCBI GI
BLAST score
                      149
E value
                      1.0e-09
Match length
                      92
% identity
                      35
                      (AC005679) Similar to gi_2244754 heat shock transcription
NCBI Description
                      factor HSF30 homolog from Arabidopsis thaliana chromosome 4
                      contig gb Z97335. [Arabidopsis thaliana]
                      29270
Seq. No.
                      189019 2.R1040
Contig ID
```

kl1701213812.hl

5'-most EST

5'-most EST

```
Seq. No.
                    29271
                    189024 1.R1040
 Contig ID
                    zzp700\overline{8}34874.h1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g4567279
 BLAST score
                    455
 E value
                    2.0e-45
 Match length
                    140
 % identity
                    63
                    (AC006841) putative serine/threonine protein kinase
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    29272
                    189062 1.R1040
 Contig ID
 5'-most EST
                    jC-qmf102220064q02a1
 Seq. No.
                    189077 1.R1040
 Contig ID
 5'-most EST
                    zzp700834944.h1
 Seq. No.
                    29274
                    189082 1.R1040
 Contig ID
 5'-most EST
                    zzp700834949.h1
 Method
                    BLASTX
 NCBI GI
                    q119640
 BLAST score
                    163
 E value
                    2.0e-11
 Match length
                    74
                    42
 % identity
 NCBI Description
                    1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
                    E8) >gi_82109_pir__S01642 ripening protein E8 - tomato
                    >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
                    esculentum]
 Seq. No.
                    29275
                    189091 1.R1040
 Contig ID
5'-most EST
                    jC-qmst02400055c07a1
                    29276
 Seq. No.
 Contig ID
                    189100 1.R1040
                    uC-gmropic022b04b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q1854443
 BLAST score
                    585
 E value
                    2.0e-60
 Match length
                    132
 % identity
 NCBI Description
                    (D83970) CPRD8 protein [Vigna unguiculata]
 Seq. No.
                    29277
                    189103 1.R1040
 Contig ID
 5'-most EST
                    zzp700834976.h1
 Seq. No.
                    29278
 Contig ID
                    189120 1.R1040
```

jC-gmle01810012a03a1

BLAST score

```
Seq. No.
                   29279
                   189126 1.R1040
Contig ID
                   jC-gmle01810004e12d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4538987
BLAST score
                   182
E value
                   2.0e-13
Match length
                   47
% identity
                   68
                   (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
NCBI Description
                   29280
Seq. No.
                   189173 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}06401.h1
                   29281
Seq. No.
                   189202 1.R1040
Contig ID
5'-most EST
                   q43974\overline{3}0
Seq. No.
                   29282
Contig ID
                   189207 1.R1040
5'-most EST
                   zzp700835112.h1
Seq. No.
                   29283
                   189235 1.R1040
Contig ID
5'-most EST
                   zzp700835146.h1
                   29284
Seq. No.
                   189248 1.R1040
Contig ID
5'-most EST
                   zzp700835167.h1
                   BLASTX
Method
NCBI GI
                   q3402704
BLAST score
                   177
E value
                   8.0e-13
Match length
                   83
% identity
                   41
NCBI Description
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
                   29285
Seq. No.
Contig ID
                   189279 1.R1040
5'-most EST
                   q42925\overline{4}1
Method
                   BLASTX
NCBI GI
                   g559237
BLAST score
                   351
                   2.0e-33
E value
Match length
                   110
% identity
NCBI Description
                   (L36982) tyrosine-rich hydroxyproline-rich glycoprotein
                    [Petroselinum crispum]
                   29286
Seq. No.
Contig ID
                   189286 1.R1040
5'-most EST
                   zzp700835214.h1
                   BLASTX
Method
                   q1170626
NCBI GI
```

```
8.0e-45
E value
Match length
                   103
                   84
% identity
                   CALCIUM/CALMODULIN-DEPENDENT SERINE/THREONINE PROTEIN
NCBI Description
                   KINASE >gi 478408 pir JQ2251 calcium/calmodulin-binding
                   protein kinase - apple tree >gi_311320_emb_CAA78961_(Z17313) calcium/calmodulin-dependent serine/threonine
                   protein kinase [Malus domestica] >gi 984160_emb_CAA86286_
                   (Z38126) calmodulin-binding protein kinase [Malus
                   domestica]
                   29287
Seq. No.
                   189295 1.R1040
Contig ID
5'-most EST
                   zzp700835225.h1
Method
                   BLASTX
NCBI GI
                   g4432860
BLAST score
                   166
                   3.0e-11
E value
Match length
                   120
% identity
                   8
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   29288
                   189325 1.R1040
Contig ID
5'-most EST
                   zzp700835263.h1
                   29289
Seq. No.
                   189344 1.R1040
Contig ID
5'-most EST
                   zzp700835285.h1
                   29290
Seq. No.
                   189349 1.R1040
Contig ID
5'-most EST
                   uC-gmropic074c08b1
Seq. No.
                   189375 1.R1040
Contig ID
5'-most EST
                   zzp700835330.h1
                   29292
Seq. No.
Contig ID
                   189382 1.R1040
5'-most EST
                   dpv701098653.h1
                   29293
Seq. No.
                   189395 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810069h03d1
Seq. No.
                   29294
                   189399 1.R1040
Contig ID
5'-most EST
                   zzp700835359.h1
Method
                   BLASTX
NCBI GI
                   q2829912
BLAST score
                   308
E value
                   2.0e-28
Match length
                   72
% identity
```

NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis

E value

Match length

```
thaliana]
Seq. No.
                   29295
                   189406 1.R1040
Contig ID
5'-most EST
                   zzp700835367.h1
                   BLASTX
Method
NCBI GI
                   q4510344
BLAST score
                   210
E value
                   9.0e-17
Match length
                   50
% identity
                   78
NCBI Description
                   (AC006921) hypothetical protein [Arabidopsis thaliana]
                   29296
Seq. No.
Contig ID
                   189432 1.R1040
5'-most EST
                   jC-qmst02400071a12a1
                   BLASTX
Method
                   g3641845
NCBI GI
BLAST score
                   172
E value
                   4.0e-12
Match length
                   74
% identity
                   49
NCBI Description
                   (AJ223358) stelar K+ outward rectifying channel
                   [Arabidopsis thaliana]
                   29297
Seq. No.
                   189460 1.R1040
Contig ID
5'-most EST
                   asj700967492.h1
                   29298
Seq. No.
Contig ID
                   189481 1.R1040
5'-most EST
                   zzp700835461.h1
Method
                   BLASTX
                   g2335096
NCBI GI
BLAST score
                   164
E value
                   8.0e-12
Match length
                   55
% identity
                   (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29299
Seq. No.
Contig ID
                   189519 1.R1040
5'-most EST
                   zhf700\overline{9}61719.h1
                   29300
Seq. No.
                   189532_1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}01315.h1
Method
                   BLASTX
                   g3023519
NCBI GI
BLAST score
                   210
```

% identity ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT NCBI Description

7.0e-29

113

58

(ENDOPEPTIDASE CLP) >gi_2384690 (AF013216) proteosome major

subunit [Myxococcus xanthus]

Contig ID

```
29301
Seq. No.
                   189548 1.R1040
Contig ID
5'-most EST
                   uC-gmropic022a06b1
                   29302
Seq. No.
                   189557 1.R1040
Contig ID
5'-most EST
                   g5175508
                   29303
Seq. No.
                   189565 1.R1040
Contig ID
                   jC-gmle01810005b06a1
5'-most_EST
Seq. No.
                   29304
                   189575 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810080a08d1
                   29305
Seq. No.
                   189589 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}03654.h1
                   29306
Seq. No.
                   189638 1.R1040
Contig ID
5'-most EST
                   zzp700835668.h1
Seq. No.
                   29307
                   189641 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy219d04b1
                   29308
Seq. No.
Contig ID
                   189643 1.R1040
5'-most EST
                   zzp700835673.h1
Seq. No.
                   29309
                   189650 1.R1040
Contig ID
5'-most EST
                   uC-gmropic056e01b1
Seq. No.
                   29310
                   189653 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400031c10a1
Method
                   BLASTX
NCBI GI
                   g4567304
BLAST score
                   583
E value
                   6.0e-60
Match length
                   238
% identity
                   53
NCBI Description
                   (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                   189670 1.R1040
Contig ID
5'-most EST
                   zzp700835712.h1
Seq. No.
                   29312
                   189678 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810010g04a1
Seq. No.
```

189725 1.R1040

BLAST score

E value

542 2.0e-55

```
zsg701125908.h1
5'-most EST
Seq. No.
                  29314
                  189729 1.R1040
Contig ID
                   fC-gmse700854605a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3482919
BLAST score
                   657
E value
                   5.0e-69.
Match length
                   135
% identity
                  87
                   (AC003970) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  29315
Seq. No.
                  189748 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910024g04a1
Method
                  BLASTX
NCBI GI
                  q3461845
BLAST score
                   460
E value
                   9.0e-46
Match length
                   163
                   59
% identity
                   (AC005315) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29316
Seq. No.
                  189748 2.R1040
Contig ID
                  bth700848410.h1
5'-most EST
                  29317
Seq. No.
                  189775 1.R1040
Contig ID
5'-most EST
                   zzp700835838.h1
Method
                  BLASTX
                  g3153889
NCBI GI
BLAST score
                   513
E value
                   4.0e-52
Match length
                  118
% identity
                  81
                   (AF065444) root iron transporter protein [Pisum sativum]
NCBI Description
Seq. No.
                   29318
                  189803 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220079b06a1
Method
                  BLASTX
                  g4510427
NCBI GI
                   232
BLAST score
                  2.0e-19
E value
Match length
                  124
% identity
                   (AC006929) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29319
Seq. No.
                  189857 1.R1040
Contig ID
5'-most EST
                  pmv700889134.h1
Method
                  BLASTX
NCBI GI
                  g3021355
```

29327

```
Match length
                  133
                   78
% identity
                   (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   29320
Seq. No.
                   189888 1.R1040
Contig ID
5'-most EST
                   zzp700835984.h1
Method
                   BLASTX
NCBI GI
                   q3395439
BLAST score
                   191
                   1.0e-14
E value
Match length
                   94
% identity
                   41
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29321
Seq. No.
                   189917_1.R1040
Contig ID
5'-most EST
                   zzp700836026.h1
                   29322
Seq. No.
                   189936 1.R1040
Contig ID
                   zzp700836048.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3281849
BLAST score
                   830
E value
                   4.0e-89
Match length
                   193
% identity
                   79
                   (AL031004) methyltransferase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   29323
Seq. No.
                   189945 1.R1040
Contig ID
5'-most EST
                   zzp700836163.hl
                   29324
Seq. No.
                   189953 1.R1040
Contig ID
                   sat701\overline{0}04288.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1420936
BLAST score
                   293
E value
                   1.0e-26
Match length
                   91
                   66
% identity
NCBI Description
                   (U61396) Vigna unguiculata aspartic proteinase mRNA,
                   complete cds. [Vigna unguiculata]
                   29325
Seq. No.
                   189959 1.R1040
Contig ID
5'-most EST
                   zzp700836078.hl
                   29326
Seq. No.
                   190014 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810004e05a1
```

\$1.00 P

Match length

```
190037 1.R1040
Contig ID
                   crh700\overline{8}55395.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2688822
BLAST score
                   518
                   2.0e-52
E value
                   132
Match length
% identity
                   73
NCBI Description
                   (U93272) pyrophosphate-dependent phosphofructo-1-kinase
                   [Prunus armeniaca]
Seq. No.
                   29328
                   190066 1.R1040
Contig ID
5'-most EST
                   zzp700836223.h1
Method
                   BLASTX
NCBI GI
                   g4056403
BLAST score
                   191
E value
                   9.0e-15
Match length
                   72
% identity
                   62
NCBI Description
                   (AD001673) lipoxygenase [Persea americana]
Seq. No.
                   29329
Contig ID
                   190069 1.R1040
5'-most EST
                   zzp700836236.hl
Method
                   BLASTX
                   q3402675
NCBI GI
BLAST score
                   248
                   8.0e-21
E value
Match length
                   137
% identity
                   40
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29330
Seq. No.
                   190078 1.R1040
Contig ID
5'-most EST
                   zzp700836239.h1
Seq. No.
                   29331
                   190081 1.R1040
Contig ID
5'-most EST
                   zzp700836243.h1
Seq. No.
                   29332
                   190088 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy028d10b1
                   29333
Seq. No.
Contig ID
                   190214_1.R1040
5'-most EST
                   uC-gmrominsoy099e05b1
Seq. No.
                   29334
                   190220 1.R1040
Contig ID
                   sat701002720.h2
5'-most EST
                   BLASTX
Method
                   g3819699
NCBI GI
                   431
BLAST score
                   2.0e-42
E value
```

Match length

```
% identity
                   (AJ009609) BnMAP4K alpha2 [Brassica napus]
NCBI Description
                   29335
Seq. No.
                   190226_1.R1040
Contig ID
5'-most EST
                   g4301764
Method
                   BLASTX
NCBI GI
                   q4091080
BLAST score
                   224
                   2.0e-18
E value
                   75
Match length
                   59
% identity
NCBI Description
                   (AF045571) nucleic acid binding protein [Oryza sativa]
                   29336
Seq. No.
                   190237 1.R1040
Contig ID
                   sat701\overline{0}02744.h2
5'-most EST
Seq. No.
                   29337
                   190244 1.R1040
Contig ID
                   sat701002754.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244940
BLAST score
                   329
E value
                   2.0e-30
Match length
                   128
% identity
                   61
NCBI Description
                   (297339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29338
                   190246 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800035d05a1
Seq. No.
Contig ID
                   190246 2.R1040
5'-most EST
                   asn701133567.h2
                   29340
Seq. No.
                   190258 1.R1040
Contig ID
5'-most EST
                   gsv701053458.hl
Seq. No.
                   29341
                   190303 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}02823.h1
                   29342
Seq. No.
Contig ID
                   190327 1.R1040
5'-most EST
                   yz1700967050.h1
                   29343
Seq. No.
                   190344_1.R1040
Contig ID
5'-most EST
                   uC-gmropic023b02b1
Method
                   BLASTX
NCBI GI
                   g2809253
BLAST score
                   228
E value
                   1.0e-18
```

Contig ID

```
% identity
NCBI Description
                   (AC002560) F21B7.22 [Arabidopsis thaliana]
                  29344
Seq. No.
                  190395 1.R1040
Contig ID
5'-most EST
                  gsv701050433.hl
Method
                  BLASTX
NCBI GI
                  g1532167
BLAST score
                  192
E value
                   2.0e-14
Match length
                   65
% identity
                   49
NCBI Description
                   (U63815) localized according to blastn similarity to EST
                  sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
Seq. No.
                  29345
                  190399 1.R1040
Contig ID
5'-most EST
                  jC-gmf\overline{1}02220094a02a1
Method
                  BLASTX
NCBI GI
                  q3242715
BLAST score
                  183
E value
                   2.0e-13
Match length
                  139
% identity
NCBI Description
                   (AC003040) hypothetical protein [Arabidopsis thaliana]
                  29346
Seq. No.
Contig ID
                  190421 1.R1040
                  jC-gmf102220052h06a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2618698
BLAST score
                  587
E value
                   6.0e-61
Match length
                  134
% identity
NCBI Description
                   (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                  29347
                  190446 1.R1040
Contig ID
                  pmv700891419.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2598575
BLAST score
                  224
E value
                  2.0e-18
Match length
                  117
% identity
                  41
NCBI Description
                  (Y15293) MtN21 [Medicago truncatula]
Seq. No.
                  29348
                  190448 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy069d04b1
Seq. No.
```

190485 1.R1040

```
sat701003065.h1
5'-most EST
                      500
                   29350
Seq. No.
                   190516 1.R1040
Contig ID
                   sat701\overline{0}03104.h1
5'-most EST
                   29351
Seq. No.
                   190522 1.R1040
Contig ID
                   sat701003112.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1619601
BLAST score
                   112
E value
                   3.0e-56
Match length
                   188
% identity
                   90
NCBI Description
                   M.truncatula mRNA for MtN3 gene
Seq. No.
                   29352
                   190526 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063h04a1
Seq. No.
                   29353
                   190534 1.R1040
Contig ID
5'-most EST
                   sat701003129.hl
Method
                   BLASTX
NCBI GI
                   q4455232
BLAST score
                   167
E value
                   2.0e-11
Match length
                   164
% identity
NCBI Description
                   (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                   29354
Contig ID
                   190556_1.R1040
5'-most EST
                   sat701\overline{0}03164.h1
Method
                   BLASTN
NCBI GI
                   q2224910
BLAST score
                   58
E value
                   5.0e-24
Match length
                   170
                   84
% identity
NCBI Description
                   Daucus carota somatic embryogenesis receptor-like kinase
                   mRNA, complete cds
                   29355
Seq. No.
                   190592 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}03209.h1
Seq. No.
                   29356
                   190599 1.R1040
Contig ID
5'-most EST
                   pmv700894036.hl
Method
                   BLASTX
NCBI GI
                   q3834306
BLAST score
                   165
E value
                   2.0e-11
Match length
                   90
% identity
                  42
```

Contig ID

5'-most EST

```
(AC005679) EST gb R65024 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  29357
Seq. No.
                  190615 1.R1040
Contig ID
5'-most EST
                  sat701003239.hl
Method
                  BLASTX
NCBI GI
                  q3805960
BLAST score
                  260
E value
                  3.0e - 33
Match length
                  91
                  79
% identity
NCBI Description (Y13771) laccase [Populus balsamifera subsp. trichocarpa]
Seq. No.
                  29358
                  190646 1.R1040
Contig ID
                  zsq701120890.hl
5'-most EST
Method
                  BLASTX
                  g3176709
NCBI GI
BLAST score
                  285
                  2.0e-25
E value
Match length
                  162
                  36
% identity
                   (AC002392) putative anthranilate
NCBI Description
                  N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                  thaliana]
                  29359
Seq. No.
                  190700 1.R1040
Contig ID
5'-most EST
                  sat701003354.hl
Method
                  BLASTX
NCBI GI
                  g2464905
BLAST score
                  207
E value
                  4.0e-16
                  95
Match length
                  52
% identity
NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]
                  29360
Seq. No.
                  190704 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220103g10d1
Seq. No.
                  29361
                  190746 1.R1040
Contig ID
5'-most EST
                  sat701\overline{0}06016.h2
                  BLASTX
Method
NCBI GI
                  g3805956
BLAST score
                  537
                  9.0e-55
E value
Match length
                  100
                  91
% identity
NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]
Seq. No.
                  29362
```

190763 1.R1040

bth700847786.h1

```
29363
Seq. No.
                   190774 1.R1040
Contig ID
                   sat701004372.hl
5'-most EST
                   29364
Seq. No.
                   190782 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy058b04b1
Seq. No.
                   29365
                   190782 2.R1040
Contig ID
                   sat701004554.hl
5'-most EST
Seq. No.
                   29366
                   190794 1.R1040
Contiq ID
                   zhf700953746.hl
5'-most EST
                   29367
Seq. No.
                   190815 1.R1040
Contig ID
5'-most EST
                   sat701003537.hl
Method
                   BLASTX
NCBI GI
                   q1402879
BLAST score
                   104
E value
                   9.0e-09
Match length
                   65
                   49
% identity
NCBI Description
                   (X98130) unknown [Arabidopsis thaliana]
                   >gi 1495247 emb_CAA66220 (X97616) orf 05 [Arabidopsis
                   thaliana]
Seq. No.
                   29368
                   190817 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}03539.h1
                   29369
Seq. No.
Contig ID
                   190822 1.R1040
5'-most EST
                   bth700846694.h1
Method
                   BLASTX
NCBI GI
                   g3242717
BLAST score
                   145
E value
                   2.0e-09
Match length
                   55
% identity
NCBI Description
                   (AC003040) putative APG protein [Arabidopsis thaliana]
                   29370
Seq. No.
                   190824 1.R1040
Contig ID
5'-most EST
                   pxt700944659.h1
Seq. No.
                   29371
                   190841 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy063a12b1
Seq. No.
                   29372
                   190843 1.R1040
Contig ID
5'-most EST
                   zhf700959449.h1
```

```
190873 1.R1040
Contiga ID
5'-most EST
                   sat701003613.hl
                   29374
Seq. No.
                   190882 1.R1040
Contig ID
                   sat701003623.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2795804
BLAST score
                   178
E value
                   3.0e-13
                   74
Match length
% identity
NCBI Description
                    (AC003674) unknown protein [Arabidopsis thaliana]
                   >gi 3355492 (AC004218) unknown protein [Arabidopsis
                   thalianal
                   29375
Seq. No.
                   190899 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}03647.h1
                   29376
Seq. No.
                   190920 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910027e08a1
Method
                   BLASTX
                   q114974
NCBI GI
BLAST score
                   1742
                   0.0e + 00
E value
                   484
Match length
                   67
% identity
                   NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21)
                   precursor (clone TRE361) - white clover >gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
                    [Trifolium repens]
                   29377
Seq. No.
Contig ID
                   190926 1.R1040
                   leu701147471.hl
5'-most EST
                   29378
Seq. No.
                   190926 2.R1040
Contig ID
5'-most EST
                   leu701154868.hl
                   29379
Seq. No.
                   190967 1.R1040
Contig ID
5'-most EST
                   asn701142641.h1
Method
                   BLASTX
                   g4455359
NCBI GI
BLAST score
                   721
E value
                   2.0e-76
                   201
Match length
```

% identity
NCBI Description

Contig ID 190977 1.R1040 5'-most EST sat701003770.h1

(AL035524) putative protein [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   29381
                   191020 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy074g01b1
Method
                   BLASTX
NCBI GI
                   g4056496
BLAST score
                   263
E value
                   6.0e-23
Match length
                   68
% identity
                   76
                   (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29382
Seq. No.
                   191043 1.R1040
Contig ID
5'-most EST
                   k11701202887.h1
Seq. No.
                   29383
                   191054 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}03880.h1
Seq. No.
                   29384
Contig ID
                   191063 1.R1040
5'-most EST
                   q5175467
Method
                   BLASTX
NCBI GI
                   q3080401
BLAST score
                  . 480
E value
                   5.0e-48
Match length
                   140
% identity
                   64
NCBI Description
                   (AL022603) putative protein [Arabidopsis thaliana]
                   >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
                   [Arabidopsis thaliana]
                   29385
Seq. No.
Contig ID
                   191143 1.R1040
5'-most EST
                   sat701004031.hl
                   29386
Seq. No.
                   191147 1.R1040
Contig ID
5'-most EST
                   pxt700944436.h1
Method
                   BLASTX
NCBI GI
                   g1841464
BLAST score
                   390
E value
                   1.0e-37
Match length
                   109
% identity
NCBI Description
                   (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
Seq. No.
                   29387
Contig ID
                   191153 1.R1040
5'-most EST
                   sat701004047.hl
Seq. No.
                   29388
                   191172 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810020g12a1
Method
                   BLASTX
```

q2335096

Contig ID

5'-most EST

```
BLAST score
                   281
                   5.0e-25
E value
                   63
Match length
% identity
                   81
                   (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29389
Seq. No.
                   191172 2.R1040
Contig ID
5'-most EST
                   sat701\overline{0}05843.h1
                   29390
Seq. No.
Contig ID
                   191187 1.R1040
                   leu701151195.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2213594
BLAST score
                   356
E value
                   6.0e-34
Match length
                   108
                   63
% identity
NCBI Description
                   (AC000348) T7N9.14 [Arabidopsis thaliana]
                   29391
Seq. No.
                   191219 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}04140.h1
                   29392
Seq. No.
Contig ID
                   191253 1.R1040
5'-most EST
                   awf700842935.hl
                   BLASTN
Method
NCBI GI
                   g2564050
BLAST score
                   35
                   3.0e-10
E value
                   135
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   29393
                   191271 1.R1040
Contig ID
5'-most EST
                   sat701012823.h1
                   29394
Seq. No.
Contig ID
                   191344 1.R1040
5'-most EST
                   zsg701118002.h2
                   BLASTX
Method
NCBI GI
                   g4530126
BLAST score
                   241
E value
                   2.0e-20
                   81
Match length
% identity
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                   29395
Seq. No.
```

191350 1.R1040

 $sat701\overline{0}04324.h1$

```
Seq. No.
                   29396
                   191377 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400072h03a1
Method
                   BLASTX
NCBI GI
                   g3522942
BLAST score
                   397
E value
                   2.0e-38
Match length
                   120
% identity
NCBI Description
                   (AC004411) hypothetical protein [Arabidopsis thaliana]
                   29397
Seq. No.
                   191427 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}04421.h1
                   29398
Seq. No.
                   191441 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810002d05d1
Seq. No.
                   29399
                   191442 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}04440.h1
Method
                   BLASTX
NCBI GI
                   q4006829
BLAST score
                   468
E value
                   9.0e-47
Match length
                   136
% identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   29400
                   191461 1.R1040
Contig ID
5'-most EST
                   kl1701\overline{2}09210.h1
Method
                   BLASTX
NCBI GI
                   q3402679
BLAST score
                   408
E value
                   3.0e-40
Match length
                   95
% identity
                   81
                   (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29401
Seq. No.
                   191494 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}08312.h1
                   29402
Seq. No.
Contig ID
                   191514 1.R1040
5'-most EST
                   hrw701061533.hl
Method
                   BLASTX
                   q1709358
NCBI GI
BLAST score
                   206
                   2.0e-16
E value
Match length
                   57
% identity
                   74
                   NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
NCBI Description
                   PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
```

nucleoside triphosphatase - garden pea

```
precursor, chromatin-associated - garden pea
>gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase
                    [Pisum satīvum] >gi 4519173_dbj_BAA75506.1_ (AB022319)
                    nucleoside triphosphatase (NTPase) [Pisum sativum]
                    29403
Seq. No.
                    191527 1.R1040
Contig ID
                    rlr700897515.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    g544134
BLAST score
                    321
E value
                    1.0e-29
Match length
                    113
% identity
                    54
                    DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                    >gi_99720_pir__S22863 hypothetical protein - Arabidopsis
thaliana >gi_421844_pir__A46260 RecA functional analog
                    DRT100 - Arabidopsis thaliana (fragment)
                   -29404
Seq. No.
                    191561 1.R1040
Contig ID
5'-most EST
                    uC-qmflminsoy089e08b1
                    29405
Seq. No.
                    191575 1.R1040
Contig ID
5'-most EST
                    rlr700899927.hl
                    BLASTX
Method
NCBI GI
                    q2498732
BLAST score
                    208
E value
                    3.0e-18
Match length
                    104
                    46
% identity
                    PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
NCBI Description
                    >gi_1362014_pir__S57612 zeta-crystallin homolog -
                    Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268)
                    zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                    29406
                    191594 1.R1040
Contig ID
5'-most EST
                    q44056\overline{2}1
Method
                    BLASTX
NCBI GI
                    q4467156
BLAST score
                    390
E value
                    1.0e-37
Match length
                    99
% identity
                    (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    191600 1.R1040
Contig ID
5'-most EST
                    jC-gmro02910008h08a1
                    29408
Seq. No.
                    191603 1.R1040
Contig ID
```

>gi 2129890 pir S65147 nucleoside triphosphatase

pxt700943255.h1

BLASTX

5'-most EST Method

BLAST score

```
q1076274
NCBI GI
                   333
BLAST score
E value
                   3.0e - 31
                   121
Match length
                   59
% identity
                  cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
Seq. No.
                  29409
                  191605 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy224a09b1
Method
                  BLASTX
NCBI GI
                  g2224933
BLAST score
                  171
E value
                   5.0e-12
Match length
                   56
% identity
NCBI Description
                   (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
                  >gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                  thaliana]
                  29410
Seq. No.
                  191625 1.R1040
Contig ID
5'-most EST
                   sat701004679.hl
Method
                  BLASTX
NCBI GI
                  g2129859
BLAST score
                  534
                   1.0e-54
E value
Match length
                   141
                   69
% identity
                  vestitone reductase - alfalfa >gi_973249 (U28213) vestitone
NCBI Description
                  reductase [Medicago sativa subsp. sativa]
                   29411
Seq. No.
                   191633 1.R1040
Contig ID
5'-most EST
                   sat701004688.hl
Seq. No.
                   29412
                   191646 1.R1040
Contig ID
                   jC-gmle01810061h01a1
5'-most EST
                  29413
Seq. No.
                  191655 1.R1040
Contig ID
                   fua701037394.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3668085
BLAST score
                  171
E value
                  1.0e-11
Match length
                  124
% identity
                  52
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29414
Seq. No.
                  191655 2.R1040
Contig ID
5'-most EST
                  qsv701\overline{0}44364.h1
                  BLASTX
Method
                  g3668085
NCBI GI
```

```
1.0e-09
E value
Match length
                   95
% identity
                   41
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29415
                   191659 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}09643.h1
Method
                   BLASTX
NCBI GI
                   g4538934
                   288
BLAST score
                   3.0e-26
E value
Match length
                   91
% identity
                   37
                    (AL049483) putative leucine-rich-repeat protein
NCBI Description
                    [Arabidopsis thaliana]
                   29416
Seq. No.
Contig ID
                   191700 1.R1040
5'-most EST
                   sat701\overline{0}04787.h1
                   29417
Seq. No.
                   191737 1.R1040
Contig ID
5'-most EST
                   gsv701051086.hl
Seq. No.
                   29418
                   191779 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220138g07a1
Method
                   BLASTX
NCBI GI
                   g1076664
BLAST score
                   356
                   9.0e-34
E value
Match length
                   150
% identity
                   leucine zipper transcription factor - potato
NCBI Description
                   >gi_575418_emb_CAA57894_ (X82544) leucine zipper
                   transcription factor [Solanum tuberosum]
Seq. No.
                   29419
                   191811 1.R1040
Contig ID
5'-most EST
                   sat701004943.hl
Method
                   BLASTX
                   g3426039
NCBI GI
BLAST score
                   234
                   2.0e-19
E value
Match length
                   101
% identity
                   50
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   29420
                   191825 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910023e02d1
Method
                   BLASTX
NCBI GI
                   g2827992
BLAST score
                   587
                   7.0e-61
E value
```

145

Match length

Seq. No.

29426

```
% identity
NCBI Description -(AF034743) UDP-qlucuronosyltransferase [Pisum sativum]
Seq. No.
                   29421
                   191835 1.R1040
Contig ID
                   sat701\overline{0}04975.h1
5'-most EST
Seq. No.
                   29422
                   191869 1.R1040
Contig ID
                   sat701\overline{0}05029.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3242717
BLAST score
                   230
E value
                   2.0e-19
                   79
Match length
% identity
                   62
NCBI Description
                   (AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.
                   29423
                   191878 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir071f04b1
Method
                   BLASTX
NCBI GI
                   q3176662
BLAST score
                   1155
E value
                   1.0e-127
Match length
                   325
% identity
                   66
NCBI Description
                   (AC004393) Similar to mannosyl-oligosaccharide glucosidase
                   gb X87237 from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                   29424
                   191898 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}14033.h1
Method
                   BLASTX
NCBI GI
                   q3242062
BLAST score
                   264
E value
                   6.0e-23
Match length
                   80
% identity
                   (Z97058) NRT2;1p [Arabidopsis thaliana] >gi 3608362
NCBI Description
                   (AF019748) high-affinity nitrate transporter ACH1
                   [Arabidopsis thaliana] >gi_3747058 (AF093754)
                   trans-membrane nitrate transporter protein AtNRT2:1
                   [Arabidopsis thaliana]
                   29425
Seq. No.
Contig ID
                   191901 1.R1040
5'-most EST
                   zhf700956811.hl
Method
                   BLASTX
NCBI GI
                   g1418990
BLAST score
                   199
E value
                   3.0e-15
Match length
                   136
% identity
NCBI Description
                  (Z75524) unknown [Lycopersicon esculentum]
```

NCBI GI

```
191913 1.R1040
·Contig ID
                    sat701005116.hl
5'-most EST
Seq. No.
                    29427
                    191931 1.R1040
Contig ID
                    sat701\overline{0}05170.h1
5'-most EST
Method
                    BLASTX
                    g2961385
NCBI GI
BLAST score
                    183
E value
                    8.0e-14
Match length
                    73
% identity
                    52
                    (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
                    29428
Seq. No.
                    191944 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}05164.h1
                    BLASTX
Method
NCBI GI
                    g4455328
BLAST score
                    154
E value
                    2.0e-10
                    42
Match length
                    69
% identity
                    (AL035525) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    29429
Contig ID
                    191978 1.R1040
5'-most EST
                    jC-gmro02910067b11a1
Method
                    BLASTX
                    g2739008
NCBI GI
BLAST score
                    378
E value
                    4.0e-36
                    145
Match length
                    50
% identity
                    (AF022463) CYP78A3p [Glycine max]
NCBI Description
                    29430
Seq. No.
                    192004 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}08551.h1
                    29431
Seq. No.
                    192014 1.R1040
Contig ID
5'-most EST
                    g56881<u>9</u>2
                    29432
Seq. No.
                    192016 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}05301.h1
                    29433
Seq. No.
                    192046 1.R1040
Contig ID
                    sat701005365.hl
5'-most EST
                    29434
Seq. No.
                    192052 1.R1040
Contig ID
5'-most EST
                    uC-gmropic107f07b1
Method
                    BLASTX
```

g3461820

```
BLAST score
                   258
E value
                   3.0e-22
Match length
                   75
% identity
                   59
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
                   29435
Seq. No.
Contig ID
                   192070 1.R1040
5'-most EST
                   awf700841401.h1
Method
                   BLASTX
NCBI GI
                   q2914703
BLAST score
                   337
E value
                   2.0e-31
Match length
                   104
% identity
                   62
NCBI Description
                   (AC003974) unknown protein [Arabidopsis thaliana]
                   29436
Seq. No.
                   192078 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}05415.h1
                   29437
Seq. No.
Contig ID
                   192082 1.R1040
5'-most EST
                   sat701\overline{0}05419.h1
                   29438
Seq. No.
                   192104 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}05451.h1
                   29439
Seq. No.
Contig ID
                   192119 1.R1040
                   bth700845486.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2245682
BLAST score
                   127
E value
                   6.0e-65
Match length
                   243
% identity
NCBI Description
                   Glycine max peroxidase precursor (GMIPER1) mRNA, complete
                   cds
                   29440
Seq. No.
Contig ID
                   192131 1.R1040
                   zhf700959074.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829895
BLAST score
                   146
E value
                   1.0e-09
Match length
                   55
% identity
                   (AC002311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29441.
                   192138 1.R1040
Contig ID
5'-most EST
                   r1r700\overline{9}00359.h1
```

29442

Seq. No.

```
192139 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014c07d1
Seq. No.
                   192196 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06082.h2
Seq. No.
                   29444
                   192207 1.R1040
Contig ID
                   zsq701119825.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455286
BLAST score
                   151
E value
                   8.0e-10
Match length
                   91
% identity
                   46
                   (AL035527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29445
                   192216 1.R1040
Contig ID
                   sat701\overline{0}05901.h1
5'-most EST
Seq. No.
                   29446
                   192259 1.R1040
Contig ID
5'-most EST
                   sat701005847.hl
Method
                   BLASTX
NCBI GI
                   q4508076
BLAST score
                   186
E value
                   1.0e-13
Match length
                   70
% identity
                   46
NCBI Description
                   (AC005882) 55659 [Arabidopsis thaliana]
                   29447
Seq. No.
Contig ID
                   192326 1.R1040
5'-most EST
                   epx701109214.hl
Method
                   BLASTX
NCBI GI
                   q4406780
BLAST score
                   232
E value
                   2.0e-19
Match length
                   63
% identity
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
                   29448
Seq. No.
Contig ID
                   192346 1.R1040
5'-most EST
                   sat701005981.h1
Method
                   BLASTN
NCBI GI
                   q3005575
BLAST score
                   160
E value
                   1.0e-84
Match length
                   356
% identity
                   Glycine max putative high affinity nitrate transporter
NCBI Description
```

(NRT2) mRNA, complete cds

Contig ID

```
Seq. No.
                   29449
                   192376 1.R1040
Contig ID
5'-most EST
                   bth700844904.h1
Method
                   BLASTX
NCBI GI
                   g3063471
                   279
BLAST score
E value
                   5.0e-25
Match length
                   80
% identity
                   (AC003981) F22013.33 [Arabidopsis,thaliana]
NCBI Description
                   29450
Seq. No.
                   192383 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06027.h2
Method
                   BLASTX
NCBI GI
                   g4567227
BLAST score
                   273
E value
                   3.0e-24
Match length
                   83
% identity
NCBI Description
                   (AC007119) putative transport protein [Arabidopsis
                   thaliana]
Seq. No.
                   29451
Contig ID
                   192405 1.R1040
5'-most EST
                   uC-qmrominsoy070b12b1
                   29452
Seq. No.
                   192437 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06110.h1
Method
                   BLASTX
NCBI GI
                   q2275218
BLAST score
                   492
                   7.0e-50
E value
Match length
                   114
% identity
NCBI Description
                   (AC002337) G-beta-repeat containing protein isolog
                   [Arabidopsis thaliana]
                   29453
Seq. No.
Contig ID
                   192444 1.R1040
5'-most EST
                   epx701\overline{1}06795.h1
                   29454
Seq. No.
                   192446_1.R1040
Contig ID
5'-most EST
                   uC-gmronoir008h08b1
Method
                   BLASTX
                   g2388580
NCBI GI
BLAST score
                   174
E value
                   2.0e-12
Match length
                   56.
% identity
NCBI Description
                   (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb 1253956). [Arabidopsis thaliana]
                   29455
Seq. No.
```

192449_1.R1040

Seq. No.

29466

```
5'-most EST
                   q4290719
Seq. No.
                   29456
                   192475 1.R1040
Contig ID
                   sat701015349.hl
5'-most EST
                   29457
Seq. No.
                   192508 1.R1040
Contig ID
                   sat701\overline{0}06191.h1
5'-most EST
                   29458
Seq. No.
                   192518 1.R1040
Contiq ID
                   fua701040190.hl
5'-most EST
                   29459
Seq. No.
                   192520 1.R1040
Contig ID
                   k11701212647.h1
5'-most EST
Seq. No.
                   29460
                   192532 1.R1040
Contig ID
                   sat701006225.h2
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2104674
BLAST score
                   72
E value
                   3.0e-32
Match length
                   171
                   86
% identity
                   V.faba mRNA for transcription factor containing bZIP
NCBI Description
                   29461
Seq. No.
                   192565 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220063g08a1
                   BLASTX
Method
NCBI GI
                   g2738982
BLAST score
                   316
E value
                   4.0e-29
Match length
                   96
% identity
                   61
                   (AF022157) CYP71A10 [Glycine max]
NCBI Description
                   29462
Seq. No.
                   192568 1.R1040
Contig ID
                   sat701\overline{0}06272.h2
5'-most EST
                   29463
Seq. No.
                   192588 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06401.h1
Seq. No.
                   29464
                   192596 1.R1040
Contig ID
5'-most EST
                   g4302555
Seq. No.
                   29465
                   192598 1.R1040
Contig ID
                   sat701\overline{0}06326.h1
5'-most EST
```

```
192599 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir053c02b1
Method
                   BLASTX
NCBI GI
                   g1360088
BLAST score
                   336
                   4.0e-31
E value
                   76
Match length
% identity
                   72
NCBI Description
                   (X97947) Zn finger protein [Nicotiana tabacum]
                   29467
Seq. No.
                   192608 1.R1040
Contig ID
                   sat701006345.hl
5'-most EST
                   29468
Seq. No.
                   192611 1.R1040
Contig ID
                   sat701006353.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2281627
BLAST score
                   151
E value
                   4.0e-10
Match length
                   40
% identity
NCBI Description
                   (AF003094) AP2 domain containing protein RAP2.1
                   [Arabidopsis thaliana]
Seq. No.
                   29469
                   192614 1.R1040
Contig ID
5'-most EST
                   sat701006358.h1
Seq. No.
                   29470
                   192616 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06371.h1
                   29471
Seq. No.
                   192620 1.R1040
Contig ID
5'-most EST
                   sat701006375.h1
Seq. No.
                   29472
                   192621 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06376.h1
Seq. No.
                   29473
                   192639 1.R1040
Contig ID
5'-most EST
                   sat701006407.hl
Method
                   BLASTX
NCBI GI
                   q3176687
BLAST score
                   515
E value
                   3.0e-74
Match length
                   164
% identity
NCBI Description
                   (AC003671) Strong similarity to trehalose-6-phosphate
                   synthase homolog from A. thaliana chromosome 4 contig
                   gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and
                   gb R64855 come from this gene. [Arabidopsis thaliana]
```

Seq. No. 29474

5'-most EST

```
Contig ID
                   192694 1.R1040
5'-most EST
                   uC-gmrominsoy217b04b1
Method
                   BLASTX
NCBI GI
                   g2292921
BLAST score
                   419
                   2.0e-52
E value
                   152
Match length
% identity
                   73
NCBI Description
                   (Y10252) pantoate--beta-alanine ligase [Lotus japonicus]
Seq. No.
                   29475
                   192722 1.R1040
Contig ID
5'-most EST
                   uC-gmropic032c09b1
Method
                   BLASTX
NCBI GI
                   q4530585
BLAST score
                   208
E value
                   2.0e-16
Match length
                   51
% identity
NCBI Description
                   (AF130978) B12D protein [Ipomoea batatas]
                   29476
Seq. No.
                   192722 2.R1040
Contig ID
5'-most EST
                   sat701006550.hl
Method
                   BLASTX
NCBI GI
                   q4530585
BLAST score
                   354
E value
                   2.0e-33
Match length
                   87
% identity
NCBI Description
                  (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                   29477
Contig ID
                   192730 1.R1040
5'-most EST
                   zsg701\overline{1}28511.h1
Method
                   BLASTX
NCBI GI
                   g3201627
BLAST score
                   363
E value
                   2.0e-40
Match length
                   114
% identity
NCBI Description
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
                   29478
Seq. No.
Contig ID
                   192760 1.R1040
5'-most EST
                   sat701\overline{0}06609.h1
Method
                   BLASTX
NCBI GI
                   q3688173
BLAST score
                   454
E value
                   3.0e-45
Match length
                   134
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   29479
                   192777 1.R1040
Contig ID
```

sat701006632.hl

E value

4.0e-10

```
Seq. No.
                   29480
                   192784 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910067a10d1
                   BLASTN
Method
                   g728482
NCBI GI
BLAST score
                   119
E value
                   3.0e-60
Match length
                   263
% identity
                   86
                   Pisum sativum endo-1,4-beta-glucanase (EGL1) gene, complete
NCBI Description
                   cds
Seq. No.
                   29481
                   192788 1.R1040
Contig ID
                   zsg701\overline{1}18194.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2947063
BLAST score
                   227
E value
                   1.0e-18
Match length
                   82
% identity
                   48
NCBI Description
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
Seq. No.
                   29482
                   192790 1.R1040
Contig ID
5'-most EST
                   iC-qmst02400014e12d1
Seq. No.
                   29483
                   192846 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}06802.h1
                   29484
Seq. No.
Contig ID
                   192865 1.R1040
5'-most EST
                   jC-qmf102220148f04a1
                   29485
Seq. No.
                   192903 1.R1040
Contig ID
5'-most EST
                   asn701142412.h1
Method
                   BLASTX
NCBI GI
                   g3402746
BLAST score
                   241
E value
                   4.0e-20
Match length
                   76
% identity
NCBI Description
                   (AL022603) putative protein [Arabidopsis thaliana]
                   >gi_3402762_emb_CAA20208.1_ (AL031187) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   29486
Contig ID
                   192909 1.R1040
5'-most EST
                   sat701007001.hl
Method
                   BLASTX
NCBI GI
                   g2392895
BLAST score
                   151
```

```
Match length
                     73
                     47
% identity
                     (AF017056) brassinosteroid insensitive 1 [Arabidopsis
NCBI Description
                     thaliana]
                     29487
Seq. No.
                     192917 1.R1040
Contig ID
5'-most EST
                     sat701007016.hl
Seq. No.
                     29488 -
                     192945 1.R1040
Contig ID
                     kl1701207211.h1
5'-most EST
Seq. No.
                     29489
                     192952 1.R1040
Contig ID
                     sat701\overline{0}07114.h1
5'-most EST
Seq. No.
                     29490
                     193009 1.R1040
Contig ID
5'-most EST
                     dpv701\overline{0}98378.h1
Seq. No.
                     29491
                     193029 1.R1040
Contig ID
5'-most EST
                     sat701\overline{0}07212.h2
Method
                     BLASTX
NCBI GI
                     a416651
BLAST score
                     314
E value
                     9.0e-29
Match length
                     92
% identity
                     63
NCBI Description
                     PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
                     PCNT103) >gi_100301_pir__S16269 auxin-induced protein (clone pCNT103) - common tobacco >gi_19791_emb_CAA39704_
                     (X56263) auxin-induced protein [Nicotiana tabacum]
Seq. No.
                     29492
                     193077 1.R1040
Contig ID
                     sat701\overline{0}07277.h2
5'-most EST
                     29493
Seq. No.
                     193080 1.R1040
Contig ID
5'-most EST
                     sat701\overline{0}07280.h2
                     29494
Seq. No.
                     193108 1.R1040
Contig ID
5'-most EST
                     zsg701\overline{1}27564.h1
Seq. No.
                     29495
                     193118 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy022c01b1
                     29496
Seq. No.
                     193128 1.R1040
Contig ID
5'-most EST
                     epx701\overline{1}04056.h1
                     29497
Seq. No.
Contig ID
                    193147 1.R1040
```

Method

BLASTX

```
5'-most EST
                    sat701007370.h2
                   29498
Seq. No.
                   193153 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}07377.h2
Seq. No.
                   29499
                    193161 1.R1040
Contig ID
5'-most EST
                   uC-gmropic069h12b1
                   29500
Seq. No.
Contig ID
                   193166 1.R1040
5'-most EST
                   jC-gmst02400029f06a1
Seq. No.
                   29501
                   193180 1.R1040
Contig ID
                   k11701\overline{2}07080.h1
5'-most EST
Seq. No.
                   29502
                   193209 1.R1040
Contig ID
                    g43140<u>9</u>1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3822223
BLAST score
                    1022
E value
                    1.0e-111
Match length
                    255
% identity
                    73
NCBI Description
                    (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   29503
                   193214 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}07463.h2
Method
                   BLASTX
NCBI GI
                   q1495804
BLAST score
                    497
                                           1.30
E value
                    4.0e-50
Match length
                   161
% identity
                    63
NCBI Description
                    (X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   29504
                   193302 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}07613.h1
Method
                   BLASTX
NCBI GI
                   q3170230
BLAST score
                   185
E value
                   7.0e-14
Match length
                   78
% identity
NCBI Description
                    (AF041848) fructose-6-phosphate 2-kinase
                   /fructose-2,6-bisphosphatase [Spinacia oleracea]
                   29505
Seq. No.
                   193348 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014b05d1
```

```
NCBI GI
                  q4490310
BLAST score
                  185
E value
                  1.0e-13
Match length
                  62
                  58
% identity
                   (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  29506
                  193352 1.R1040
Contig ID
5'-most EST
                  gsv701054114.hl
                  BLASTX
Method
NCBI GI
                  q3367574
BLAST score
                  168
E value
                   6.0e-12
Match length
                  117
                  36
% identity
                   (AL031135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29507
Seq. No.
                  193369 1.R1040
Contig ID
                  awf700841301.hl
5'-most EST
Method
                  BLASTX
                  g2894594
NCBI GI
BLAST score
                  155
E value
                  1.0e-09
Match length
                  46
                  59
% identity
                  (AL021889) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29508
Seq. No.
                  193371 1.R1040
Contig ID
                  asn701133458.hl
5'-most EST
                  29509
Seq. No.
                  193395_1.R1040
Contig ID
5'-most EST
                  sat701007806.hl
Method
                  BLASTX
NCBI GI
                  g2346988
BLAST score
                  141
                  8.0e-09
E value
Match length
                  52
% identity
                  40
                   (AB006606) ZPT4-4 [Petunia x hybrida]
NCBI Description
                  29510
Seq. No.
                  193431_1.R1040
Contig ID
5'-most EST
                  fua701040268.hl
Method
                  BLASTX
                  g2598575
NCBI GI
BLAST score
                  159
                  5.0e-11
E value
                  51
Match length
                  63
% identity
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
```

este.

29511

Seq. No.

```
Contig ID
                   193450 1.R1040
                   sat701008113.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3643085
BLAST score
                   228
E value
                   4.0e-19
Match length
                   85
% identity
NCBI Description
                   (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                   crystallinum]
Seq. No.
                   29512
                   193467 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}07943.h1
Method
                   BLASTX
NCBI GI
                   g2499882
BLAST score
                   141
E value
                   1.0e-08
Match length
                   51
% identity
                   49
NCBI Description
                   PROTEASE IV HOMOLOG (ENDOPEPTIDASE IV)
                   >gi 1652816_dbj_BAA17735_ (D90908) protease IV
                   [Synechocystis sp.]
Seq. No.
                   29513
Contig ID
                   193468 1.R1040
                   jC-gmle01810011f08a1
5'-most EST
Method
                   BLASTX
                   g4335751
NCBI GI
BLAST score
                   476
E value
                   8.0e-48
Match length
                   157
% identity
                   57
                   (AC006284) putative methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   29514
Seq. No.
                   193482 1.R1040
Contig ID
                   sat701\overline{0}08130.h1
5'-most EST
Method
                   BLASTX
                   g3548806
NCBI GI
BLAST score
                   166
                   3.0e-19
E value
Match length
                   75
% identity
                   77
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                   29515
Contig ID
                   193486 1.R1040
5'-most EST
                   gsv701\overline{0}54389.h1
                   29516
Seq. No.
Contig ID
                   193538 1.R1040
                   sat701\overline{0}08054.h1
5'-most EST
Method
                   BLASTX
                   g2749982
NCBI GI
                   351
BLAST score
```

```
E value
                   4.0e-33
Match length
                   139
% identity
                   53
NCBI Description
                   (AF036705) Similar to phytoene desaturase; coded for by C.
                   elegans cDNA CEESX74F; coded for by C. elegans cDNA
                   yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded
                   for by C. elegans cDNA yk303f4.5; coded for by C. elegans
                   cDNA yk257d4.5;
Seq. No.
                   29517
                   193542 1.R1040
Contig ID
5'-most EST
                   sat701008061.hl
Method
                   BLASTX
NCBI GI
                   q1707412
BLAST score
                   235
E value
                   6.0e-20
Match length
                   65
% identity
                   (X95906) Cleavage and Polyadenylation Specifity Factor
NCBI Description
                   protein [Bos taurus]
                   29518
Seq. No.
Contig ID
                   193558 1.R1040
5'-most EST
                   zsq701123432.h1
Method
                   BLASTX
NCBI GI
                   a1087073
BLAST score
                   240
                   1.0e-20
E value
Match length
                   62
% identity
                   68
NCBI Description
                   (S79243) calmodulin-binding heat-shock protein, CaMBP
                   [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]
                   [Nicotiana tabacum]
                   29519
Seq. No.
Contig ID
                   193559 1.R1040
5'-most EST
                   sat701\overline{0}08090.h1
Method
                   BLASTX
NCBI GI
                   g2244902
BLAST score
                   174
E value
                   1.0e-12
Match length
                   59
                   47
% identity
                   (Z97339) allene oxide synthase [Arabidopsis thaliana]
NCBI Description
                   29520
Seq. No.
Contig ID
                   193565 1.R1040
5'-most EST
                   sat701\overline{0}08102.h1
Seq. No.
                   29521
                   193569 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy077g05b1
                   29522
Seq. No.
                   193586 1.R1040
Contig ID
```

jsh701070376.hl

BLASTX

5'-most EST Method

```
NCBI GI
                   g3551956
BLAST score
                   406
                   9.0e-40
E value
Match length
                   88
                   77
% identity
                   (AF082031) senescence-associated protein 6 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  29523
Seq. No.
                   193588 1.R1040
Contig ID
5'-most EST
                  sat701\overline{0}10616.h1
Seq. No.
                  29524
                  193596 1.R1040
Contig ID
5'-most EST
                  g4289887
                  BLASTX
Method
                  g3242717
NCBI GI
BLAST score
                   264
                                                        E value
                   5.0e-23
Match length
                   113
% identity
                   51
                   (AC003040) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  29525 --- --- ---
Seq. No. ----
                   193597 1.R1040
Contig ID
                   jC-qmst02400052e03d1
5'-most EST
Method
                  BLASTN
NCBI GI
                   g2252848
BLAST score
                   39
                   2.0e-12
E value
                   143
Match length
                   82
% identity
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                   29526
                   193598 1.R1040
Contig ID
                   sat701\overline{0}08164.h1
5'-most EST
Seq. No.
                   29527
                   193624 1.R1040
Contig ID
5'-most EST
                  pmv700890406.h1
                   29528
Seq. No.
                   193629 1.R1040
Contig ID
5'-most EST
                   pmv700890281.hl
Method
                   BLASTX
NCBI GI
                   g3540182
BLAST score
                   193
E value
                   8.0e-15
                   79
Match length
% identity
NCBI Description
                   (AC004122) Unknown protein [Arabidopsis thaliana]
                   29529
Seq. No.
                   193665 1.R1040
Contig ID
```

fua701037777.h1

5'-most EST

```
29530
Seq. No.
                   193666 1.R1040
Contig ID
                   epx701\overline{1}09858.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3114968
                   300
BLAST score
                   1.0e-27
E value
Match length
                   83
% identity
                   67
NCBI Description
                   (Y14997) prolidase [Suberites domuncula]
                   29531
Seq. No.
                   193678 1.R1040
Contig ID
5'-most EST
                   sat701008303.hl
Method
                   BLASTN
NCBI GI
                   g19506
BLAST score
                   132
E value
                   3.0e-68
Match length
                   208
% identity
                   91
NCBI Description
                   L.polyphyllus mRNA for pPLZ02 protein
Seq. No.
                   29532
                   193694 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy145b02b1
                   29533
Seq. No.
                   193727 1.R1040
Contig ID
                   sat701\overline{0}08405.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335349
BLAST score
                   658
                   4.0e-69
E value
                   177
Match length
% identity
                   69
NCBI Description
                   (AC004512) Similar to gb U46691 putative chromatin
                   structure regulator (SUPT6H) from Homo sapiens.
                   gb T42908, gb AA586170 and gb_AA395125 come from this gene.
                   [Arabidopsis thaliana]
                   29534
Seq. No.
Contig ID
                   193738 1.R1040
                   sat701\overline{0}08420.h1
5'-most EST
                   29535
Seq. No.
                   193739 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810045d06a1
Method
                   BLASTX
NCBI GI
                   q2191171
                   259
BLAST score
                   1.0e-22
E value
Match length
                   81
% identity
                   48
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
```

29536

Seq. No.

```
193795 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy276e05b1
                   29537
Seq. No.
                   193816 1.R1040
Contig ID
5'-most EST
                   sat701008663.hl
Seq. No.
                   29538
                   193828 1.R1040
Contig ID
                   sat701\overline{0}08568.h1
5'-most EST
                   29539
Seq. No.
                   193831 1.R1040
Contig ID
                   rlr700900159.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3152579
                   225
BLAST score
                 . 1.0e-27
E value
Match length
                   98
                   72
% identity
                   (AC002986) YUP8H12R.9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29540
                   193855 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}12568.h1
Method
                   BLASTX
NCBI GI
                   q2723496
BLAST score
                   244
E value
                   3.0e-25
Match length
                   128
% identity
                   52
                   (AB009972) beta-1,4-xylosidase [Aspergillus oryzae]
NCBI Description
Seq. No.
                   29541
Contig ID
                   193859 1.R1040
5'-most EST
                   sat701008602.h1
Method
                   BLASTX
NCBI GI
                   q3647355
BLAST score
                   301
                   1.0e-27
E value
Match length
                   105
% identity
                   58
                   (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w),
NCBI Description
                   Human hypothetical protein KIAA0249-related protein len:
                   1160 aa; Similarity to 2 human and an yeast hypothetical
                   gene. Human hypothetical protein KIAA0249 (SW:Y249 HUMA
                   29542
Seq. No.
                   193868 1.R1040
Contig ID
                   sat701\overline{0}08613.h1
5'-most EST
Seq. No.
                   29543
                   193870 1.R1040
Contig ID
5'-most EST
                   g5057567
                   29544
Seq. No.
                   193929 1.R1040
Contig ID
```

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NCBI Description

```
5'-most EST
                   zhf700965246.h1
Seq. No.
                   29545
                   193951 1.R1040
Contig ID
                   bth700845382.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3241943
BLAST score
                   677
E value
                   2.0e-71
Match length
                   152
% identity
                   80
                   (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29546
Seq. No.
                   193969 1.R1040
Contig ID
5'-most EST
                   g5057839
                   29547
Seq. No.
Contig ID
                   193990 1.R1040
5'-most EST
                   sat701008819.hl
                   29548
Seq. No.
Contig ID
                   193995 1.R1040
5'-most EST
                   epx701109276.h1
Method
                   BLASTX
NCBI GI
                   q4544451
BLAST score
                   163
                   2.0e-11
E value
Match length
                   72
% identity
                   46
NCBI Description
                   (AC006592) unknown protein [Arabidopsis thaliana]
                   29549
Seq. No.
                   194008 1.R1040
Contig ID
                   jC-gmr002910067h09a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245032
BLAST score
                   234
E value
                   3.0e-19
Match length
                   106
% identity
                   51
                   (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
                   29550
Seq. No.
                   194016 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}08859.h1
Seq. No.
                   29551
Contig ID
                   194045_1.R1040
5'-most EST
                   k11701\overline{2}09619.h1
Method
                   BLASTX
NCBI GI
                   g2827556
BLAST score
                   169
                   3.0e-15
E value
                   127
Match length
% identity
                   44
```

(AL021635) predicted protein [Arabidopsis thaliana]

E value

1.0e-27

```
29552
Seq. No.
Contig ID
                    194051 1.R1040
 5'-most EST
                   uC-gmrominsoy111f07b1
                    29553
Seq. No.
Contig ID
                   194066 1.R1040
5'-most EST
                   uC-gmronoir030b03b1
Seq. No.
                   29554
                   194073 1.R1040
Contig ID
                   sat701\overline{0}08951.h1
5'-most EST
Seq. No.
                   29555
                   194089 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}08972.h1
Method
                   BLASTX
NCBI GI
                   g2944423
BLAST score
                   183
E value
                    1.0e-13
Match length
                   116
% identity
                    41
NCBI Description
                    (AF049850) hypothetical protein [Mus musculus]
Seq. No.
                    29556
                   194097 1.R1040
Contig ID
5'-most EST
                   sat701009149.h1
Seq. No.
                   29557
                   194107 1.R1040
Contig ID
5'-most EST
                    fua701042312.hl
Method
                   BLASTX
NCBI GI
                   q3402684
BLAST score
                   183
E value
                    6.0e-14
Match length
                   51
% identity
                    63
NCBI Description
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29558
Contig ID
                   194109 1.R1040
5'-most EST
                   awf700838967.hl
Method
                   BLASTX
NCBI GI
                   q3021409
BLAST score
                   497
E value
                   4.0e-50
Match length
                   139
% identity
NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens]
                   29559
Seq. No.
Contig ID
                   194126 1.R1040
5'-most EST
                   pxt700943384.h1
Method
                   BLASTX
                   g3482929
NCBI GI
BLAST score
                   301
```

Contig ID

```
Match length .
                   67
                   79
% identity
NCBI Description
                   (AC003970) Putative transcription factor [Arabidopsis
                  thaliana]
                   29560
Seq. No.
                   194127 1.R1040
Contig ID
                   sat701009961.h2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2293067
BLAST score
                   49
E value
                   3.0e-18
                   281
Match length
% identity
                   89
NCBI Description
                  S.rostrata mRNA for early nodulin
Seq. No.
                   29561
                   194157 1.R1040
Contig ID
5'-most EST
                   pxt700944035.h1
Seq. No.
                   29562
Contig ID
                   194202 1.R1040
5'-most EST
                   jC-gmle01810094g08d1
                   29563
Seq. No.
Contig ID
                   194217 1.R1040
5'-most EST
                   jC-gmro02910004a07a1
Seq. No.
                   29564
Contig ID
                   194247 1.R1040
5'-most EST
                   sat701\overline{0}09196.h1
Method
                   BLASTX
NCBI GI
                   q461812
BLAST score
                   232
E value
                   3.0e-19
Match length
                   128
% identity
                   34
NCBI Description
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                   >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                   roseus]
Seq. No.
                  29565
                   194256 1.R1040
Contig ID
5'-most EST
                   sat701009212.hl
Method
                   BLASTX
NCBI GI
                   q4115379
BLAST score
                   223
E value
                   1.0e-18
Match length
                   80
% identity
NCBI Description
                   (AC005967) putative carbonyl reductase (Arabidopsis
                   thaliana]
Seq. No.
                   29566
```

194276 1.R1040

```
5'-most EST
                   jC-qmst02400057q06a1
                   29567
Seq. No.
                   194289 1.R1040
Contig ID
                   sat701009252.hl
5'-most EST
Seq. No.
                   29568
                   194294 2.R1040
Contig ID
                   qsv701\overline{0}56852.h1
5'-most EST
                   29569
Seq. No.
                   194333 1.R1040
Contig ID
                   sat701\overline{0}09314.h1
5'-most EST
                   29570
Seq. No.
                   194337 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir062f12b1
Seq. No.
                   29571
                   194339 1.R1040
Contig ID
                   pmv700892839.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1076274
BLAST score
                   188
E value
                   1.0e-26
Match length
                   129
                   52
% identity
                   cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
Seq. No.
                   29572
                   194381 1.R1040
Contig ID
                   sat701\overline{0}09375.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4490736
BLAST score
                   345
E value
                   1.0e-32
Match length
                   114
% identity
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   29573
                   194384 1.R1040
Contig ID
                   sat701\overline{0}09378.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g125415
BLAST score
                   214
E value
                   3.0e-17
Match length
                   110
% identity
                   42
                   KINESIN HEAVY CHAIN >gi_102714_pir_ A35075 kinesin heavy
NCBI Description
                   chain - longfin squid >gi 161290 (J05258) kinesin heavy
                   chain [Loligo pealii]
Seq. No.
                   29574
                   194385 1.R1040
Contig ID
```

 $sat701\overline{0}09379.h1$

5'-most EST

5'-most EST

```
29575
Seq. No.
                   194394 1.R1040
Contig ID
                   sat701009392.hl
5'-most EST
                   29576
Seq. No.
                   194414 1.R1040
Contig ID
5'-most EST
                   zhf700953808.hl
Method
                   BLASTX
NCBI GI
                   g2832686
BLAST score
                   519
E value
                   6.0e-53
Match length
                   139
% identity
                   63
NCBI Description
                   (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                   29577
                   194463 2.R1040
Contig ID
5'-most EST
                   pxt700945306.hl
Method
                   BLASTX
NCBI GI
                   g3033389
BLAST score
                   147
E value
                   2.0e-09
Match length
                   70
% identity
                  ~24
                   (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29578
                   194466 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}09506.h1
Seq. No.
                   29579
                   194468 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}09512.h1
Seq. No.
                   29580
                   194482 1.R1040
Contig ID
5'-most EST
                   bth700849483.hl
Seq. No.
                   29581
                   194499 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910063b03a1
Seq. No.
                   29582
                   194546 1.R1040
Contig ID
5'-most EST
                   pxt700943786.hl
Seq. No.
                   29583
Contig ID
                   194553 1.R1040
5'-most EST
                   jC-gmst02400065d04a2
Seq. No.
                   29584
Contig ID
                   194575 1.R1040
5'-most EST
                   gsv701047130.hl
Seq. No.
                   29585
                   194623 1.R1040
Contig ID
```

 $sat701\overline{0}09739.h1$

```
Seq. No.
                   29586
                   194731 1.R1040
Contig ID
                   sat701\overline{0}09879.h1
5'-most EST
Seq. No.
                   29587
Contig ID
                   194735 1.R1040
                   sat701009886.hl
5'-most EST
                   29588
Seq. No.
                   194735 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy078c02b1
Seq. No.
                   29589
                   194747 1.R1040
Contig ID
                   bth700846381.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3367594
BLAST score
                   222
                   4.0e-18
E value
                   88
Match length
% identity
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                   29590
                   194760 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}09926.h2
                   29591
Seq. No.
                   194789 1.R1040
Contig ID
                   sat701\overline{0}09960.h2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g298018
BLAST score
                   141
E value
                   2.0e-73
Match length
                   225
% identity
                   94
NCBI Description M.sativa mRNA msk7 for map kinase
Seq. No.
                   29592
                   194793 1.R1040
Contig ID
5'-most EST
                   uC-gmropic033d02b1
                   29593
Seq. No.
                   194813 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}12812.h1
                   29594
Seq. No.
                   194814 1.R1040
Contig ID
                   sat701\overline{0}09994.h2
5'-most EST
Seq. No.
                   29595
                   194816 1.R1040
Contig ID
                   hrw701061964.hl
5'-most EST
Seq. No.
                   29596
                   194833 1.R1040
Contig ID
```

```
5'-most EST
                  uC-qmrominsoy272c09b1
Method
                  BLASTX
NCBI GI
                  q3413704
BLAST score
                  560
E value
                  2.0e-57
Match length
                  147
% identity
                  70
                   (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  194833 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy109c12b1
Method
                  BLASTX
NCBI GI
                  q3413704
BLAST score
                  272
E value
                  7.0e-24
Match length
                  82
% identity
                   65
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
                  29598
Seq. No.
                  194858 1.R1040
Contig ID
5'-most EST
                  sat701010054.h2
Method - ---
                  BLASTX -
                  g2507229
NCBI GI
BLAST score
                  297
                   6.0e-27
E value
                  90
Match length
                   66
% identity
                  40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
NCBI Description
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
                  PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
                  >gi_423247_pir__A46579 estrogen receptor-binding
                  cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
                  cyclophilin [Bos taurus]
Seq. No.
                  29599
                  194860 1.R1040
Contig ID
                  sat701010057.h2
5'-most EST
Method
                  BLASTN
                  q312988
NCBI GI
BLAST score
                  127
                   3.0e-65
E value
                  227
Match length
                  89
% identity
NCBI Description G.max mRNA for beta-tubulin, partial cds
Seq. No.
                  29600
Contig ID
                  194870 1.R1040
5'-most EST
                  leu701148749.h1
                  BLASTX
Method
NCBI GI
                  q4249380
BLAST score
                  252
                  1.0e-21
E value
Match length
                  90
                  52
% identity
                  (AC005966) ESTs gb_Z37637, gb_AA042498 and gb_AA042269 come
NCBI Description
```

Match length

92

```
29601
Seq. No.
                   194875_1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}10075.h2
Seq. No.
                   29602
                   194900 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400029f07d1
                   BLASTX
Method
                   g2623297
NCBI GI
BLAST score
                   192
                   2.0e-14
E value
                   59
Match length
                   56
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3790583 (AF079180) RING-H2 finger protein RHC1a
                   [Arabidopsis thaliana]
Seq. No.
                   29603
                   194900_2.R1040
Contig ID
5'-most EST
                   jC-gmro02910071b07d1
                   BLASTX
Method
NCBI-GI-
                   g2982466
                   155
BLAST score
                   3.0e-10
E value
                   39
Match length
                   59
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   29604
Seq. No.
                   194904 1.R1040
Contig ID
                   jsh701\overline{0}66235.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3540180
BLAST score
                   232
                   2.0e-19
E value
                   104
Match length
                   49
% identity
NCBI Description
                   (AC004122) Unknown protein [Arabidopsis thaliana]
                   29605
Seq. No.
                   194930 1.R1040
Contig ID
5'-most EST
                   sat701010158.h2
Seq. No.
                   29606
                   194936 1.R1040
Contig ID
5'-most EST
                   sat701010170.h2
                   29607
Seq. No.
                   194946 1.R1040
Contig ID
5'-most EST
                   sat701010189.h2
                   BLASTX
Method
                   g3695019
NCBI GI
BLAST score
                   297
E value
                   3.0e-27
```

from this gene. [Arabidopsis thaliana]

Contig ID

```
% identity
                    (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    194957 1.R1040
Contig ID
5'-most EST
                    jC-gmst02400027d10a1
Seq. No.
                    29609
                    194970 1.R1040
Contig ID
5'-most EST
                    sat701010228.h2
                    29610
Seq. No.
                    194982 1.R1040
Contig ID
5'-most EST
                    pmv700889887.h1
                    29611
Seq. No.
                    195033 1.R1040
Contig ID
5'-most EST
                    q5677757
Method
                    BLASTX
NCBI GI
                    g3600049
BLAST score
                    378
E value
                    2.0e-36
Match length
                    123
%-identity
                    64-
                    (AF080120) similar to initiation factor IF2-beta (Pfam:
NCBI Description
                    GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana]
Seq. No.
                    29612
                    195062 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}10365.h1
Method
                    BLASTX
NCBI GI
                    g3600032
BLAST score
                    378
                    1.0e-36
E value
Match length
                    102
% identity
                    61
                    (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
NCBI Description
                    ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
Seq. No.
                    29613
                    195094 1.R1040
Contig ID
5'-most EST
                    g5606044
Method
                    BLASTX
NCBI GI
                    q4559333
BLAST score
                    182
E value
                    9.0e-17
Match length
                    122
% identity
                    49
NCBI Description
                    (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                    29614
                    195207 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}10565.h1
Seq. No.
```

195227 1.R1040

```
jex700904394.h1
5'-most EST
                   29616
Seq. No.
                   195290 1.R1040
Contig ID
                   sat701\overline{0}10670.h1
5'-most EST
                   29617
Seq. No.
                   195299 1.R1040
Contig ID
5'-most EST
                   uC-gmropic019a01b1
                   29618
Seq. No.
                   195313 1.R1040
Contig ID
5'-most EST
                   asn701137390.h1
Method
                   BLASTX
NCBI GI
                   q3249105
BLAST score
                   396
E value
                   1.0e-38
Match length
                   98
% identity
                   69
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   29619
                   195326 1.R1040
Contig ID
5'-most EST
                   sat701010719.h1
                   29620
Seq. No.
                   195354 1.R1040
Contig ID
                   asn701\overline{1}38694.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2342423
BLAST score
                   274
E value
                   2.0e-24
Match length
                   101
% identity
                   62
NCBI Description
                   (AB000797) NPK1-related protein kinase 1S [Arabidopsis
                   thaliana]
                   29621
Seq. No.
                   195465 1.R1040
Contig ID
5'-most EST
                   sat701010931.hl
                   29622
Seq. No.
                   195499 1.R1040
Contig ID
                   sat701\overline{0}10979.h1
5'-most EST
Seq. No.
                   29623
                   195533 1.R1040
Contig ID
                   sat701\overline{0}11065.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539314
BLAST score
                   161
E value
                   1.0e-11
Match length
                   54
% identity
                   57
```

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Method

BLASTX

```
29624
Seq. No.
                   195555 1.R1040
Contig ID
5'-most EST ...
                   sat701011073.hl
                   29625
Seq. No.
                   195587 1.R1040
Contig ID
                   sat701011116.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4432835
BLAST score
                   196
                   2.0e-15
E value
Match length
                   54
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
                   29626
Seq. No.
                   195588 1.R1040
Contig ID
5'-most EST
                   sat701011117.hl
Method
                   BLASTN
NCBI GI
                   g2598586
BLAST score
                   152
E value
                   4.0e-80
Match length
                   272
% identity
                   89 -
NCBI Description Medicago truncatula mRNA for cycloartenol synthase, partial
Seq. No.
                   29627
Contig ID
                   195612 1.R1040
5'-most EST
                   sat701\overline{0}11145.h1
Method
                   BLASTX
NCBI GI
                   q4220535
BLAST score
                   369
E value
                   1.0e-35
Match length
                   85
% identity
NCBI Description
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
                   thaliana]
                   29628
Seq. No.
                   195622 1.R1040
Contig ID
5'-most EST
                   asn701139014.h1
Seq. No.
                   29629
                   195663 1.R1040
Contig ID
5'-most EST
                   leu701146071.h1
Method
                   BLASTX
NCBI GI
                   g1651736
BLAST score
                   241
E value
                   3.0e-20
Match length
                   69
% identity
NCBI Description
                   (D90899) cysteine synthase [Synechocystis sp.]
                   29630
Seq. No.
                   195667 1.R1040
Contig ID
                   jsh701\overline{0}66652.h1
5'-most EST
```

5'-most EST

```
NCBI GI
                   g4432855
BLAST score
                   392
E value
                   5.0e-38
                   140
Match length
% identity
                   68
NCBI Description
                   (AC006300) unknown protein [Arabidopsis thaliana]
Seq. No.
                   195670 1.R1040
Contig ID
                   sat701011220.hl
5'-most EST
Seq. No.
                   29632
                   195692 1.R1040
Contig ID
5'-most EST
                   zsq701\overline{1}27909.h1
Seq. No.
                   29633
                   195710 1.R1040
Contig ID
                   sat701\overline{0}11269.h1
5'-most EST
Seq. No.
                   29634
                   195715 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}11275.h1
Seq. No.
                   29635---------
                   195739 1.R1040
Contig ID
5'-most EST
                   sat701011311.hl
                   29636
Seq. No.
                   195761 1.R1040
Contig ID
5'-most EST
                   fua701036962.hl
Method
                   BLASTX
NCBI GI
                   g3269296
BLAST score
                   145
E value
                   5.0e-09
Match length
                   76
% identity
                   41
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
                   29637
Seq. No.
                   195771 1.R1040
Contiq ID
5'-most EST
                   jC-qmle01810093d04d1
                   29638
Seq. No.
                   195772 1.R1040
Contig ID
5'-most EST
                   g4292625
                   BLASTX
Method
                   g4512681
NCBI GI
BLAST score
                   372
E value
                   1.0e-35
Match length
                   160
% identity
                   52
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29639
                   195775 1.R1040
Contig ID
```

 $qsv701\overline{0}50635.h1$

```
29640
Seq. No.
                   195791 1.R1040
Contig ID
                   gsv701045616.h1
5'-most EST
                   29641
Seq. No.
                   195810 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400040d05a1
Method
                   BLASTX
                   g2135172
NCBI GI
BLAST score
                   186
                   1.0e-13
E value
                   133
Match length
                   32
% identity
                   gene anonymous protein - human >gi 388012 (L18972)
NCBI Description
                   anonymous [Homo sapiens]
                   >gi 4505829_ref_NP_003669.1_pPK1.3_ gene from
                   NF2/meningioma region of 22q12
Seq. No.
                   29642
                   195824 1.R1040
Contig ID
                   yz1700966927.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2344890
                   244----
BLAST score
E value
                   5.0e-27
Match length
                   83
% identity
                   76
                    (AC002388) TINY transcription factor isolog [Arabidopsis
NCBI Description
                   thaliana]
                   29643
Seq. No.
                   195832 1.R1040
Contig ID
                   sat701\overline{0}11429.h1
 5'-most EST
Seq. No.
                   29644
                   195846 1.R1040
Contig ID
                   leu701145620.h1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q2739372
BLAST score
                   180
E value
                    2.0e-13
Match length
                   66
% identity
                    64
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29645
                   195849 1.R1040
Contig ID
5'-most EST
                   epx701105188.h1
Seq. No.
                   29646
                   195857 1.R1040
Contig ID
                   sat701\overline{0}11463.h1
5'-most EST
                   29647
Seq. No.
                   195867 1.R1040
Contig ID
```

zhf700965170.hl

5'-most EST

Match length

186

```
29648
Seq. No.
                   195880 1.R1040
Contig ID
                   sat701\overline{0}11503.h1
5'-most EST
                   29649
Seq. No.
                   195983 1.R1040
Contig ID
                   leu701155819.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1223579
BLAST score
                   305
E value
                   3.0e-28
                   85
Match length
% identity
                   68
NCBI Description
                   (X96481) cDNA101 [Arabidopsis thaliana]
Seq. No.
                   29650
                   196011 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy168c03b1
Method
                   BLASTX
NCBI GI
                   g3355640
BLAST score
                   477
E value
                   3.0e-48
Match length
                   120
% identity
                   81 --
NCBI Description (AJ009684) IVR-like protein [Nicotiana tabacum]
                   29651
Seq. No.
                   196036 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}11749.h1 = 0
Method
                   BLASTX
NCBI GI
                   g3080435
BLAST score
                   637
E value
                   2.0e-66
Match length
                   147
                   82
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                   29652
                   196068 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}07228.h1
Seq. No.
                   29653
                   196101 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}11846.h1
                   29654
Seq. No.
Contig ID
                   196144 1.R1040
5'-most EST
                   sat701012096.hl
Seq. No.
                   29655
                   196150 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy010a02b1
                   BLASTX
Method
NCBI GI
                   q3033392
BLAST score
                   723
                   1.0e-76
E value
```

Method

BLASTX

```
% identity
                   (AC004238) putative translation initiation factor
NCBI Description
                   EIF-2B-epsilon subunit [Arabidopsis thaliana]
Seq. No.
                   29656
                   196152 1.R1040
Contig ID
                   jC-gmle01810062d11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2864618
BLAST score
                   605
E value
                   8.0e-63
Match length
                   191
% identity
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
                   29657
Seq. No.
                   196202 1.R1040
Contig ID
5'-most EST
                   sat701012010.h1
Method
                   BLASTX
NCBI GI
                   g4544399
BLAST score
                   296
E value
                   8.0e-27
Match length
                   133
% identity --
                  68
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   29658
Seq. No.
                   196209 1.R1040
Contig ID
                   sat701\overline{0}12020.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g927575
BLAST score
                   112
                   4.0e-11
E value
Match length
                   125
% identity
NCBI Description (U12926) alpha galactosidase [Glycine max]
                   29659
Seq. No.
                   196216 1.R1040
Contig ID
5'-most EST
                   pxt700946306.hl
Method
                   BLASTX
                   g2244792
NCBI GI
BLAST score
                   342
E value
                   1.0e-32
Match length
                   75
% identity
NCBI Description
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
                   29660
Seq. No.
                   196233 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy089g03b1
                   29661
Seq. No.
                   196234 1.R1040
Contig ID
                   jC-gmf\overline{1}02220053g12a1
5'-most EST
```

```
NCBI GI
                   g3152582
BLAST score
                   361
                   2.0e-34
E value
Match length
                  151
% identity
                   50
                   (AC002986) YUP8H12R.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  29662
                  196243 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy021h04b1
Seq. No.
                  29663
                  196251 1.R1040
Contig ID
5'-most EST
                   zsq701130316.hl
Method
                  BLASTX
NCBI GI
                  g2190548
BLAST score
                  186
E value
                   5.0e-14
Match length
                   69
% identity
                   55
NCBI Description
                   (AC001229) EST gb ATTS1121 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  29664-
                  196277 1.R1040
Contig ID
5'-most EST
                   sat701012132.h1
Method
                  BLASTX
NCBI GI
                  q3176690
BLAST score
                  325
E value
                   4.0e-30
Match length
                  75
                  83
% identity
                   (AC003671) Similar to ubiquitin ligase gb D63905 from S.
NCBI Description
                  cerevisiae. EST gb R65295 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  29665
                  196282 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}65685.h1
                  BLASTN
Method
NCBI GI
                  q2627180
BLAST score
                  241
                  1.0e-133
E value
Match length
                  453
                  88
% identity
NCBI Description
                  Pisum sativum mRNA for cycloartenol synthase, complete cds
Seq. No.
                  29666
                  196303 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir033g10b1
                  29667
Seq. No.
Contig ID
                  196326 1.R1040
5'-most EST
                  zhf700957964.h1
                  29668
Seq. No.
                  196395 1.R1040
Contig ID
```

Contig ID

```
5'-most EST
                   jC-gmro02910029f11d1
Seq. No.
                   29669
                   196421 1.R1040
Contig ID
                   sat701012409.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1865721
BLAST score
                   348
E value
                   4.0e-33
Match length
                   80
% identity
                   76
                   (Y08067) mitochondrial single-subunit DNA-dependent RNA
NCBI Description
                   polymerase [Chenopodium album]
Seq. No.
                   29670
                   196426 1.R1040
Contig ID
5'-most EST
                   zhf700959816.h1
                   29671
Seq. No.
                   196442_1.R1040
Contig ID
                   jC-gmst02400055e08a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2827556
BLAST score
                   192---
E value
                   1.0e-14
Match length
                   79
                   48
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   29672
Seq. No.
Contig ID
                   196453 1.R1040
5'-most EST
                   sat701\overline{0}12406.h1
Method
                   BLASTN
NCBI GI
                   g4115338
BLAST score
                   112
E value
                   3.0e-56
Match length
                   220
% identity
                   22
NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds
                   29673
Seq. No.
Contig ID
                   196651 1.R1040
5'-most EST
                   gsv701046508.hl
                   29674
Seq. No.
                   196699 1.R1040
Contig ID
5'-most EST
                   g5752704
Method
                   BLASTX
NCBI GI
                   g4322940
BLAST score
                   384
E value
                   7.0e-37
Match length
                   113
% identity
                   37
                   (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   29675
```

196730 1.R1040

```
5'-most EST
                   dpv701100906.h1
                   29676
Seq. No.
                   196753 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir007e01b1
                   29677
Seq. No.
                   196755 1.R1040
Contig ID
5'-most EST
                   zhf700951721.hl
                   BLASTX
Method
NCBI GI
                   q2959781
BLAST score
                   676
                   5.0e-90
E value
Match length
                   192
% identity
                   86
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   29678
Seq. No.
                   196758 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}12844.h1
                   29679
Seq. No.
Contig ID
                   196763 1.R1040
5-'-most EST
                   sat701\overline{0}12849.h1
                   29680
Seq. No.
                   196801 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}12906.h1
Method
                   BLASTX
NCBI GI
                   q4539324
BLAST score
                   175
E value
                   9.0e-13
Match length
                   60
                   60
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   29681
                   196816 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}62093.h1
                   29682
Seq. No.
Contig ID
                   196827 1.R1040
5'-most EST
                   sat701012935.h1
Method
                   BLASTX
                   g4204259
NCBI GI
BLAST score
                   211
E value
                   4.0e-17
Match length
                   51
                   76
% identity
NCBI Description
                   (AC005223) 18074 [Arabidopsis thaliana]
                   29683
Seq. No.
                   196841 1.R1040
Contig ID
                   sat701012958.h1
5'-most EST
Method
                   BLASTX
                   g3287270
NCBI GI
```

.

208

BLAST score

```
1.0e-16
E value
Match length
                   86
% identity
                   56
                   (Y09533) involved in starch metabalism [Solanum tuberosum]
NCBI Description
                   29684
Seq. No.
                   196912 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}66923.h1
Method
                   BLASTX:
NCBI GI
                   q482404
BLAST score
                   145
E value
                   6.0e-09
Match length
                   160
                   11
% identity
NCBI Description
                   T-complex-associated-testes-expressed-1 protein - mouse
                   >gi 201910 (M28821) Tcte-1 peptide [Mus musculus]
                   29685
Seq. No.
                   196940 1.R1040
Contig ID
5'-most EST
                   bth700849266.h1
                   BLASTX
Method
                   g1402918
NCBI GI
BLAST score
                   404
E-value
                   2.0e-39-
                   106
Match length
% identity
                   71
                   (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
Seq. No.
                   29686
                   196952 1.R1040
Contig ID
5'-most EST
                   sat701013110.hl
                   29687
Seq. No.
Contig ID
                   196976 1.R1040
5'-most EST
                   sat701013323.hl
                   29688
Seq. No.
                   197022 1.R1040
Contig ID
                   leu701155607.hl
5'-most EST
                   29689
Seq. No.
                   197029 1.R1040
Contig ID
                   r1r700897547.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4417287
BLAST score
                   185
E value
                   7.0e-14
                   78
Match length
% identity
                   51
                   (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29690
Seq. No.
                   197032 1.R1040
Contig ID
                   sat701\overline{0}13224.h1
5'-most EST
```

BLASTX

Method

NCBI Description

```
NCBI, GI
                   q4056460
BLAST score
                   257
E value
                   3.0e-22
                   89
Match length
% identity
                   52
                   (AC005990) Contains similarity to gb_L26505 Met30p from
NCBI Description
                   Saccharomyces cerevisiae. ESTs gb F14133, gb T46217,
                   gb AA404758 and gb Z37647 come from this gene. [Arabidopsis ...
                   thaliana]
Seq. No.
                   29691
                   197142 1.R1040
Contig ID
5'-most EST
                   sat701013408.hl
Seq. No.
                   29692
                   197147 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910071h01d1
                   29693
Seq. No.
                   197160 1.R1040
Contig ID
                   dpv701\overline{1}01082.h1
5'-most EST
                   29694
Seq. No.
Contig ID -
                   197161_1.R1040 -
5'-most EST
                   fC-gmse700838708c1
Method
                   BLASTX
                   q1877397
NCBI GI
                   187
BLAST score
                   6.0e-14
E value
Match length
                   46
% identity
                   74
                   (Y11591) shaggy-like kinase [Ricinus communis]
NCBI Description
                   29695
Seq. No.
                   197170 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810082e07a1
                   29696
Seq. No.
                   197228 1.R1040
Contig ID
5'-most EST
                   g4298019
                   29697
Seq. No.
                   197233 1.R1040
Contig ID
5'-most EST
                   fua701038023.hl
                   29698
Seq. No.
Contig ID
                   197235_1.R1040
                   fC-gmro700845003f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1246403
BLAST score
                   237
                   1.0e-29
E value
Match length
                   91
% identity
```

TINY [Arabidopsis thaliana]

(X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405)

Method

BLASTX

```
29699
Seq. No.
                   197236 1.R1040
Contig ID
5'-most EST
                   bth700849379.h1
Method
                   BLASTX
NCBI GI
                   g3128176
BLAST score
                   373
                   1.0e-35
E value
Match length
                   118
% identity
                   55
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29700
Seq. No.
                   197237 1.R1040
Contig ID
                   qsv701\overline{0}46729.h1
5'-most EST
Seq. No.
                   29701
                   197355 1.R1040
Contig ID
5'-most EST
                   sat701013738.hl
Seq. No.
                   29702
                   197357 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071e07d1
Method
                   BLASTX
NCBI GI
                   q2344894
BLAST score
                   152
E value
                   7.0e-10
Match length
                   60
% identity
                   52
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   29703
                   197382 1.R1040
Contig ID
5'-most EST
                   q56064\overline{5}2
Method
                   BLASTX
NCBI GI
                   q2275213
BLAST score
                   473
E value
                   3.0e-47
                                                                 1.0
Match length
                   182
% identity
                   56
NCBI Description
                   (AC002337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   197403 1.R1040
Contig ID
5'-most EST
                   uC-gmropic041h04b1
Seq. No.
Contig ID
                   197406 1.R1040
5'-most EST
                   jC-gmf102220053f04a1
Seq. No.
                   197406 2.R1040
Contig ID
5'-most EST
                   pxt700944637.h1
Seq. No.
                   29707
                   197411 1.R1040
Contig ID
5'-most EST
                   g5509811
```

- 4

```
NCBI GI
                   q4006886
BLAST score
                   460
E value
                   9.0e-46
Match length
                   131
% identity
                   67
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
                   29708
Seq. No.
Contig ID
                   197434 1.R1040
5'-most EST
                   bth700845640.h1
Method
                   BLASTN
NCBI GI
                   q2245682
BLAST score
                   145
E value
                   1.0e-75
Match length
                   305
                   87
% identity
                   Glycine max peroxidase precursor (GMIPER1) mRNA, complete
NCBI Description
Seq. No.
                   29709
                   197444 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}13865.h1
                   29710
Seq. No.
                   197454_1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}13877.h1
                   29711
Seq. No.
                   197484 1.R1040
Contig ID
                   sat701\overline{0}13920.h1
5'-most EST
Method
                   BLASTX
                   g2558516
NCBI GI
BLAST score
                   206
E value
                   2.0e-16
Match length
                   84
% identity
NCBI Description
                   (AJ001119) Rab5 GDP/GTP exchange factor, Rabex5 [Bos
                   taurus]
Seq. No.
                   29712
                   197554 1.R1040
Contig ID
                   k11701\overline{2}11259.h1
5'-most EST
Seq. No.
                   29713
                   197564 1.R1040
Contig ID
5'-most EST
                   sat701014050.h1
Seq. No.
                   29714
Contig ID
                   197607 1.R1040
5'-most EST
                   sat701014106.hl
Method
                   BLASTN
NCBI GI
                   g1396053
BLAST score
                   74
E value
                   6.0e - 34
                   142
Match length
                   88
% identity
NCBI Description Pisum sativum mRNA for phosphoribosylanthranilate
```

transferase, partial cds

```
29715
Seq. No.
                   197627 1.R1040
Contig ID
                   sat701014139.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4115383
BLAST score
                   300
                   1.0e-27
E value
Match length
                   92
% identity
                   (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29716
                   197632 1.R1040
Contig ID
                   sat701014146.hl
5'-most EST
                   BLASTX
Method
                   q2827699
NCBI GI
BLAST score
                   147
                   4.0e-09
E value
                   182
Match length
                   25
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   29717
Seq. No.
                   197661 1.R1040
Contig ID
                   fC-qmse700660311r5
5'-most EST
                   29718
Seq. No.
                   197689 1.R1040
Contig ID
                   bth700844437.h1
5'-most EST
                   29719
Seq. No.
                   197725 4.R1040
Contig ID
5'-most EST
                   zsg701126981.h1
                   29720
Seq. No.
                   197747 1.R1040
Contig ID
5'-most EST
                   asn701137866.h1
                   29721
Seq. No.
                   197748 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}67605.h1
                   29722
Seq. No.
Contig ID
                   197764 1.R1040
5'-most EST
                   jC-gmf102220096c03d1
Method
                   BLASTX
                   q1161167
NCBI GI
                   220
BLAST score
                   1.0e-17
E value
Match length
                   80
% identity
                   44
                   (L42466) ethylene-forming enzyme [Picea glauca]
NCBI Description
```

29723

Seq. No.

```
197797 1.R1040
Contig ID
5'-most EST
                    dpv701\overline{1}01334.h1
Seq. No.
                    29724
                    197832 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}14423.h1
Method
                    BLASTX
NCBI GI
                    q4063751
BLAST score
                    160
E value
                    6.0e-11
Match length
                    118
                    33
% identity
                    (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                    >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
                    29725
Seq. No.
                    197891 1.R1040
Contig ID
5'-most EST
                    sat701014510.hl
                    29726
Seq. No.
                    197893 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}14593.h1
Seq. No.
                    29727
Contig ID
                    197943 1.R1040
                    jC-gmle01810029c10d1
5'-most EST
Method
                    BLASTX
                    q3236255
NCBI GI
BLAST score
                    147
E value
                    4.0e-09
Match length
                    89
% identity
                    33
NCBI Description
                    (AC004684) hypothetical protein [Arabidopsis thaliana]
                    29728
Seq. No.
Contig ID
                    197965 1.R1040
5'-most EST
                    jC-gmf102220130d06a1
                    29729
Seq. No.
                    197986 1.R1040
Contig ID
5'-most EST
                    zhf700958990.h1
                    29730
Seq. No.
                    198008 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}06491.h1
Seq. No.
                   29731
Contig ID
                   198012_1.R1040
5'-most EST
                    zsg701119896.hl
                    29732
Seq. No.
                   198110 1.R1040
Contig ID
5'-most EST
                    sat701\overline{0}14822.h1
Method
                   BLASTX
                   q3924598
NCBI GI
BLAST score
                    228
```

```
E value
                  1.0e-18
Match length
                  167
% identity
                  31
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                  29733
Seq. No.
                  198111 1.R1040
Contig ID
5'-most EST
                  sat701014823.hl
                  29734
Seq. No.
                  198125 1.R1040
Contig ID
5'-most EST
                  kl1701207269.h1
                  29735
Seq. No.
                  198139 1.R1040
Contig ID
5'-most EST
                  sat701014863.hl
Method
                  BLASTX
NCBI GI
                  q1418331
BLAST score
                  593
E value
                  2.0e-61
Match length
                  169
% identity
                  66
NCBI Description
                  (X95909) receptor like protein kinase [Arabidopsis
                  29736
Seq. No.
                  198142 1.R1040
Contig ID
5'-most EST
                  q4303640
Method
                  BLASTX
NCBI GI
                  g1853968
BLAST score
                  391
E value
                  2.0e-41
                  150
Match length
% identity
                  62
NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]
Seq. No.
                  29737
                  198152 1.R1040
Contig ID
5'-most EST
                  zsg701127620.h1
                  29738
Seq. No.
                  198299 1.R1040
Contig ID
5'-most EST
                  sat701\overline{0}15140.h1
                  29739
Seq. No.
                  198306 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy042d09b1
Seq. No.
                  29740
                  198309 1.R1040
Contig ID
                  leu701153759.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4128133
BLAST score
                  141
                  8.0e-09
E value
Match length
                  56
```

% identity

```
NCBI Description
                   (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                   29741
Seq. No.
                   198316 1.R1040
Contig ID
                   sat701015161.hl
5'-most EST
                   29742
Seq. No.
                   198427 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}15304.h1
Method
                   BLASTX
NCBI GI
                   q4099090
BLAST score
                   572
E value
                   9.0e-59
Match length
                   137
                   75
% identity
NCBI Description
                   (U83178) unknown [Arabidopsis thaliana]
                   29743
Seq. No.
                   198434 1.R1040
Contig ID
5'-most EST
                   asn701141557.hl
                   29744
Seq. No.
                   198451 1.R1040
Contig ID
5'-most EST
                   pxt700945140.hl
Method
                   BLASTX
NCBI GI
                   g3927836
BLAST score
                   212
                   3.0e-17
E value
Match length
                   47
                   79
% identity
                  (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29745
Seq. No.
                   198453 1.R1040
Contig ID
5'-most EST
                   sat701015335.hl
Seq. No.
                   29746
                   198458 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}15342.h1
                   29747
Seq. No.
                   198461 1.R1040
Contig ID
5'-most EST
                   rlr700901985.hl
                   BLASTX
Method
                   g3068713
NCBI GI
BLAST score
                   253
                   5.0e-22
E value
Match length
                   87
% identity
                   60
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
                   29748
Seq. No.
                   198515 1.R1040
Contig ID
                   sat701\overline{0}15414.h1
5'-most EST
                   29749
Seq. No.
```

198519 1.R1040

Contig ID

```
5'-most EST
                   uC-gmrominsov209a04b1
Method
                   BLASTX
NCBI GI
                   q4455260
BLAST score
                   819
E value
                   1.0e-87
Match length
                   173
% identity
                   83
NCBI Description
                   (AL035353) protein kinase-like protein [Arabidopsis
                   thaliana]
                   29750
Seq. No.
                   198553 1.R1040
Contig ID
5'-most EST
                   sat701015458.hl
Method
                   BLASTX
NCBI GI
                   q1931652
BLAST score
                   147
E value
                   3.0e-09
Match length
                   39
                   22
% identity
NCBI Description
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   29751
                   198556 1.R1040
Contig ID
                   jC-gmro02910036b05d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4490736
BLAST score
                   479
E value
                   3.0e-48
Match length
                   112
% identity
                   64
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   29752
                   198577 1.R1040
Contig ID
5'-most EST
                   sat701\overline{0}15493.h1
                   29753
Seq. No.
Contig ID
                   198633 1.R1040
5'-most EST
                   awf700836368.h1
Seq. No.
                   29754
Contig ID
                   198663 1.R1040
5'-most EST
                   a50583\overline{2}7
Method
                   BLASTX
NCBI GI
                   g710465
BLAST score
                   309
E value
                   3.0e-28
Match length
                   142
% identity
NCBI Description
                   OEP86=outer envelope protein [Peas, Peptide Chloroplast,
                   878 aa1
Seq. No.
                   29755
                   198672 1.R1040
Contig ID
```

awf700836424.hl

5'-most EST

```
29756
Seq. No.
Contig ID
                   198681 1.R1040
5'-most EST
                   awf700836435.h1
Method
                   BLASTN
                   q609343
NCBI GI
BLAST score
                   101
                   2.0e-49
E value
                   342
Match length
% identity
                   85
                   Pisum sativum Wando aspartate carbamoyltransferase (pyrB3)
NCBI Description
                   mRNA, complete cds
                   29757
Seq. No.
                   198729 1.R1040
Contig ID
                   awf700836507.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2947070
BLAST score
                   213
E value
                   6.0e-19
Match length
                   160
% identity
                   44
NCBI Description
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
                   thaliana]
                   29758
Seq. No.
Contig ID
                   198749 1.R1040
5'-most EST
                   jC-gmf102220090g03a1
Method
                   BLASTX
                   g2130210
NCBI GI
BLAST score
                   156
E value
                   5.0e-10
Match length
                   70
                   44
% identity
NCBI Description
                   hypothetical protein - fission yeast (Schizosaccharomyces
                   pombe)
Seq. No.
                   29759
                   198749_2.R1040
Contig ID
5'-most EST
                   g4286231
                   29760
Seq. No.
                   198758 1.R1040
Contig ID
                   awf700836543.hl
5'-most EST
                   29761
Seq. No.
                   198818 1.R1040
Contig ID
5'-most EST
                   awf700\overline{8}36625.h1
                   29762
Seq. No.
                   198835 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy001c03b1
                   29763
Seq. No.
                   198862 1.R1040
Contig ID
                   awf700842302.hl
5'-most EST
Method
                   BLASTX
```

q3063444

NCBI GI

```
BLAST score
                   174
E value
                   3.0e-12
Match length
                   60
% identity
                   57
NCBI Description
                   (AC003981) F22013.5 [Arabidopsis thaliana]
                   29764
Seq. No.
                   198933 1.R1040
Contig ID
5'-most EST
                   awf700836778.h1
                   29765
Seq. No.
                   198949 1.R1040
Contig ID
                   awf700836802.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q13384
                   169
BLAST score
                   3.0e-90
E value
                   278
Match length
                   90
% identity
                   Pea mitochondrial coxI gene for cytochrome oxidase subunit
NCBI Description
                   29766
Seq. No.
Contig ID ...
                   198997 1.R1040 ---
5'-most EST
                   all700863227.hl
                   29767
Seq. No.
                   199013 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy261d11b1
                   29768
Seq. No.
                   199020 1.R1040
Contig ID
5'-most EST
                   awf700836913.h1
                   BLASTN
Method
NCBI GI
                   g3868723
BLAST score
                   44
E value
                   1.0e-15
Match length
                   192
                   81
% identity
                  Arabidopsis thaliana chromosome V map 60.5 cM, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   29769
Seq. No.
                   199035 1.R1040
Contig ID
                   awf700836932.h1
5'-most EST
                   29770
Seq. No.
Contig ID
                   199038_1.R1040
                   awf700836937.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4106395
BLAST score
                   294
E value
                   2.0e-26
Match length
                   111
                   55
% identity
```

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

NCBI Description

```
29771
Seq. No.
                   199039 1.R1040
Contig ID
5'-most EST
                   awf700842414.hl
                   29772
Seq. No.
                   199056 1.R1040
Contig ID
                   awf700\overline{8}36959.h1
5'-most EST
                  29773
Seq. No.
                   199075 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400026d02a1
                   29774
Seq. No.
                   199081 1.R1040
Contig ID
5'-most EST
                   zhf700953761.h1
                   29775
Seq. No.
                   199151 1.R1040
Contig ID
5'-most EST
                   uC-gmropic113a07b1
                   29776
Seq. No.
                   199167 1.R1040
Contig ID
5'-most EST
                   awf700837156.hl
                   29777
Seq. No.
                   199186 1.R1040
Contig ID
5'-most EST
                   awf700837147.h1
                   29778
Seq. No.
                   199260 1.R1040
Contig ID
                   awf700837255.hl
5'-most EST
                   29779
Seq. No.
                   199274 1.R1040
Contig ID
                   awf700\overline{8}37280.h1
5'-most EST
                   29780
Seq. No.
Contig ID
                   199297 1.R1040
                   jC-gmst02400016e07a1
5'-most EST
Method
                   BLASTX
                   g4490708
NCBI GI
BLAST score
                   214
E value
                   2.0e-17
Match length
                   51
% identity
                   80
NCBI Description
                   (AL035680) putative protein [Arabidopsis thaliana]
                   29781
Seq. No.
                   199312 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220104h04d1
Method
                   BLASTN
NCBI GI
                   g18731
BLAST score
                   194
E value
                   1.0e-105
                   218
Match length
% identity
```

Soybean RPB1-B1 gene for the largest subunit of RNA

polymerase II (EC 2.7.7.6)

```
29782
Seq. No.
                   199313 1.R1040
Contig ID
                   awf700837341.hl
5'-most EST
                   29783
Seq. No.
                   199315 1.R1040
Contig ID
5'-most EST
                   crh700852559.hl
                   BLASTX
Method
NCBI GI
                   g1363749
BLAST score
                   152
                   5.0e-10
E value
                   93
Match length
% identity
                   35
                   probable membrane protein YLR418c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi 632679 (U20162) Cdc73p [Saccharomyces
                   cerevisiae]
                   29784
Seq. No.
                   199383 1.R1040
Contig ID
                   awf700837445.hl
5'-most EST
                   -29785 ------
Seq. No. --
                   199443_1.R1040
Contig ID
5'-most EST
                   fC-gmse700841524f1
                   29786
Seq. No.
                   199451 1.R1040
Contig ID
                   dpv701098501.hl
5'-most EST
                   29787
Seq. No.
                   199455 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy066d02b1
                   29788
Seq. No.
Contig ID
                   199482 1.R1040
                   hrw701\overline{0}59258.h1
5'-most EST
                   29789
Seq. No.
                   199482 3.R1040
Contig ID
5'-most EST
                   bth700\overline{8}44906.h1
                   29790
Seq. No.
                   199498 1.R1040
Contig ID
                   k11701213363.hl
5'-most EST
Seq. No.
                   29791
                   199515 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220103b07d1
Seq. No.
                   29792
                   199531 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118d07b1
                   BLASTX
Method
                   g2459421
NCBI GI
                   248
BLAST score
```

NCBI GI

```
E value
                   5.0e-21
Match length
                   73
                   63
% identity
NCBI Description
                   (AC002332) putative calcium-binding EF-hand protein
                   [Arabidopsis thaliana]
                   29793
Seq. No.
                   199533 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}56160.h1
Seq. No.
                   29794
                   199535 1.R1040
Contig ID
                   uC-gmrominsoy032b01b1
5'-most EST
Method
                  BLASTN
                  g22635
NCBI GI
                   35
BLAST score
E value
                   5.0e-10
                  59
Match length
                   90
% identity
NCBI Description P.vulgaris mRNA for 70 kD heat shock protein
                  29795
Seq. No.
                  199670 1.R1040
Contig ID
5'-most-EST-
                  crh700850007.h1
                   29796
Seq. No.
Contig ID
                   199801 1.R1040
5'-most EST
                  dpv701100931.hl
                   29797
Seq. No.
                   199813 1.R1040
Contig ID
5'-most EST
                   awf700838065.hl
                  29798
Seq. No.
                   199813 3.R1040
Contig ID
5'-most EST
                   jex700905882.hl
Seq. No.
                  29799
                  199844 1.R1040
Contig ID
5'-most EST
                  awf700838110.h1
                  29800
Seq. No.
Contig ID
                  199921 1.R1040
5'-most EST
                   awf700838214.hl
                  BLASTX
Method
NCBI GI
                  g4417267
BLAST score
                   286
E value
                   2.0e-42
                  114
Match length
% identity
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29801
Seq. No.
                  199925 1.R1040
Contig ID
                  zhf700953264.h1
5'-most EST
                  BLASTX
Method
```

g1652942

```
BLAST score
                   145
                   3.0e-09
E value
Match length
                  118
% identity
                   31
NCBI Description
                   (D90909) extragenic suppressor [Synechocystis sp.]
Seq. No.
                  29802
Contig ID
                  200013 1.R1040
5'-most EST
                  awf700838363.hl
Method
                  BLASTN
NCBI GI
                  q3413510
BLAST score
                  77
E value
                  2.0e-35
Match length
                  197
% identity
                  85
NCBI Description
                  Spinacia oleracea mRNA (nuclear-encoded) for chloroplast
                  glucose-6-phosphate isomerase
                  29803
Seq. No.
Contig ID
                  200043 1.R1040
5'-most EST
                  awf700838485.hl
Method
                  BLASTX
                  q3063693
NCBI GI
BLAST score
                   301
                  8.0e-28
E value
Match length.
                  78
% identity
                   64
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  29804
Seq. No.
Contig ID
                  200080 1.R1040
5'-most EST
                  crh700852040.hl
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                   390
E value
                   4.0e-38
Match length
                  91
% identity
                  85
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
                  29805
Seq. No.
                  200088 1.R1040
Contig ID
5'-most EST
                  awf700838455.h1
Seq. No.
                  29806
Contig ID
                  200103 1.R1040
5'-most EST
                  jC-gmle01810008d10a1
Seq. No.
Contig ID
                  200188 1.R1040
5'-most EST
                  awf700839224.h1
Seq. No.
```

200237 1.R1040

Contig ID

```
5'-most EST
                   zhf700953591.hl
Method
                   BLASTX
NCBI GI
                   q4558673
BLAST score
                   188
E value
                   1.0e-13
Match length
                   148
% identity
                   34
NCBI Description
                   (AC007063) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   200317 1.R1040 c
Contiq ID
                   epx701\overline{1}08756.h1
5'-most EST
                   29810
Seq. No.
                   200336 1.R1040
Contig ID
5'-most EST
                   fC-gmse700838355b1
Method
                   BLASTN
                   g576508
NCBI GI
BLAST score
                   171
E value
                   3.0e-91
Match length
                   474
% identity
NCBI Description
                   Pisum sativum GTP-binding protein (IAP86) mRNA, complete
Seq. No.
                   29811
                   200363 1.R1040
Contig ID
5'-most EST
                   awf700838891.hl
                   29812
Seq. No.
                   200388 1.R1040
Contig ID
5'-most EST
                   awf700838927.hl
                   29813
Seq. No.
                   200414 1.R1040
Contig ID
                   g43960<del>6</del>2
5'-most EST
Method
                   BLASTX
                   g3928086
NCBI GI
BLAST score
                   577
                   1.0e-59
E value
Match length
                   160
% identity
                   71
                   (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29814
Seq. No.
                   200443 1.R1040
Contig ID
5'-most EST
                   asn701137407.hl
Seq. No.
                   29815
                   200450 1.R1040
Contig ID
5'-most EST
                   awf700839014.hl
                   BLASTX
Method
                   g3043529
NCBI GI
BLAST score
                   322
                   5.0e-30
E value
Match length
                   109
                   57
% identity
```

NCBI GI

```
(AJ002204) polyamine oxidase [Zea mays]
NCBI Description
Seq. No.
                   29816
                   200470 1.R1040
Contig ID
                   awf700839042.hl
5'-most EST
                   29817
Seq. No.
Contig ID
                   200473 1.R1040
5'-most EST
                   epx701104690.h1
                   29818
Seq. No.
Contig ID
                   200482 1.R1040
5'-most EST
                   awf700839061.h1
                   BLASTX
Method
NCBI GI
                   q2979498
BLAST score
                   181
E value
                   2.0e-13
Match length
                   101
                   35
% identity
NCBI Description
                   (AB012143) mRNA capping enzyme [Homo sapiens]
                   29819
Seq. No.
Contig ID
                   200503 1.R1040
                   jC-gmle01810044c10a1
5'-most EST
                   29820
Seq. No.
                   200568 1.R1040
Contig ID
5'-most EST
                   uC-gmropic063h11b1
                   29821
Seq. No.
Contig ID
                   200590 1.R1040
                   asn701142174.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244806
BLAST score
                   325
E value
                   5.0e-30
Match length
                   123
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   29822
Seq. No.
Contig ID
                   200617 1.R1040
5'-most EST
                   awf700\overline{8}42228.h1
                   29823
Seq. No.
                   200651 1.R1040
Contig ID
5'-most EST
                   awf700839338.hl
                   29824
Seq. No.
                   200662 1.R1040
Contig ID
                   jC-gmf\overline{1}02220083g01a1
5'-most EST
                   29825
Seq. No.
Contig ID
                   200725 1.R1040
5'-most EST
                   fC-gmse700841319f1
Method
                   BLASTX
```

q4185136

NCBI Description

```
BLAST score
                   343
E value
                   3.0e-32
Match length
                   93
                   69
% identity
                   (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   29826
                   200736 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}06335.h1
Method
                   BLASTX
NCBI GI
                   q4557060
BLAST score
                   375
E value
                   2.0e-36
Match length
                   94
% identity
NCBI Description
                   (ACO07154) putative chromosome-associated polypeptide, 5'
                  partial [Arabidopsis thaliana]
Seq. No.
                   200776 1.R1040
Contig ID
5'-most EST
                   awf700839527.hl
                  29828 --- -
Seq. No. --
                   200778 1.R1040
Contig ID
5'-most EST
                   awf700839530.h1
                   29829
Seq. No.
                   200782 1.R1040
Contig ID
5'-most EST
                   awf700839602.hl
Seq. No.
                   29830
                   200875_1.R1040
Contig ID
5'-most EST
                   jC-gmst02400065g06a2
Seq. No.
                   29831
                   200891 1.R1040
Contig ID
5'-most EST
                   awf700839780.h1
                   29832
Seq. No.
                   200942 1.R1040
Contig ID
5'-most EST
                   zhf700958504.h1
                                                                    4,
                  29833
Seq. No.
                   200951 1.R1040
Contig ID
5'-most EST
                   zhf700963648.h1
Seq. No.
                  29834
Contig ID
                   200953 1.R1040
                  k11701\overline{2}12871.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4490330
BLAST score
                  713
E value
                  1.0e-75
Match length
                  132
% identity
```

50.5

(AL035656) splicing factor-like protein [Arabidopsis

```
thaliana]
                   29835
Seq. No.
                  200956 1.R1040
Contig ID
                   fC-gmse700839826a5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g113595
BLAST score
                   696
                   2.0e-73
E value
                  194
Match length
                  64
% identity
                  ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
NCBI Description
                  >gi_100562_pir__S15024 aldose reductase-related protein -
                  barley >gi 18891 emb_CAA40747_ (X57526) aldose
                  reductase-related protein [Hordeum vulgare]
                   29836
Seq. No.
                   201015 1.R1040
Contig ID
                   awf700839928.hl
5'-most EST
                   29837
Seq. No.
                   201019 1.R1040
Contig ID
5'-most EST
                   crh700853734.h1
                   29838
Seq. No.
                   201122 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy028a09b1
Method
                   BLASTX
NCBI GI
                   g4206122
BLAST score
                   290
E value
                   5.0e-28
Match length
                   94
% identity
NCBI Description
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                   crystallinum]
Seq. No.
                   29839
                   201144 1.R1040
Contig ID
                   awf700840151.hl
5'-most EST
Seq. No.
                   29840
                   201146 1.R1040
Contig ID
5'-most EST
                   awf700840154.hl
                   BLASTX
Method
NCBI GI
                   q4091808
BLAST score
                   129
E value
                   8.0e-13
Match length
                   103
% identity
                   40
```

Seq. No. 29841

NCBI Description

Contig ID 201155_1.R1040 5'-most EST kl1701213171.h1

Method BLASTX NCBI GI g4539005

[Catharanthus roseus]

(AF053307) deacetylvindoline 4-0-acetyltransferase

```
BLAST score
                   326
                   2.0e-30
E value
Match length
                   108
                   77
% identity
                   (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   29842
Seq. No.
Contig ID
                   201173 1.R1040
5'-most EST
                   awf700840201.h1
Seq. No.
                   29843
                   201250 1.R1040
Contig ID
5'-most EST
                   dpv701100926.h1
Method
                   BLASTX
NCBI GI
                   q2506985
BLAST score
                   220
E value
                   5.0e-18
Match length
                   78
                   55
% identity
NCBI Description
                   CDC4-LIKE PROTEIN >gi_1580781 (M83822) beige-like protein
                   [Homo sapiens]
Seq. No.
                   29844
Contig ID----
                   201258 1.R1040------
                   awf700\overline{8}40338.h1
5'-most EST
Method
                   BLASTX
                   q3402754
NCBI GI
BLAST score
                   251
                   9.0e-22
E value
                   61
Match length
                   75
% identity
                   (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
                   29845
Seq. No.
                   201314 1.R1040
Contig ID
5'-most EST
                   awf700840446.hl
                   29846
Seq. No.
                   201381 1.R1040
Contig ID
5'-most EST
                   zhf700964591.h1
                   29847
Seq. No.
                   201396_1.R1040
Contig ID
                   uC-gmflminsoy014c07b1
5'-most EST
Method
                   BLASTX
                   g2262113
NCBI GI
BLAST score
                   716
E value
                   6.0e-76
Match length
                   165
% identity
NCBI Description
                   (AC002343) unknown protein [Arabidopsis thaliana]
                   29848
Seq. No.
                   201410 1.R1040
Contig ID
5'-most EST
                   awf700840648.hl
```

Seq. No.

Seq. No.

29856

```
201494 1.R1040
Contig ID
5'-most EST
                   awf700840829.hl
                   29850
Seq. No.
                   201523 1.R1040
Contig ID
5'-most EST
                   fC-gmse700840889f1
Method
                   BLASTX
NCBI GI
                   g2708745
BLAST score
                   694
E value
                   2.0e-73
Match length
                   148
                   90
% identity
                   (AC003952) putative calcium-dependent ser/thr protein
NCBI Description
                   kinase [Arabidopsis thaliana]
Seq. No.
                   29851
                   201596 1.R1040
Contig ID
                   awf700841048.h1
5'-most EST
Seq. No.
                   29852
                   201650 1.R1040
Contig ID
5'-most EST
                   q56070\overline{5}4
Method
                   BLASTX
NCBI GI-
                   q4455358
BLAST score
                   198
E value
                   6.0e-15
Match length
                   75
% identity
                   52
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   29853
                   201728 1.R1040
Contig ID
5'-most EST
                   awf700842888.h1
Seq. No.
                   29854
Contig ID
                   201752 1.R1040
5'-most EST
                   all700863237.hl
Method
                   BLASTX
NCBI GI
                   q2853087
BLAST score
                   171
E value
                   3.0e-12
Match length
                   105
% identity
                   41
NCBI Description
                   (AL021768) putative protein [Arabidopsis thaliana]
                   29855
Seq. No.
Contig ID
                   201813 1.R1040
5'-most EST
                   kl1701214532.h1
Method
                   BLASTX
NCBI GI
                   q4544422
BLAST score
                   655
E value
                   7.0e-69
Match length
                   144
% identity
NCBI Description
                   (AC006955) putative fimbrin [Arabidopsis thaliana]
```

Contig ID

```
201845 1.R1040
Contig ID
                   bth700848401.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4512685
BLAST score
                   301
E value
                   2.0e-27
Match length
                   117
% identity
                   49
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4559325_gb_AAD22987.1_AC007087 6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
                   29857
Seq. No.
                   201887 1.R1040
Contig ID
5'-most EST
                   awf700842954.h1
                   29858
Seq. No.
                   201896 1.R1040
Contig ID
5'-most EST
                   awf700841536.h1
                   29859
Seq. No.
                   201899 1.R1040
Contig ID
                   zsg701119244.h1
5'-most EST
Method ---
                   BLASTX
                   g1778376
NCBI GI
BLAST score
                   373
E value
                   5.0e-36
Match length
                   104
% identity
                   71
                   (U81288) PsRT17-1 [Pisum sativum]
NCBI Description
Seq. No.
                   29860
                   202021 1.R1040
Contig ID
5'-most EST
                   pmv700890618.hl
Seq. No.
                   29861
                   202037 1.R1040
Contig ID
5'-most EST
                   awf700841816.h1
                   29862
Seq. No.
                   202045 1.R1040
Contig ID
5'-most EST
                   a11700863107.h1
Method
                   BLASTX
NCBI GI
                   g2462750
BLAST score
                   316
                   3.0e-29
E value
Match length
                   80
% identity
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   29863
                   202071 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400073g02a1
Seq. No.
                   29864
```

202174_1.R1040

```
5'-most EST
                   uC-gmrominsoy102h10b1
Method
                   BLASTX
                                                          NCBI GI
                   g3461820
                  252
BLAST score
                   8.0e-22
E value
                   113
Match length
                   42
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   29865
                   202200 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220141h10a1
Method
                   BLASTN
NCBI GI
                   q416257
BLAST score
                   75
                   6.0e-34
E value
Match length
                   191
% identity
                   86
                   Rice mRNA for elongation factor G, partial sequence
NCBI Description
                   >gi 3107867 dbj D42263 D42263 Rice callus cDNA, S155
Seq. No.
                   29866
                   202215 1.R1040
Contig ID
5'-most EST
                   awf700842019.h1- --
Method
                   BLASTX
NCBI GI
                   q2829912
BLAST score
                   285
E value
                   3.0e - 32
Match length
                   131
% identity
                   (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29867
Contig ID
                   202272 1.R1040
5'-most EST
                   uC-gmrominsoy284a09b1
Method
                   BLASTN
NCBI GI
                   q2618602
BLAST score
                   175
E value
                   1.0e-93
Match length
                   483
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   29868
Seq. No.
Contig ID
                   202309 1.R1040
5'-most EST
                   awf700842163.hl
Method
                   BLASTX
NCBI GI
                   q4415914
BLAST score
                   382
                   9.0e-37
E value
Match length
                   170
% identity
NCBI Description
                   (AC006282) unknown protein [Arabidopsis thaliana]
```

Seq. No.

```
Contig ID
                  202317 1.R1040
5'-most EST
                  bth700849528.h1
Seq. No.
                  29870
                  202320 1.R1040
Contig ID
5'-most EST
                  g5605865
                  29871
Seq. No.
Contig ID
                  202334 1.R1040
5'-most EST
                  awf700842202.hl
                  29872
Seq. No.
                  202342 1.R1040
Contig ID
                  awf700842212.h1
5'-most EST
                  29873
Seq. No.
                  202387 1.R1040
Contig ID
                  awf700842274.h1
5'-most EST
                  29874
Seq. No.
                  202404 1.R1040
Contig ID
5'-most EST
                  crh700852351.h1
                  BLASTX
Method
NCBI GI ---
                  g2911049- ---
BLAST score
                  241
                  1.0e-20
E value
Match length
                  75
                  57
% identity
                  (AL021961) glucosyltransferase -like protein [Arabidopsis
NCBI Description
                  thaliana]
                  29875
Seq. No.
                  202446 1.R1040
Contig ID
5'-most EST
                  g5676878
Method
                  BLASTX
NCBI GI
                  g3914212
BLAST score
                  594
E value
                  2.0e-61
                  181
Match length
% identity
                  5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)
NCBI Description
                   (5-OPASE) >gi 1732065 (U70825) 5-oxo-L-prolinase [Rattus
                  norvegicus]
                                                                          29876
Seq. No.
                  202470 1.R1040
Contig ID
                  g5126398
5'-most EST
                  29877
Seq. No.
                  202481_1.R1040
Contig ID
5'-most EST
                  q4305630
Method
                  BLASTX
                  q31504·10
NCBI GI
BLAST score
                  325
                  5.0e-30
E value
                  98
Match length
                  60
% identity
```

```
NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 29878
Contig ID 202489_1.R1040
5'-most EST uC-gmrominsoy238e05b1

Seq. No. 29879
```

Contig ID 202531_1.R1040 5'-most EST pxt700944238.h1

Seq. No. 29880
Contig ID 202661_1.R1040
5'-most EST crh700856508.h1

Seq. No. 29881 Contig ID 202673_1.R1040 5'-most EST dpv701097491.h1

Seq. No. 29882 Contig ID 202710_1.R1040

5'-most EST uC-gmflminsoy027b12b1

 Seq. No.
 29883

 Contig ID
 202762_1.R1040

 5'-most EST
 awf700842852.h1

Method BLASTX
NCBI GI g2292907
BLAST score 176
E value 3.0e-13
Match length 77

% identity 48

NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]

 Seq. No.
 29884

 Contig ID
 202789_1.R1040

 5'-most EST
 awf700842907.h1

Method BLASTX
NCBI GI g2190544
BLAST score 260
E value 2.0e-22
Match length 64

Match length 64 % identity 84

NCBI Description (AC001229) Similar to Saccharomyces hypothetical protein

P9642.2 (gb_U40828). [Arabidopsis thaliana]

Seq. No. 29885

Contig ID 202806_1.R1040 5'-most EST zhf700956048.h1

Seq. No. 29886

Contig ID 202857_1.R1040 5'-most EST awf700843008.h1

Method BLASTX
NCBI GI g1619946
BLAST score 364
E value 3.0e-34
Match length 251

NCBI GI

```
% identity
                    (U71300) snRNA activating protein complex 50kD subunit
NCBI Description
                    [Homo sapiens] >gi 4097682 (U66413) proximal sequence
                   element-binding transcription factor beta subunit [Homo
                   sapiens] >gi_4507105_ref_NP_003075.1_pSNAPC3_ small nuclear
RNA activating complex, polypeptide 3, 50kD
Seq. No.
Contig ID
                   202878 1.R1040
5'-most EST
                   leu701\overline{1}47877.h1
                   29888 °
Seq. No.
                   202962_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy212g10b1
Method
                   BLASTN
NCBI GI
                   q18729
BLAST score
                   124
                   3.0e-63
E value
Match length
                   132
% identity
                   Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
                   29889
Seq. No.
Contig ID-----
                   202962-2.R1040---
                   asn701\overline{1}36722.h1
5'-most EST
Method
                   BLASTN
                   q18729
NCBI GI
                   167
BLAST score
                   7.0e-89
E value
                   285
Match length
% identity
                   99
                   Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
                   29890
Seq. No.
                   202962 3.R1040
Contig ID
5'-most EST
                   rlr700896170.h1
Method
                   BLASTN
NCBI GI
                   g18729
BLAST score
                   235
                   1.0e-129
E value
                   251
Match length
% identity
NCBI Description
                   Soybean (Glycine max) 18S ribosomal RNA
Seq. No.
                   29891
                   202962 5.R1040
Contig ID
5'-most EST
                   jC-gmle01810084g01d1
Seq. No.
                   29892
                   202971 1.R1040
Contig ID
5'-most EST
                   awf700843186.h1
Seq. No.
                   29893-
                   203016 1.R1040
Contig ID
                   g4291629
5'-most EST
Method
                   BLASTX
```

g2224931

- 7 Mar - 1

```
BLAST score
                   669
                   2.0e-70
E value
Match length
                   165
% identity
                   75
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                   thaliana]
                   29894
Seq. No.
                   203019 1.R1040
Contig ID
5'-most EST
                   awf700843274.h1
                   29895
Seq. No.
                   203056_1.R1040
Contig ID
5'-most EST
                   fC-gmse700843342f1
Method
                   BLASTX
NCBI GI
                   g3024425
BLAST score
                   417
                   3.0e-41
E value
Match length
                   101
% identity
                   80
                   PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
NCBI Description
                   (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi_1076700_pir__S53297
                   pyruvate, orthophosphate dikinase (EC 2.7.9.1) - Flaveria
                   pringlei >gi_577776_emb_CAA53223_ (X75516) -
pyruvate,orthophosphate dikinase [Flaveria pringlei]
                   29896
Seq. No.
Contig ID
                   203103 1.R1040
                   awf700843412.h1
5'-most EST
                   29897
Seq. No.
                   203167 1.R1040
Contig ID
5'-most EST
                   yuv700862711.h1
                   29898
Seq. No.
Contig ID
                   203172_1.R1040
5'-most EST
                   uC-gmropic071e12b1
Method
                   BLASTX
                   g2781351
NCBI GI
                   376
BLAST score
E value
                   4.0e-36
Match length
                   99
% identity
                   82
                   (AC003113) F2401.7 [Arabidopsis thaliana]
NCBI Description
                   29899
Seq. No.
                   203172_2.R1040
Contig ID
5'-most EST
                   yuv700862718.hl
Method
                   BLASTX
NCBI GI
                   q2781351
                   193
BLAST score
                   7.0e-15
E value
Match length
                   52
% identity
                   79
                   (AC003113) F2401.7 [Arabidopsis thaliana]
NCBI Description
```

29900

Seq. No.

```
203263 1.R1040
Contig ID
                   uC-gmrominsoy062b06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2262136
BLAST score
                   254
                   9.0e-22
E value
                   87
Match length
% identity
                   57
NCBI Description
                   (AC002330) predicted protein of unknown function
                   [Arabidopsis thaliana] >gi_4263520_gb_AAD15346_ (AC004044)
                   predicted protein of unknown function [Arabidopsis
                   thaliana]
Seq. No.
                   29901
                   203306 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910014h03d1
                   29902
Seq. No.
Contig ID
                   203318 1.R1040
5'-most EST
                   gsv701\overline{0}56554.h1
                   29903
Seq. No.
                   203335 1.R1040
Contig ID
5'-most EST
                   zhf700955211.h1
Seq. No.
                   29904
                   203404 1.R1040
Contig ID
5'-most EST
                   zvp700764256.hl
                   29905
Seq. No.
                   203430 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400024g05d1
                   29906
Seq. No.
                   203449 1.R1040
Contig ID
5'-most EST
                   fC-gmro7000764321f1
Method
                   BLASTX
NCBI GI
                   a2062174
BLAST score
                   148
E value
                   4.0e-09
Match length
                   77
% identity
                   (AC001645) transcription factor (TINY) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   29907
Seq. No.
Contig ID
                   203499 1.R1040
5'-most EST
                   uC-gmrominsoy111f11b1
Method
                   BLASTX
NCBI GI
                   a3540207
BLAST score
                   220
E value
                   7.0e-18
Match length
                   97
% identity
                   (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
203501 1.R1040
Contig ID
5'-most EST
                  bth700844066.h1
Seq. No.
                  29909
                  203506 1.R1040
Contig ID
                  fC-gmro7000764393f1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  610
E value
                  3.0e-63
                  214
Match length
                  10
% identity
                   (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  29910
Seq. No.
                  203514 1.R1040
Contig ID
                  fua701040193.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4314363
BLAST score
                  394
E value
                  2.0e-38
Match length
                  111
                  64 . - -
% identity -
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  29911
Seq. No.
                  203534 1.R1040
Contig ID
5'-most EST
                  ary700764437.hl
                  29912
Seq. No.
                  203552 1.R1040
Contig ID
5'-most EST
                  yz1700966943.h1
                  29913
Seq. No.
                  203564 1.R1040
Contig ID
5'-most EST
                  ary700764472.h1
Method
                  BLASTX
                  g1086601
NCBI GI
BLAST score
                  139
                   9.0e-09
E value
Match length
                  81
% identity
                  35
                   (U41008) Similar to reverse transcriptase [Caenorhabditis
NCBI Description
                  elegans]
                  29914
Seq. No.
Contig ID
                  203592_1.R1040
                  bth700843507.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4559382
BLAST score
                  213
                  2.0e-17
E value
Match length
                   62
                  58
% identity
                   (AC006526) putative DNA binding protein [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                    29915
Contig ID
                    203595 1.R1040
5'-most EST
                    leu701149186.hl
Method
                   BLASTX
NCBI GI
                    q2827552
BLAST score
                    159
                    5.0e-11
E value
Match length
                    40
% identity
                    70
                    (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                    29916
Seq. No.
                    203607 1.R1040
Contig ID
5'-most EST
                   dkc700968027.h1
                    29917
Seq. No.
                    203620 1.R1040
Contig ID
                   bth700843540.hl
5'-most EST
Seq. No.
                   29918
                   203623 1.R1040
Contig ID
5'-most EST
                   leu701156525.h1
                    29919
Seq. No.
                    203639 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy232a01b1
Method
                   BLASTX
NCBI GI
                   g728868
BLAST score
                   169
E value
                    1.0e-11
Match length
                    91
                    49
% identity
NCBI Description
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
                   >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                   protein [Brassica napus]
                   29920
Seq. No.
Contig ID
                   203656 1.R1040
5'-most EST
                   uC-gmrominsoy122a12b1
Method
                   BLASTX
NCBI GI
                   g2275204
BLAST score
                   523
E value
                    6.0e-53
Match length
                   202
                   58
% identity
NCBI Description
                    (AC002337) DNA binding protein isolog [Arabidopsis
                   thaliana]
                   29921
Seq. No.
                   203656 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy047b10b1
Method
                   BLASTX
                   g2275204
NCBI GI
BLAST score
                   172
```

7.0e-15

E value

```
69
Match length
                   70
% identity
NCBI Description
                   (AC002337) DNA binding protein isolog [Arabidopsis
                   thaliana]
                   29922
Seq. No.
                   203656 3.R1040
Contig ID
5'-most EST
                   dpv701102808.h1
                   29923
Seq. No.
                   203684 1.R1040
Contig ID
5'-most EST
                   bth700843616.h1
                   29924
Seq. No.
                   203687 1.R1040
Contig ID
5'-most EST
                   bth700843620.h1
                   29925
Seq. No.
                   203695 1.R1040
Contig ID
5'-most EST
                   r1r700\overline{9}01381.h1
                   29926
Seq. No.
Contig ID
                   203700 1.R1040
5'-most EST
                   bth700843635.h1
                   BLASTX
Method
NCBI GI
                   q2245081
BLAST score
                   303
                   9.0e-28
E value
                   127
Match length
                   54
% identity
NCBI Description
                   (Z97343) myosin II heavy chain homolog [Arabidopsis
                   thaliana]
                   29927
Seq. No.
                   203724 1.R1040
Contig ID
5'-most EST
                   bth700843661.hl
Method
                   BLASTX
                   q4490309
NCBI GI
BLAST score
                   418
                   4.0e-41
E value
                   134
Match length
                   63
% identity
                   (AL035678) peroxidase ATP17a-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   29928
Seq. No.
Contig ID
                   203728 1.R1040
5'-most EST
                   bth700843665.h1
Seq. No.
                   29929
                   203754_1.R1040
Contig ID
                   jC-gmle01810094g10a1
5'-most EST
Method
                   BLASTX
                   q4006861
NCBI GI
BLAST score
                   339
                   8.0e-32
E value
```

Match length

```
% identity
NCBI Description
                   (299707) tubulin-like protein [Arabidopsis thaliana]
Seq. No.
                   29930
                   203784 1.R1040
Contig ID
5'-most EST
                   bth700843730.h1
Method
                   BLASTX
NCBI GI
                   q2499903
BLAST score
                   393
                   2.0e-38
E value
Match length
                   108
% identity
                   64
                   PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA) >gi 1184161
NCBI Description
                   (U35646) aminopeptidase [Mus musculus]
                   >gi_1585925_prf__2202260A puromycin sensitive
                   aminopeptidase [Mus musculus]
Seq. No.
                   29931
                   203828 1.R1040
Contig ID
5'-most EST
                  bth700843779.h1
Method
                   BLASTX
NCBI GI
                   g4314387
BLAST score
                   705
E value
                   2.0e-74
Match length
                  152
% identity
NCBI Description
                   (AC006232) putative beta-alanine synthetase [Arabidopsis
                   thaliana]
                   29932
Seq. No.
Contig ID
                   203847 1.R1040
5'-most EST
                   jC-gmro02910020b02a1
                  29933
Seq. No.
Contig ID
                   203870 1.R1040
5'-most EST
                  dpv701\overline{1}01957.h1
                  BLASTX
Method
NCBI GI
                   g4538981
BLAST score
                   261
E value
                   2.0e-22
Match length
                  73
% identity
                   63
NCBI Description
                   (AL049487) putative protein [Arabidopsis thaliana]
                  29934
Seq. No.
Contig ID
                  203895 1.R1040
5'-most EST
                  bth700843863.h1
Method
                  BLASTX
NCBI GI
                  g1483150
BLAST score
                  356
E value
                   4.0e-34
Match length
                  92
                  75
% identity
NCBI Description
                   (D84417) monodehydroascorbate reductase [Arabidopsis
                  thaliana]
```

Seq. No.

Contig ID

```
203969 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy053g11b1
                   29936
Seq. No.
                   203979 1.R1040
Contig ID
                   pmv700893093.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3287695
BLAST score
                   459
E value
                   1.0e-45
Match length
                   142
% identity
                   56
NCBI Description
                   (AC003979) Similar to hypothetical protein C34B7.2
                   gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                   thaliana]
                   29937
Seq. No.
                   203981 1.R1040
Contig ID
5'-most EST
                  bth700843977.hl
Method
                   BLASTX
NCBI GI
                   g3540207
BLAST score
                   133
                   9.0e-16
E value
                   70
Match length
                   59
% identity
                   (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   29938
Seq. No.
                   204023_1.R1040
Contig ID
5'-most EST
                   fC-qmro700844046f1
Method
                   BLASTX
NCBI GI
                   g4371296
BLAST score
                   269
E value
                   2.0e-23
                   107
Match length
% identity
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   29939
Seq. No.
                   204035 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}58057.h1
Method
                   BLASTX
NCBI GI
                   q4454468
BLAST score
                   716
                   7.0e-76
E value
                   182
Match length
% identity
                   (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   29940
Seq. No.
                   204104 1.R1040
Contig ID
5'-most EST
                   dpv701102894.h1
                   29941
Seq. No.
```

204152 1.R1040

5'-most EST

```
5'-most EST
                   q5687881
Method
                   BLASTX
-NCBI GI
                   q3047104
BLAST score
                   777
E value
                   5.0e-83
Match length
                   192
                   79
% identity
NCBI Description
                   (AF058919) No definition line found [Arabidopsis thaliana]
                   29942
Seq. No.
                   204169 1.R1040
Contig ID
5'-most EST
                   dpv701099601.h1
                   BLASTX
Method
                   q2160150
NCBI GI
BLAST score
                   514
                   5.0e-52
E value
                   184
Match length
% identity
                   (AC000375) EST gb_T43829 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   29943
Seq. No.
                   204207_1.R1040
Contig ID
5'-most EST
                   fC-gmro700844289f1
Method
                   BLASTX
                   g3582021
NCBI GI
                   443
BLAST score
                   4.0e-44
E value
Match length
                   131
% identity
                   61
NCBI Description
                   (Y09423) cytochrome P450 [Nepeta racemosa]
                   29944
Seq. No.
                   204209 1.R1040
Contig ID
                   dpv701\overline{1}01518.h1
5'-most EST
Seq. No.
                   29945
                   204260 1.R1040
Contig ID
                   fua701041238.hl
5'-most EST
                   29946
Seq. No.
Contig ID
                   204282 1.R1040
                   fC-gmro700844391a3
5'-most EST
Method
                   BLASTX
                   g129586
NCBI GI
BLAST score
                   3132
E value
                   0.0e+00
Match length
                   699
                   88
% identity
                   PHENYLALANINE AMMONIA-LYASE CLASS III >gi_81878_pir__S04128
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) class III - kidney
                   bean
                   29947
Seq. No.
                   204385 1.R1040
Contig ID
```

jC-gmro02910007c03d1

Seq. No.

29955

```
29948
Seq. No.
                  204399 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910040h01a1
                  29949
Seq. No.
                  204409 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810073e01a1
Method
                  BLASTX
NCBI GI
                  g3549679
BLAST score
                  535
E value
                  2.0e-54
Match length
                  214
% identity
NCBI Description
                   (AL031394) putative protein [Arabidopsis thaliana]
                  29950
Seq. No.
Contig ID
                  204433 1.R1040
5'-most EST
                  jC-gmro02910066d05a1
Method
                  BLASTX
NCBI GI
                  g3786008
BLAST score
                  173
                  4.0e-12
E value
Match length
                  186
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                  29951
Seq. No.
                  204467 1.R1040
Contig ID
                  bth700845393.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4105794
BLAST score
                  306
                  6.0e-28
E value
                  119
Match length
% identity
                   49
NCBI Description
                   (AF049928) PGP224 [Petunia x hybrida]
                  29952
Seq. No.
                  204473 1.R1040
Contig ID
5'-most EST
                  bth700844643.h1
Seq. No.
                  29953
                  204531 1.R1040
Contig ID
5'-most EST
                  fC-gmro700844719f1
Method
                  BLASTX
                  g1313907
NCBI GI
BLAST score
                  469
E value
                  8.0e-47
Match length
                  122
% identity
                  (D84507) CDPK-related protein kinase [Zea mays]
NCBI Description
Seq. No.
                  29954
                  204563 1.R1040
Contig ID ·
5'-most EST
                  jC-gmro02910038d02d1
```

```
204600 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy257f01b1
 Method
                    BLASTX
 NCBI GI
                    g1616741
 BLAST score
                    336
 E value
                    2.0e-31
 Match length
                    135
 % identity
                    49
 NCBI Description
                    (U60276) hASNA-I [Homo sapiens]
                    29956
 Seq. No.
                    204600 2.R1040
 Contig ID
 5'-most EST
                    g5606382
 Method
                    BLASTX
 NCBI GI
                    q267453
 BLAST score
                    383
 E value
                    5.0e-37
 Match length
                    127
 % identity
                    61
                   HYPOTHETICAL 37.5 KD PROTEIN ZK637.5 IN CHROMOSOME III
 NCBI Description
                    >gi 102496 pir S15791 arsenical pump-driving ATPase
                   homolog - Caenorhabditis elegans >gi_3881667_emb_CAA77452
                    (Z11115) predicted using Genefinder; ArsA homologue; cDNA
                   EST EMBL:D73741 comes from this gene; cDNA EST EMBL:D71137
                    comes from this gene; cDNA EST EMBL:C08164 comes from this
                    gene; cDNA EST EMBL: C09807 comes from this gene; cD
                    29957
 Seq. No.
                    204643 1.R1040
 Contig ID
 5'-most EST
                    g56062\overline{3}9
                    29958
 Seq. No.
                    204649 1.R1040
 Contig ID
 5'-most EST
                   bth700844872.h1
 Method
                    BLASTX
 NCBI GI
                    g2494736
 BLAST score
                    763
 E value
                    1.0e-88
Match length
                    228
 % identity
                    71
                   GLUCOSE INHIBITED DIVISION PROTEIN A
 NCBI Description
                    >gi 1001595 dbj BAA10223 (D64000) glucose inhibited
                   division protein A [Synechocystis sp.]
                    29959
 Seq. No.
                    204668 1.R1040
 Contig ID
                    fua701038236.hl
 5'-most EST
Method
                   BLASTX
                    g3947735
NCBI GI
BLAST score
                    147
E value
                    2.0e-10
Match length
                   135
 % identity
                    36
NCBI Description
                    (AJ009720) NL27 [Solanum tuberosum]
                   29960
Seq. No.
```

204713 1.R1040

Contig ID

```
5'-most EST
                   jC-gmle01810012d08a1
                   29961
Seq. No.
Contig ID
                   204716 1.R1040
                   uC-gmrominsoy176b11b1
5'-most EST
                   BLASTX
Method
                   q4415924
NCBI GI
                   403
BLAST score
                   2.0e-48
E value
Match length
                   174
                   57
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   29962
Seq. No.
Contig ID
                   204718 1.R1040
                   leu701155225.h1
5'-most EST
                   BLASTX
Method
                   g3367522
NCBI GI
BLAST score
                   284
E value
                   2.0e-25
Match length
                   102
                   52
% identity
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   29963
                   204731 1.R1040
Contig ID
                   uC-gmflminsoy016b12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2191136
BLAST score
                   289
                   5.0e-26
E value
Match length
                   131
                   50
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   29964
Seq. No.
Contig ID
                   204764 1.R1040
5'-most EST
                   dpv701\overline{1}01540.h1
                   29965
Seq. No.
                   204773 1.R1040
Contig ID
                   leu701156438.hl
5'-most EST
                  29966
Seq. No.
                  204791 1.R1040
Contig ID
5'-most EST
                  kl1701207611.h1
Method
                  BLASTX
                  g2459441
NCBI GI
BLAST score
                   315
                  5.0e-30
E value
                  108
Match length
```

% identity

5'-most EST

```
NCBI Description (AC002332) putative SWI/SNF complex subunit BAF170
                   [Arabidopsis thaliana]
                   29967
Seq. No.
                   204791 2.R1040
Contig ID
5'-most EST
                   fua701037770.hl
                   29968
Seq. No.
Contig ID
                   204793 1.R1040
5'-most EST
                  g5126294
Seq. No.
                   29969
Contig ID
                   204811 1.R1040
5'-most EST
                  g4286952
Seq. No.
                  29970
                   204818 1.R1040
Contig ID
5'-most EST
                   zsg701118888.hl
                  29971
Seq. No.
Contig ID
                   204852 1.R1040
5'-most EST
                  bth700846660.h1
                  BLASTX
Method
                  g4467156 --
NCBI GI - -
BLAST score
                  170
                   2.0e-12
E value
Match length
                  56
                                               40
% identity
                   62
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  29972
Seq. No.
Contig ID
                  204862 1.R1040
                  bth700848868.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3005575
BLAST score
                  169
E value
                   1.0e-89
Match length
                  397
                  86
% identity
NCBI Description Glycine max putative high affinity nitrate transporter
                   (NRT2) mRNA, complete cds
Seq. No.
                  29973
                  204866 1.R1040
Contig ID
                   jC-qmro02910008f11a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2746086
BLAST score
                  504
                   4.0e-51
E value
Match length
                  159
% identity
                   65
                   (AF025292) putative high-affinity potassium transporter
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                  29974
                  204870 1.R1040
Contig ID
```

34.

bth700845152.h1

5'-most EST

```
Method
                    BLASTX
                    g4056506
 NCBI GI
 BLAST score
                    544
 E value
                    1.0e-55
 Match length
                    228
 % identity
                    46
                    (AC005896) nodulin-like protein [Arabidopsis thaliana]
 NCBI Description
                    29975
 Seq. No.
                    204922 1.R1040
 Contig ID
 5'-most EST
                    jC-gmst02400025a10d1
                    29976
 Seq. No.
                    204933 1.R1040
 Contig ID
 5'-most EST
                    qsv701\overline{0}48851.h1
 Method
                    BLASTX
                    q1169421
 NCBI GI
 BLAST score
                    504
 E value
                    3.0e-51
                    125
 Match length
                    74
 % identity
                    DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG (XDRG)
 NCBI Description
                    >gi_2120159_pir__I51426 GTP-binding protein DRG - African
                    clawed frog >gi_433422_dbj_BAA02978_ (D13865) GTP-binding
                    protein DRG [Xenopus laevis]
· Seq. No.
                    29977
                    204937 1.R1040
 Contig ID
                    k11701\overline{2}03446.h1
 5'-most EST
                    29978
 Seq. No.
                    204938 1.R1040
 Contig ID
 5'-most EST
                    epx701\overline{1}10347.h1
 Method
                    BLASTX
                    g2342682
 NCBI GI
 BLAST score
                    390
 E value
                    5.0e-38.
 Match length
                    102
                    73
 % identity
 NCBI Description
                    (AC000106) Contains similarity to Rattus AMP-activated
                    protein kinase (gb X95577). [Arabidopsis thaliana]
                    29979
 Seq. No.
 Contig ID
                    204941 1.R1040
                    jC-qmle01810051e07a1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g4467096
 BLAST score
                    241
 E value
                    1.0e-25
 Match length
                    87
 % identity
                    (AL035538) putative protein [Arabidopsis thaliana]
 NCBI Description
                    29980
 Seq. No.
                    204956 1.R1040
 Contig ID
```

uC-gmropic068e03b1

E value

1.0e-25

```
29981
Seq. No.
                   204970 1.R1040
Contig ID
                   bth700845277.h1
5'-most EST
Method
                   BLASTX
                   g3152576
NCBI GI
BLAST score
                   295
                   1.0e-26
E value
Match length
                   155
                   39
% identity
                   (AC002986) Similar to liver-specific transport protein
NCBI Description
                   gb L27651 from Rattus norviegicus. [Arabidopsis thaliana]
                   29982
Seq. No.
                   204995 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400026c11d1
                   29983
Seq. No.
                   205005 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}52539.h1
                   29984
Seq. No.
                   205088_1.R1040
Contig ID
                   uC-gmflminsoy046e06b1
5'-most EST
Method --
                   BLASTX
                   g3953475
NCBI GI
BLAST score
                   216
E value
                   2.0e-17
                   68
Match length
% identity
                   65
                   (AC002328) F2202.20 [Arabidopsis thaliana]
NCBI Description
                   29985
Seq. No.
                   205090 1.R1040
Contig ID
5'-most EST
                   g4292651
                   29986
Seq. No.
Contig ID
                   205118 1.R1040
5'-most EST
                   asn701135365.h1
                   29987
Seq. No.
                   205121 1.R1040
Contig ID
5'-most EST
                   bth700845459.h1
Method
                   BLASTX
NCBI GI
                   g2262113
BLAST score
                   527
                   1.0e-53
E value
                   142
Match length
                   70
% identity
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   29988
Seq. No.
                   205136 1.R1040
Contig ID
                   uC-gmropic056e02b1
5'-most EST
Method
                   BLASTX
                   g3184082
NCBI GI
BLAST score
                   288
```

```
Match length
                  145
                  39
% identity
                   (AL023781) N-terminal acetyltransferase 1
NCBI Description
                   [Schizosaccharomyces pombe]
                  29989
Seq. No.
                  205179 1.R1040
Contig ID
                  bth700845537.h1
5'-most EST
                  29990
Seq. No.
                  205198 1.R1040
Contig ID
5'-most EST
                  bth700845558.h1
                  BLASTX
Method
                  g3510251
NCBI GI
                  280
BLAST score
                  5.0e-25
E value
                  118
Match length
% identity
                  46
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  29991
Seq. No.
                  205215 1.R1040
Contig ID
                  jex700905993.hl
5'-most EST
                  29992
Seq. No.
                  205244 1.R1040
Contig ID
                  bth700845626.h1
5'-most EST
Method
                  BLASTX
                  q3250676
NCBI GI
                  284
BLAST score
                  9.0e-26
E value
                  85
Match length
                  61
% identity
                  (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
                  29993
Seq. No.
                  205294 1.R1040
Contig ID
5'-most EST
                  dpv701099773.hl
                  29994
Seq. No.
                  205295 1.R1040
Contig ID
5'-most EST
                  bth700845691.hl
                  BLASTX
Method
                  q3643088
NCBI GI
                  128
BLAST score
                  5.0e-09
E value
                  55
Match length
% identity
                  (AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
                  29995
Seq. No.
                  205333 1.R1040
Contig ID
                  fC-gmf1700863043f1
5'-most EST
                  BLASTX
Method
                  g2459435
NCBI GI
```

BLAST score

Contig ID

5'-most EST

```
4.0e-10
E value
Match length
                  34
                  82
% identity
                   (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  29996
Seq. No.
                  205413 1.R1040
Contig ID
                  bth700845840.h1
5'-most EST
                  29997
Seq. No.
                  205432 1.R1040
Contig ID
                   zhf700954646.hl
5'-most EST
                  29998
Seq. No.
                  205488 1.R1040
Contig ID
5'-most EST
                  k11701203633.h2
                  29999
Seq. No.
                  205494 1.R1040
Contig ID
5'-most EST
                  g5175573
Method
                  BLASTX
NCBI GI
                  g4006864
BLAST score
                   447....
E value
                   4.0e-45
Match length
                  227
% identity
                  52
NCBI Description
                  (Z99707) nucleoporin-like protein [Arabidopsis thaliana]
Seq. No.
                  30000
                  205502 1.R1040
Contig ID
5'-most EST
                  q4260099
Method
                  BLASTX
NCBI GI
                  q3559805
BLAST score
                  378
E value
                   3.0e-36
Match length
                   95
% identity
NCBI Description
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
                  thaliana]
                  30001
Seq. No.
Contig ID
                  205526 1.R1040
5'-most EST
                  uC-qmrominsoy187f10b1
Method
                  BLASTX
NCBI GI
                  q3122957
BLAST score
                  222
E value
                  6.0e-18
Match length
                  149
% identity
                  30
                  TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi 2649967
NCBI Description
                   (AE001060) DNA topoisomerase VI, subunit B (top6B)
                   [Archaeoglobus fulgidus]
                  30002
Seq. No.
```

205551 1.R1040

bth700846004.h1

```
30003
Seq. No.
                   205573 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}53977.h1
                   30004
Seq. No.
                   205588 1.R1040
Contig ID
                   fC-gmro700847605a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1161167
BLAST score
                   331
                   7.0e-31
E value
Match length
                   120
% identity
                   53
                  (L42466) ethylene-forming enzyme [Picea glauca]
NCBI Description
                   30005
Seq. No.
                   205645 1.R1040
Contig ID
                   q4296319
5'-most EST
                   30006
Seq. No.
                   205683_1.R1040
Contig ID
5'-most EST
                   fC-gmro700748726d3
                   30007
Seq. No.
                   205683 2.R1040
Contig ID
5'-most EST
                   zhf700957022.h1
                   30008
Seq. No.
                   205697 1.R1040
Contig ID
                   bth700846175.h1
5'-most EST
Method
                   BLASTN
                   g4200043
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
Match length
                   84
                   88
% identity
                   Glycyrrhiza echinata CYP Ge-31 mRNA for cytochrome P450,
NCBI Description
                   complete cds
                   30009
Seq. No.
                   205698 1.R1040
Contig ID
                   jex700908673.hl
5'-most EST
                   30010
Seq. No.
                   205706 1.R1040
Contig ID
                   asn701\overline{1}39026.h1
5'-most EST
                   BLASTX
Method
                   q544184
NCBI GI
BLAST score
                   340
                   7.0e-32
E value
Match length
                   81
% identity
                   70
                   4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
NCBI Description
                   (DISPROPORTIONATING ENZYME) (D-ENZYME)
                   >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC
                   2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664)
```

```
Seq. No.
                   30011
Contig ID
                   205768 1.R1040
                   bth700846263.h1
5'-most EST
                   BLASTX
Method
                   g4262224
NCBI GI
BLAST score
                   288
                   6.0e-26
E value
Match length
                   126
                   4.5
% identity
NCBI Description
                   (AC006200) putative amino acid or GABA permease
                   [Arabidopsis thaliana]
                   30012
Seq. No.
                   205797 1.R1040
Contig ID
                   bth700846303.h1
5'-most EST
                   30013
Seq. No.
                   205871 1.R1040
Contig ID
5'-most EST
                   bth700846401.h1
                   30014
Seq. No.
                  205875 1.R1040-
Contig ID --
                   bth700846406.h1
5'-most EST
                   30015
Seq. No.
                   205884 1.R1040
Contig ID
                   bth700846417.h1
5'-most EST
                   30016
Seq. No.
                   205923 1.R1040
Contig ID
                   k11701\overline{2}14749.h1
5'-most EST
                   30017
Seq. No.
                   205927 1.R1040
Contig ID
5'-most EST
                   bth700846470.hl
Method
                   BLASTX
                   g2827556
NCBI GI
BLAST score
                   213
                   6.0e-17
E value
Match length
                   83
                   51
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   30018
Seq. No.
                   206044 1.R1040
Contig ID
5'-most EST
                   bth700846633.h1
Method
                   BLASTX
NCBI GI
                   g4467156
BLAST score
                   291
                   5.0e-47
E value
                   122
Match length
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
```

4-alpha-glucanotransferase [Solanum tuberosum]

30019

Seq. No.

```
206060 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400077e12a1
Seq. No.
                  30020
                  206088 1.R1040
Contig ID
5'-most EST
                  bth700846687.h1
Method
                  BLASTX
NCBI GI
                  g3157932
BLAST score
                  309
                  1.0e-28
E value
                                     78
Match length
                  72
% identity
NCBI Description
                   (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
                  from A. thaliana. [Arabidopsis thaliana]
                  30021
Seq. No.
                  206095 1.R1040
Contig ID
5'-most EST
                  gsv701\overline{0}46866.h1
Method
                  BLASTX
NCBI GI
                  q4220517
BLAST score
                  219
E value
                  7.0e-18
                  52
Match length
                  77----
% identity
                   (AL035356) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  30022
Seq. No.
                  206102 1.R1040
Contig ID
                  bth700846712.h1
5'-most EST
                  30023
Seq. No.
                  206109 1.R1040
Contig ID
                  bth700846768.h1
5'-most EST
                  30024
Seq. No.
                  206113 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220093b10a1
                  30025
Seq. No.
                  206130 1.R1040
Contig ID
5'-most EST
                  zsq701122592.h1
                  30026
Seq. No.
                  206165 1.R1040
Contig ID
                  bth700846993.h1
5'-most EST
                  30027
Seq. No.
Contig ID
                  206181 1.R1040
                  uC-gmflminsoy030d08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4512701
                  395
BLAST score
                  2.0e-38
E value
                  88
Match length
                  83
% identity
                   (AC006569) putative tyrosine decarboxylase [Arabidopsis
NCBI Description
```

thaliana]

```
30028
Seq. No.
Contig ID
                  206185 1.R1040
5'-most EST
                  bth700846826.h1
                  30029
Seq. No.
                  206227 1.R1040
Contig ID
5'-most EST
                  pmv700890991.hl
                  30030
Seq. No.
                  206230 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910068h01a1
Seq. No.
                  30031
Contig ID
                  206233 1.R1040
                  pxt700942737.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2947063
BLAST score
                  429
E value
                  5.0e-42
Match length
                  176
% identity
                  51
NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
                  30032
Seq. No.
                  206300 1.R1040
Contig ID
                  fua701039394.hl
5'-most EST
Method
                  BLASTX
                  g4263818
NCBI GI
BLAST score
                  295
E value
                  2.0e-26
Match length
                  184
                  38
% identity
NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]
Seq. No.
                  30033
                  206355_1.R1040
Contig ID
                  jC-gmr002800030g03a1
5'-most EST
Method
                  BLASTX
                  q4063742
NCBI GI
BLAST score
                  306
E value
                  1.0e-27
Match length
                  116
% identity
                  56
NCBI Description
                  (AC005851) putative phaseolin G-box binding protein
                  [Arabidopsis thaliana]
                  30034
Seq. No.
                  206370 1.R1040
Contig ID
                  jC-gmle01810042c10a1
5'-most EST
Seq. No.
                  30035
Contig ID
                  206426 1.R1040
                  bth700847167.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3341694
```

```
BLAST score
                  143
E value
                  6.0e-09
Match length
                  77
% identity
                  44
                  (ACO03672) PREG-like protein [Arabidopsis thaliana]
NCBI Description
                  30036
Seq. No.
                  206440 1.R1040
Contig ID
5'-most EST
                  zsg701120332.h1
Seq. No.
                  30037
                  206468 1.R1040
Contig ID
5'-most EST
                  fC-gmro700848531a1
                  30038
Seq. No.
                  206469 1.R1040
Contig ID
                  bth700848245.h1
5'-most EST
                  30039
Seq. No.
                  206470 1.R1040
Contig ID
                  rlr700901269.hl
5'-most EST
                  30040
Seq. No.
                  206494 1.R1040
Contig ID
5'-most EST
                  g4284646
                  30041
Seq. No.
                  206497 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy081g09b1
                  BLASTX
Method
                  g4468812
NCBI GI
BLAST score
                  277
E value
                  1.0e-24
                  75
Match length
                  67
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30042
Contig ID
                  206513 1.R1040
                  bth700847267.h1
5'-most EST
                  30043
Seq. No.
                  206551 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810088b07d1
                  30044
Seq. No.
                  206551_2.R1040
Contig ID
5'-most EST
                  uC-gmropic027a09b1
                  30045
Seq. No.
                  206585_1.R1040
Contig ID
                  bth700847358.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4325338
BLAST score
                  564
```

. V

2.0e-58

120

E value Match length

```
% identity .
                    (AF128392) No definition line found [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    30046
 Contig ID
                    206591 1.R1040
 5'-most EST
                    bth700847364.h1
 Method
                    BLASTX
 NCBI GI
                    q4335745
 BLAST score
                    223
                    4.0e-18
 E value
 Match length
                    98
 % identity
                    43
                    (AC006284) putative hydrolase (contains an
 NCBI Description
                    esterase/lipase/thioesterase active site serine domain
                    (prosite: PS50187) [Arabidopsis thaliana]
                    30047
 Seq. No.
                    206653 1.R1040
 Contig ID
 5'-most EST
                    jex700907913.hl
 Seq. No.
                    30048
                    206675 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810077e06d1
 Seq. No.
                    30049
                    206691 1.R1040
 Contig ID
 5'-most EST
                    pmv700893634.h1
                    BLASTX
 Method
                    g2827630
 NCBI GI
 BLAST score
                    295
 E value
                    7.0e-39
 Match length
                    109
                    72
 % identity
 NCBI Description
                    (AL021636) putative protein [Arabidopsis thaliana]
                    30050
 Seq. No.
206700 1.R1040
 5'-most EST
                    fua701040870.hl
 Method
                    BLASTX
 NCBI GI
                    g2829887
 BLAST score
                    282
 E value
                    2.0e-25
 Match length
                    87
 % identity
                    (AC002396) Hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    30051
 Seq. No.
 Contig ID
                    206726 1.R1040
 5'-most EST
                    uC-gmrominsoy193g08b1
 Method
                    BLASTX
                    g3335060
 NCBI GI
 BLAST score
                    293
 E value
                    2.0e-28
 Match length
                    97
                    74
 % identity
                    (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
 NCBI Description
```

thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma

```
membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
30052
```

 Seq. No.
 30052

 Contig ID
 206750_1.R1040

 5'-most EST
 bth700848082.h1

Seq. No. 30053

Contig ID 206768_1.R1040 5'-most EST pmv700889038.h1

Seq. No. 30054

Contig ID 206773_1.R1040 5'-most EST bth700847609.h1

Method BLASTX
NCBI GI g3510259
BLAST score 268
E value 7.0e-24
Match length 66
% identity 82

NCBI Description (AC005310) putative inorganic pyrophosphatase [Arabidopsis

thaliana] >gi 3522960 (AC004411) putative inorganic

pyrophosphatase [Arabidopsis thaliana]

 Seq. No.
 -30055

 Contig ID
 206774 1.R1040

 5'-most EST
 asn701142575.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g2501494
BLAST score 162
E value 3.0e-11
Match length 85
% identity 44

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi 542015 pir S41951

UTP-glucose glucosyltransferase - cassava >gi 453249 emb CAA54612 (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No. 30056

Contig ID 206798_1.R1040 5'-most EST zhf700953387.h1

Seq. No. 30057

Contig ID 206804 1.R1040 5'-most EST bth700847649.h1

Seq. No. 30058

Contig ID 206824_1.R1040 5'-most EST gsv701051171.h1

Seq. No. 30059

Contig ID 206829_1.R1040 5'-most EST fC-gmle700870704a2

Method BLASTX
NCBI GI g3912917
BLAST score 1703
E value 0.0e+00

Method

BLASTX

```
426
Match length
                  78
% identity
                   (AF001308) putative NAK-like ser/thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  30060
Seq. No.
                  206844 1.R1040
Contig ID
5'-most EST
                  zsg701118010.h2
Method
                  BLASTX
NCBI GI
                  q2225877
BLAST score
                  484
                  1.0e-48
E value
Match length
                  119
% identity
                  77
                   (AB002406) TIP49 [Rattus norvegicus] >gi 4106528 (AF100694)
NCBI Description
                  Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_
                   (AB001581) DNA helicase p50 [Rattus norvegicus]
Seq. No.
                  30061
                  206847 1.R1040
Contig ID
5'-most EST
                  fC-qmst700892002d3
Seq. No.
                  30062
Contig ID
                  206847 2.R1040 --
5'-most EST
                  zsq701123575.h1
                   30063
Seq. No.
                  206874 1.R1040
Contig ID
                   jC-qmst02400028f01a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2781345
BLAST score
                   587
                   1.0e-60
E value
Match length
                   233
                   51
% identity
NCBI Description
                   (AC003113) F2401.2 [Arabidopsis thaliana]
Seq. No.
                   206876 1.R1040
Contig ID
5'-most EST
                   q4397509
                   30065
Seq. No.
                   206885 1.R1040
Contig ID
5'-most EST
                   leu701154624.hl
                  BLASTX
Method
                   g1809257
NCBI GI
BLAST score
                   98
E value
                   2.0e-09
Match length
                  89
% identity
                   (U59316) serine/threonine protein kinase Pto [Lycopersicon
NCBI Description
                   esculentum]
                   30066
Seq. No.
                   206885 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810021g05a1
```

```
NCBI GI
                   g1644291
                   213
BLAST score
                   6.0e-17
E value
Match length
                   109
% identity
                   45
                   (Z73295) receptor-like protein kinase [Catharanthus roseus]
NCBI Description
                   30067
Seq. No.
Contig ID
                   206885 3.R1040
5'-most EST
                   jsh701\overline{0}68122.h1
                   30068
Seq. No.
Contig ID
                   206919 1.R1040
5'-most EST
                   pmv700893156.h1
                   BLASTX
Method
                   g3228668
NCBI GI
BLAST score
                   430
                   2.0e-42
E value
                                                  :- · .
Match length
                   153
% identity
                   52
                   (AF069988) nitrilase 1 [Mus musculus]
NCBI Description
                   30069
Seq. No.
                   206958 1.R1040 ~
Contig ID
                   jC-gmro02910062a12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4314357
BLAST score
                   138
E value
                   4.0e-12
Match length
                   162
                   41
% identity
                   (AC006340) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   30070
Seq. No.
                   207003 1.R1040
Contig ID
5'-most EST
                   bth700847903.h1
Method
                   BLASTX
NCBI GI
                   g1621461
BLAST score
                   165
E value
                   1.0e-11
Match length
                   114
                   39
% identity
                   (U73103) laccase [Liriodendron tulipifera]
NCBI Description
                   30071
Seq. No.
                   207011 1.R1040
Contig ID
5'-most EST
                   bth700847911.h1
                   30072
Seq. No.
                   207016_1.R1040
Contig ID
5'-most EST
                   epx701104603.h1
Method
                   BLASTX
                   q3096947
NCBI GI
BLAST score
                   384
                   2.0e-37
E value
                   95
Match length
```

BLAST score

448

```
% identity
NCBI Description
                   (Y16327) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana]
                   30073
Seq. No.
                   207054 1.R1040
Contig ID
                   jC-gmf\overline{1}02220054d02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q539079
BLAST score
                   463
E value
                   4.0e-46
                   202
Match length
% identity
                   45
                  peroxisomal assembly protein 5 - yeast (Pichia pastoris)
NCBI Description
                   30074
Seq. No.
                  207072 1.R1040
Contig ID
                  bth700847992.h1
5'-most EST
                   30075
Seq. No.
                   207093_1.R1040
Contig ID
5'-most EST
                  asn701141385.hl
Seq. No.
                  30076
Contig ID
                   207110 1.R1040
5'-most EST
                  uC-gmrominsoy035c07b1
                   30077
Seq. No.
                   207154 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy075e07b1
                  30078
Seq. No.
                  207158 1.R1040
Contig ID
5'-most EST
                  bth700848109.h1
                  30079
Seq. No.
Contig ID.
                  207161 1.R1040
5'-most EST
                  pxt700943435.hl
                  BLASTX
Method
                  g4544432
NCBI GI
BLAST score
                  369
                   3.0e-35
E value
Match length
                  77
% identity
                   (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  30080
Seq. No.
                  207162 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810021c05d1
                  30081
Seq. No.
Contig ID
                  207163 1.R1040
5'-most EST
                  jC-gmro02910056f02a1
Method
                  BLASTX
                  g1304227
NCBI GI
```

```
2.0e-44
E value
                   154
Match length
% identity
                   51
NCBI Description
                   (D63781) Epoxide hydrolase [Glycine max]
                  >gi 2764804 emb CAA55293 (X78547) èpoxide hydrolase
                   [Glycine max]
                   30082
Seq. No.
Contig ID
                   207197 1.R1040
                   zhf700958167.h1
5'-most EST
                   30083
Seq. No.
Contig ID
                  207215 1.R1040
5'-most EST
                  bth700848183.h1
                  BLASTX
Method
                  g4567283
NCBI GI
                  222
BLAST score
                  1.0e-18
E value
Match length
                   62
% identity
                  73
                   (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                  30084
Seq. No.
                  207226 1.R1040
Contig ID
5'-most EST
                  g5510282
                  BLASTX
Method
NCBI GI
                  g3482918
BLAST score
                   308
E value
                   4.0e-28
                  79
Match length
                  75
% identity
                   (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                   30085
Seq. No.
                  207238 1.R1040 ·
Contig ID
5'-most EST
                  bth700848214.h1
Seq. No.
                  30086
                  207244 1.R1040
Contig ID
                  bth700848221.h1
5'-most EST
                  30087
Seq. No.
                  207257 1.R1040
Contig ID
                   zhf700\overline{9}56222.h1
5'-most EST
                  30088
Seq. No.
                  207331 1.R1040
Contig ID
                  fC-gmro700846765a1
5'-most EST
Method
                  BLASTX
                  g3334661
NCBI GI
BLAST score
                  440
                  1.0e-43
E value
Match length
                  123
% identity
                  63
                  (Y10490) putative cytochrome P450 [Glycine max]
NCBI Description
```

```
30089
Seq. No.
                   207346_1.R1040
Contig ID
5'-most EST
                   dpv701101241.h1
Method
                  BLASTX
NCBI GI
                   q3912919
BLAST score
                   368
E value
                   4.0e-35
Match length
                  118
                   59
% identity
NCBI Description
                   (AF001308) hypothetical protein [Arabidopsis thaliana]
                   30090
Seq. No.
Contig ID
                  207362 1.R1040
5'-most EST
                  bth700848369.h1
                  BLASTX
Method
                  g2688828
NCBI GI
                  158
BLAST score
                  1.0e-17
E value
Match length
                  84
                  52
% identity
                   (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
NCBI Description
                  armeniaca]
                  30091
Seq. No.
Contig ID
                  207421 1.R1040
5'-most EST
                  bth700848443.h1
Method
                  BLASTX
NCBI GI
                  g3402685
BLAST score
                  167
                  5.0e-15
E value
Match length
                  60
                  75
% identity
NCBI Description
                   (AC004697) unknown protein [Arabidopsis thaliana]
                  30092
Seq. No.
                  207431_1.R1040
Contig ID
                  bth700848453.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4539301
BLAST score
                  216
E value
                  1.0e-17
Match length
                  99
                  49
% identity
NCBI Description
                   (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
                  30093
Seq. No.
Contig ID
                  207455 1.R1040
5'-most EST
                  zhf700959259.hl
Seq. No.
                  30094
Contig ID
                  207461 1.R1040
5'-most EST
                  uC-gmflminsoy082e11b1
Seq. No.
                  30095
                  207532 1.R1040
Contig ID
```

fua701039758.hl

5'-most EST

Contig ID

```
Seq. No.
                   30096
                   207546 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400067d12d1
                   30097
Seq. No.
                   207574 1.R1040
Contig ID
                   uC-gmropic050g01b1
5'-most EST
                   30098
Seq. No.
                   207592 1.R1040
Contig ID
                   dpv701102879.h1
5'-most EST
                   BLASTN
Method
                   g170029
NCBI GI
BLAST score
                   56
E value
                   7.0e-23
                   95
Match length
% identity
                   91
                   Glycine max cv. Dare nodulin 26 gene fragment
NCBI Description
                   30099
Seq. No.
Contig ID
                   207615 1.R1040
5'-most EST
                   fC-gmro700848694a1
Method
                   BLASTX
NCBI GI
                   g3292831
BLAST score
                   286
E value
                   7.0e-50
Match length
                   131
% identity
                   77
                   (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                   thaliana]
                   30100
Seq. No.
Contig ID
                   207620 1.R1040
5'-most EST
                   bth700848707.h1
                   BLASTN
Method
NCBI GI
                   g3292807
BLAST score
                   55
E value
                   4.0e-22
Match length
                   153
                   85
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
Seq. No.
                   30101
Contig ID
                   207663 1.R1040
5'-most EST
                   uC-gmropic090d03b1
Method
                   BLASTX
NCBI GI
                   g2191145
BLAST score
                   227
E value
                   1.0e-18
Match length
                   146
                   41
% identity
                   (AF007269) A IG002N01.4 gene product [Arabidopsis thaliana]
NCBI Description
                   30102
Seq. No.
                   207727 1.R1040
```

```
5'-most EST
                   hrw701063119.hl
                   30103
Seq. No.
                   207746 1.R1040
Contig ID
5'-most EST
                   bth700848864.h1
                   30104
Seq. No.
                   207753_1.R1040
Contig ID
5'-most EST
                   uC-gmropic023a06b1
Method
                   BLASTX
                   g3096947
NCBI GI
                   184
BLAST score
                   2.0e-13
E value
                   103
Match length
                   45
% identity
                    (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                    [Arabidopsis thaliana]
                   30105
Seq. No.
                   207769 1.R1040
Contig ID
                   bth700848894.h1
5'-most EST
                   30106
Seq. No.
                   207784 1.R1040
Contig ID
 5'-most EST
                   bth700848917.h1
                   BLASTX
Method
                   g4559380
NCBI GI
BLAST score
                   205
                   2.0e-18
E value
Match length
                   61
                   79
% identity
NCBI Description
                    (AC006526) putative auxin-responsive GH3 protein
                    [Arabidopsis thaliana]
                   30107
Seq. No.
                   207795 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}07346.h1
Seq. No.
                   30108
                   207796 1.R1040
Contig ID
                   uC-gmropic004a12b1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g3559816
                   286
BLAST score
                    6.0e-39
E value
Match length
                   132
                    63
% identity
NCBI Description
                    (Y15782) transketolase 2 [Capsicum annuum]
Seq. No.
                   30109
                   207803 1.R1040
Contig ID
                   fua701037395.hl
5'-most EST
                   30110
Seq. No.
                   207866 1.R1040
Contig ID
```

bth700849032.h1

5'-most EST

Contig ID

```
Seq. No.
                  30111.
Contig ID
                  207883 1.R1040
5'-most EST
                  bth700849050.h1
                  30112
Seq. No.
                  207891 1.R1040
Contig ID
5'-most EST
                  uC-gmropic054f11b1
                  BLASTX
Method
NCBI GI
                  q4539383
BLAST score
                  317
                  5.0e-29
E value
Match length
                  119
% identity
                  48
NCBI Description
                   (AL035526) putative protein (fragment) [Arabidopsis
Seq. No.
                  30113
Contiq ID
                  207892 1.R1040
5'-most EST
                  bth700849061.h1
Seq. No.
                  30114
Contig ID
                  207903 1.R1040
5'-most EST
                  jC-qmst02400001f09a1
Seq. No.
                  30115
Contig ID
                  207905 1.R1040
5'-most EST
                  uC-gmropic054c04b1
Method
                  BLASTX
NCBI GI
                  q2493895
BLAST score
                  601
E value
                  3.0e-62
Match length
                  170
% identity
                  68
NCBI Description
                  CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
                  (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi 1071911 pir S46438 cysteine synthase (EC 4.2.99.8) -
                  watermelon >gi_540497 dbj BAA05965 (D28777) cysteine
                  synthase [Citrullus lanatus]
Seq. No.
                  30116
Contig ID
                  207905 2.R1040
5'-most EST
                  jC-gmle01810030e09d1
Method -
                  BLASTX
NCBI GI
                  q3127890
BLAST score
                  181
E value
                  4.0e-13
Match length
                  73
% identity
NCBI Description
                  (AJ006024) cysteine synthase, O-acetyl-L-serine
                  (thiol)-lyase [Cicer arietinum]
Seq. No.
                  30117
Contig ID
                  207905 3.R1040
5'-most EST
                  jsh701064170.hl
Seq. No.
                  30118
```

207907 1.R1040

```
5'-most EST
                  bth700849086.h1
                  30119
Seq. No.
                  207909 1.R1040
Contig ID
5'-most EST
                  bth700849090.h1
                  BLASTX
Method
                  g520570
NCBI GI
                  246
BLAST score
E value
                   4.0e-21
Match length
                   69
                   70
% identity
NCBI Description
                  (U12315) peroxidase [Cenchrus ciliaris]
                  30120
Seq. No.
                  207919 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy017e02b1
                  BLASTX
Method
                   q4191786
NCBI GI
                  592
BLAST score
                  2.0e-61
E value
                  163
Match length
                  71
% identity
                  (AC005917) unknown protein [Arabidopsis thaliana]
NCBI Description
                  30121
Seq. No.
                  207968 1.R1040
Contig ID
5'-most EST
                   fua701040728.hl
Method
                  BLASTX
                   g2829864
NCBI GI
BLAST score
                  154
                   2.0e-10
E value
Match length
                   45
                   60
% identity
                   (AC002396) similar to zinc metalloproteinases [Arabidopsis
NCBI Description
                   thaliana]
                   30122
Seq. No.
                   207983 1.R1040
Contig ID
                   uC-gmropic043g07b1
5'-most EST
                   BLASTX
Method
                   q3668087
NCBI GI
BLAST score
                   518
                   1.0e-52
E value
Match length
                   161
                   38
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30123
Seq. No.
                  208017 1.R1040
Contig ID
                  bth700849224.h1
5'-most EST
                   30124
Seq. No.
                  208024 1.R1040
Contig ID
                  bth700849231.h1
5'-most EST
                  BLASTX
Method
                  g2252847
NCBI GI
```

BLAST score

```
E value
                  3.0e-12
Match length
                  35
% identity
                  89
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                  30125
Seq. No.
                  208030 1.R1040
Contig ID
                  jC-gmro02910011c09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  908
E value
                  2.0e-98
Match length
                  191
% identity
                  (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                  30126
Seq. No.
                  208066 1.R1040
Contig ID
                  bth700849280.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4567305
BLAST score
                  195
                  7.0e-15
E value
                  81
Match length
                  48
% identity
                  (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30127
                  208109 1.R1040
Contig ID
                  uC-gmropic009e01b1
5'-most EST
                  30128
Seq. No.
Contig ID
                  208111 1.R1040
5'-most EST
                  gsv701\overline{0}50584.h1
                  30129
Seq. No.
                  208176 1.R1040
Contig ID
5'-most EST
                  g4313893
Seq. No.
                  30130
                  208183 1.R1040
Contig ID
                  zhf700955854.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3212539
BLAST score
                  657
                  9.0e-69
E value
                  200
Match length
                  63
% identity
                  Chain A, Structure Of Human Isovaleryl-Coa Dehydrogenase At
NCBI Description
                  2.6 Angstroms Resolution: Structural Basis For Substrate
                  Specificity >gi_3212540_pdb_1IVH_B Chain B, Structure Of
                  Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms
                  Resolution: Structural Basis For Substrate Specificity
                  >gi_3212541_pdb_1IVH_C Chain C, Structure Of Human
                  Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:
                  Structural Basis For Substrate Specificity
```

>gi_3212542_pdb_1IVH_D Chain D, Structure Of Human

```
Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity
```

```
Seq. No.
                   30131
                   208226 1.R1040
Contig ID
5'-most EST
                   g5677038
                   30132
Seq. No.
Contig ID
                   208260 1.R1040
                   bth700849533.h1
5'-most EST
                   30133
Seq. No.
                   208280 1.R1040
Contig ID
                   bth700849556.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4220631
BLAST score
                   49
E value
                   1.0e-18
Match length
                   204
% identity
                   86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K5J14, complete sequence [Arabidopsis thaliana]
                   30134
Seq. No. -
                   208289 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy061b05b1
Method
                   BLASTX
NCBI GI
                   g2583122
BLAST score
                   223
                   3.0e-18
E value
                   105
Match length
                   48
% identity
NCBI Description
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
                   30135
Seq. No.
                   208305 1.R1040
Contig ID
5'-most EST
                   zsg701128405.hl
                   30136
Seq. No.
                   208333 1.R1040
Contig ID
                   uC-gmropic038h11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1172584
BLAST score
                   215
                   3.0e-17
E value
                   89
Match length
                   49
% identity
NCBI Description
                   POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
                   >gi_1076478_pir__S52984 catechol oxidase (EC 1.10.3.1)
                  precursor - apple tree >gi_507280 (L29450) polyphenol
                   oxidase [Malus domestica]
                   30137
Seq. No.
                   208349 1.R1040
Contig ID
```

5'-most EST

jC-gmle01810032g11d1

```
208398 1.R1040
Contig ID
5'-most EST
                   bth700849701.h1
                   BLASTX
Method
NCBI GI
                   q559713
BLAST score
                   115
                   1.0e-10
E value
Match length
                   57
% identity
                   63
NCBI Description
                   (D38552) The half39 protein is related to cyclophilin.
                   [Homo sapiens]
                   30139
Seq. No.
                   208405 1.R1040
Contig ID
                   bth700849710.h1
5'-most EST
Method
                   BLASTX
                   q4006829
NCBI GI
BLAST score
                   208
E value
                   1.0e-16
Match length
                   93
                   54
% identity
NCBI Description
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
                   30140
Seq. No.
                   208408 1.R1040 -
Contig ID ...
5'-most EST
                   bth700849713.h1
Seq. No.
                   30141
                   208451 1.R1040
Contig ID
                   bth700849769.h1
5'-most EST
                   30142
Seq. No.
                   208501 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810016f08d1
                   30143
Seq. No.
                   208550 1.R1040
Contig ID
5'-most EST
                   bnh700764501.h1
Method
                   BLASTX
                   g4204257
NCBI GI
BLAST score
                   167
                   1.0e-20
E value
Match length
                   71
                   73
% identity
                   (AC005223) 5493 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30144
                   208583 1.R1040
Contig ID
5'-most EST
                   bnh700764543.h1
                   30145
Seq. No.
Contig ID
                   208665 1.R1040
                   dpv701\overline{0}99937.h1
5'-most EST
Seq. No.
                   30146
                   208687 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}02966.h1
```

BLASTX

Method

5'-most EST

```
NCBI GI
                   q3776025
BLAST score
                   254
                   7.0e-24
E value
Match length
                   79
                   74
% identity
NCBI Description
                   (AJ010474) RNA helicase [Arabidopsis thaliana]
                   30147
Seq. No.
Contig ID
                   208688 2.R1040
5'-most EST
                   zhf700953167.h1
Seq. No.
                   30148
Contig ID
                   208691_1.R1040
5'-most EST
                   jex700902980.hl
                   BLASTX
Method
                   g2194125
NCBI GI
BLAST score
                   509
                   1.0e-51
E value
                   115
Match length
                   77
% identity
                   (AC002062) ESTs gb R30459, gb N38441 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   30149
Seq. No.
                   208694 1.R1040
Contig ID
5'-most EST
                   jex700904478.hl
Seq. No.
                   30150
                   208715 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220073a05a1
                   30151
Seq. No.
                   208744 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}03170.h1
Method
                   BLASTX
NCBI GI
                   g624943
BLAST score
                   157
E value
                   9.0e-11
Match length
                   81
% identity
                   (X79432) unnamed protein product [Brassica oleracea]
NCBI Description
                   30152
Seq. No.
Contig ID
                   208751 1.R1040
                   jex700\overline{9}03527.h1
5'-most EST
Method
                   BLASTX
                   g3334665
NCBI GI
BLAST score
                   386
E value
                   2.0e-37
Match length
                   132
                   55
% identity
NCBI Description
                   (Y10492) putative cytochrome P450 [Glycine max]
                   30153
Seq. No.
                   208754 1.R1040
Contig ID
```

 $jex700\overline{9}04555.h1$

NCBI GI

```
30154
Seq. No.
                  208756 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810010h12a1
                  30155
Seq. No.
                  208814 1.R1040
Contig ID
                  zhf700955093.hl
5'-most EST
Method
                  BLASTX
                  g125889
NCBI GI
BLAST score
                  414
                  1.0e-40
E value
Match length
                  124
                  63
% identity
                  PROBABLE PECTATE LYASE P59 PRECURSOR >gi_280400_pir__$27098
NCBI Description
                  pectate lyase (EC 4.2.2.2) LAT59 - tomato
                  >gi_19271 emb CAA33523 (X15499) P59 protein [Lycopersicon
                  esculentum]
                  30156
Seq. No.
                  208817 1.R1040
Contig ID
                  zhf700953936.h1
5'-most EST
Method
                  BLASTX
                  g2088651
NCBI GI
BLAST score
                  162
                  5.0e-11
E value
Match length
                  83
                  55
% identity
NCBI Description
                  (AF002109) hypersensitivity-related gene 201 isolog
                  [Arabidopsis thaliana]
                  30157
Seq. No.
                  208828 1.R1040
Contig ID
5'-most EST
                  uC-gmropic027c09b1
Method
                  BLASTX
NCBI GI
                  g4220529
BLAST score
                  637
E value
                  1.0e-66
Match length
                  160
% identity
                  76
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
                  30158
Seq. No.
                  208848 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220103d01a1
Method
                  BLASTX
NCBI GI
                  g529353
BLAST score
                  414
                  1.0e-40
E value
Match length
                  121
% identity
NCBI Description
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
                  30159
Seq. No.
                  208850 1.R1040
Contig ID
5'-most EST
                  zsq701119787.h1
Method
                  BLASTN
```

g2465528

```
BLAST score
                   85
                   4.0e-40
E value
Match length
                   169
                   88
% identity
                   Medicago truncatula phosphate transporter (MtPT2) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   30160
                   208859 1.R1040
Contig ID
5'-most EST
                   g50582\overline{4}0
                   BLASTX
Method
                   g4038036
NCBI GI
BLAST score
                   155
E value
                   3.0e-17
Match length
                   185
% identity
                   43
                   (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30161
Seq. No.
                   208891 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}64182.h1
Method
                   BLASTX
NCBI GI
                   g4218120
BLAST score
                   509
E value
                   1.0e-51
Match length
                   139
% identity
                   72
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30162
                   208892 1.R1040
Contig ID
                   leu701151880.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1669341
BLAST score
                   290
E value
                   3.0e-26
                   108
Match length
                   56
% identity
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
Seq. No.
                   30163
                   208911 1.R1040
Contig ID
5'-most EST
                   jex700903566.hl
                   30164
Seq. No.
                   208926 1.R1040
Contig ID
                   jex700\overline{9}03603.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2088651
BLAST score
                   323 -
                   8.0e-30
E value
Match length
                   145
% identity
                   48
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
```

[Arabidopsis thaliana]

```
30165
Seq. No.
                   208930 1.R1040
Contig ID
5'-most EST
                   jex700903610.h1
                   30166
Seq. No.
                   208955 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}03642.h1
Method
                   BLASTX
                   q4455246
NCBI GI
BLAST score
                   188
                   5.0e-14
E value
                   94
Match length
                   50
% identity
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   30167
Seq. No.
                   208969 1.R1040
Contig ID
                   jex700\overline{9}03674.h1
5'-most EST
                   30168
Seq. No.
                   208971_1.R1040
Contig ID
                   zsg701123853.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1711618
                   444
BLAST score
E value
                   4.0e-44
                   126
Match length
                   69
% identity
                   LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir__S51765
NCBI Description
                   low affinity sulphate transporter - Stylosanthes hamata
                   >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
                   transporter [Stylosanthes hamata]
                   30169
Seq. No.
                   208991 1.R1040
Contig ID
                   fC-gmf\overline{1}700904235a1
5'-most EST
                   BLASTX
Method
                   g3047095
NCBI GI
                   272
BLAST score
                   7.0e-24
E value
                   109
Match length
                   30
% identity
                   (AF058826) similar to eukaryotic protein kinase domains
NCBI Description
                   (Pfam: pkinase.hmm, score: 72.39) [Arabidopsis thaliana]
                   30170
Seq. No.
                   209019 1.R1040
Contig ID
                   fC-gmf1700903761f4
5'-most EST
                   BLASTX
Method
                   g1150406
NCBI GI
                   293
BLAST score
                   3.0e-26
E value
                   142
Match length
% identity
                   43
                   (Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan
NCBI Description
                   glucanohydrolase [Pichia angusta]
```

```
30171
Seq. No.
                    209026 1.R1040
Contig ID
5'-most EST
                    leu701\overline{1}49594.h1
Seq. No.
                    30172
                    209044 1.R1040
Contig ID
5'-most EST
                    jex700906355.hl
Seq. No.
                    30173
                    209057 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}03826.h1
                    30174
Seq. No.
Contig ID
                    209062 1.R1040
5'-most EST
                    jC-gmro02910004g06a1
Seq. No.
                    30175
                    209078 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}03873.h1
                    30176
Seq. No.
                    209094 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}03894.h1
                    30177
Seq. No.
Contig ID
                    209127 1.R1040
5'-most EST
                    uC-gmropic010c06b1
                    BLASTX
Method
NCBI GI
                    q1297187
BLAST score
                    654
E value
                    2.0e-68
Match length
                    212
% identity
                    (U53501) similar to protein encoded by GenBank Accession
NCBI Description
                    Number U41815, nucleoporin 98 [Arabidopsis thaliana]
Seq. No.
                    30178
                    209142 1.R1040
Contig ID
5'-most EST
                    jex700\overline{9}04010.h1
                    30179
Seq. No.
Contig ID
                    209146 1.R1040
5'-most EST
                    jex700\overline{9}04018.h1
Seq. No.
                    30180
                    209173 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy012g11b1
Method
                    BLASTX
NCBI GI
                    g2576361
BLAST score
                    568
                    1.0e-58
E value
Match length
                    138
% identity
                    (U39782) lysine and histidine specific transporter
NCBI Description
```

[Arabidopsis thaliana]

```
30181
Seq. No.
                   209186 1.R1040
Contig ID
5'-most EST
                   jex700904081.h1
                   30182
Seq. No.
                   209246 1.R1040
Contig ID
                   crh700852687.h1
5'-most EST
                   30183
Seq. No.
                   209247 1.R1040
Contig ID
5'-most EST
                   leu701154524.h1
                   30184
Seq. No.
                   209293_1.R1040
Contig ID
                   uC-gmropic028a03b1
5'-most EST
                   BLASTX
Method
                   g2388971
NCBI GI
BLAST score
                   277
                   3.0e-24
E value
                   122
Match length
                   48
% identity
                   (Z98979) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   30185
Seq. No.
                   209298 1.R1040
Contig ID
                   rlr700895783.hl
5'-most EST
Method
                   BLASTX
                   g452593
NCBI GI
BLAST score
                   252
                   6.0e-22
E value
                   91
Match length
                   49
% identity
                   (D21814) ORF [Lilium longiflorum]
NCBI Description
                   30186
Seq. No.
                   209330 1.R1040
Contig ID
                   uC-gmropic109h07b1
5'-most EST
Method
                   BLASTN
                   g1165321
NCBI GI
BLAST score
                   58
                   7.0e-24
E value
                   193
Match length
                   20
% identity
                  Glycine max extensin (SbHRGP3) gene, complete cds
NCBI Description
                   30187
Seq. No.
                   209374 1.R1040
Contig ID
                   jC-gmro02800038c01d1
5'-most EST
                   30188
Seq. No.
                   209436_1.R1040
Contig ID
                   fC-gmf1700902268a1
5'-most EST
                   BLASTX
Method
                   q3641252
NCBI GI
                   280
BLAST score
                   5.0e-25
E value
```

Match length



```
% identity
NCBI Description
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
                   domestica]
                   30189
Seq. No.
                   209469 1.R1040
Contig ID
                   uC-gmflminsoy005b09b1
5'-most EST
                   30190
Seq. No.
                   209471 1.R1040
Contig ID
5'-most EST
                   leu701149690.h1
Seq. No.
                   30191
                   209485 1.R1040
Contig ID
5'-most EST
                   fC-qmf1700904490f4
Method
                   BLASTX
NCBI GI
                   g1352075
BLAST score
                   619
                   8.0e-67
E value
                   178
Match length
                   61
% identity
                   BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                   >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) -
                   wild cabbage >gi_669059_emb_CAA59162_ (X84684)
                   beta-galactosidase [Brassica oleracea]
Seq. No.
                   30192
                   209487 1.R1040
Contig ID
5'-most EST
                   fC-gmf1700904492f4
Method
                   BLASTX
NCBI GI
                   g3721856
BLAST score
                   422
E value
                   2.0e-41
                   109
Match length
                   69
% identity
                   (AB014057) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   30193
Seq. No.
Contig ID
                   209503 1.R1040
5'-most EST
                   leu701145795.h1
                   BLASTX
Method
NCBI GI
                   g1653033
BLAST score
                   163
                   3.0e-11
E value
                   36
Match length
% identity
                   (D90910) hypothetical protein [Synechocystis sp.]
NCBI Description
                   30194
Seq. No.
                   209545 1.R1040
Contig ID
5'-most EST
                   jex700905108.hl
                   30195
Seq. No.
Contig ID
                   209549 1.R1040
5'-most EST
                   jex700\overline{9}04589.h1
```

Seq. No.

5'-most EST

```
209566 1.R1040
Contig ID
5'-most EST
                   uC-qmropic022a02b1
Seq. No.
                   30197
                   209574 1.R1040
Contig ID
5'-most EST
                   zhf700958011.h1
Method
                   BLASTX
NCBI GI
                   q99808
BLAST score
                   570
E value
                   9.0e-59
Match length
                   171
                   63
% identity
                   gene Bp10 protein - rape >gi 17797 emb CAA47178 (X66609)
NCBI Description
                   Bplo [Brassica napus]
                   30198
Seq. No.
                   209577 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220142h02a1
                   30199
Seq. No.
                   209616_1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220100e08a1
Method
                   BLASTX
                   g1708972
NCBI GI
BLAST score
                   217
E value
                   3.0e-17
Match length
                   101
% identity
                   50
                   (R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR
NCBI Description
                   (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi_1262279
                   (U51562) (R)-(+)-mandelonitrile lyase isoform MDL\overline{3}
                   precursor [Prunus serotina] >gi 2343181 (AF013161)
                   (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus
                   serotina]
                   30200
Seq. No.
Contig ID
                   209640 1.R1040
                   k11701\overline{2}05153.h1
5'-most EST
                   30201
Seq. No.
                   209667 1.R1040
Contig ID
                   jex700\overline{9}04771.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455171
                   751
BLAST score
E value
                   6.0e-80
Match length
                   196
% identity
NCBI Description
                   (AL035521) hypothetical protein [Arabidopsis thaliana]
                   30202
Seq. No.
                   209683 1.R1040
Contig ID
5'-most EST
                   leu701149039.hl
                   30203
Seq. No.
                   209717 1.R1040
Contig ID
```

 $leu701\overline{1}53716.h1$

```
BLASTX
Method
                   g2842496
NCBI GI
BLAST score
                   448
E value
                   2.0e-44
Match length
                   121
                   73
% identity
                   (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
                   30204
Seq. No.
Contig ID
                   209723 1.R1040
5'-most EST
                   jex700\overline{9}04868.h1
Method
                   BLASTX
                   g4415912
NCBI GI
BLAST score
                   148
E value
                   8.0e-10
Match length
                   85
                   35
% identity
                   (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
                   30205
Seq. No.
Contig ID
                   209745_1.R1040
5'-most EST
                   gsv701051266.hl
                   BLASTX
Method
NCBI GI
                   g4559320
BLAST score
                   278
                   8.0e-25
E value
Match length
                   100
% identity
                   52
                   (ACO07087) putative 50S ribosomal protein L1 [Arabidopsis
NCBI Description
                   thaliana]
                   30206
Seq. No.
Contig ID
                   209767 1.R1040
5'-most EST
                   jex700\overline{9}04935.h1
                   BLASTX
Method
NCBI GI
                   g2114104
BLAST score
                   341
                   1.0e-64
E value
Match length
                   178
                   71
% identity
                   (AB003590) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                   >gi 2114106_dbj_BAA20085_ (AB003591) sulfate transporter
                   [Arabidopsis thaliana]
                   30207
Seq. No.
                   209780 1.R1040
Contig ID
5'-most EST
                   jex700905528.hl
                   30208
Seq. No.
                   209808 1.R1040
Contig ID
                   jex700\overline{9}04983.h1
5'-most EST
Method
                   BLASTX
                   g4008008
NCBI GI
BLAST score
                   251
                   2.0e-21
E value
                   93
Match length
```

% identity

```
NCBI Description
                   (AF084035) receptor-like protein kinase [Arabidopsis
                   thalianal
Seq. No.
                   30209
                   209826 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910010e04a1
Seq. No.
                   30210
Contig ID
                   209832 1.R1040
5'-most EST
                   jC-gmst02400044b04a1
                                                              Zini.
Method
                   BLASTX
                   g3885344
NCBI GI
BLAST score
                   172
                   4.0e-12
E value
Match length
                   126
% identity
                   (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown
                   protein [Arabidopsis thaliana]
                   30211
Seq. No.
                   209864 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05078.h1
Seq. No.
                   30212
                   209902 1.R1040
Contig ID
                   jC-gmf\overline{1}02220099h10d1
5'-most EST
                   30213
Seq. No.
                   209926 1.R1040
Contig ID
5'-most EST
                   fC-qmf1700906103a1
                   30214
Seq. No.
                   209939_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910047b05a1
                   BLASTX
Method
                   g4539335
NCBI GI
BLAST score
                   375
                   1.0e-35
E value
Match length
                   249
                   35
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30215
                   209939 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy302e03b1
Method
                   BLASTX
NCBI GI
                   g4539335
BLAST score
                   243
E value
                   1.0e-20
Match length
                   137
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   30216
Seq. No.
                   209949 1.R1040
Contig ID
                   zhf700955913.hl
5'-most EST
```

```
BLASTX
Method
NCBI GI
                   q3335359
BLAST score
                   434
E value
                   8.0e-43
Match length
                   129
                   66
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30217
Seq. No.
                   209973 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05225.h1
Method
                   BLASTX
                   g4454012
NCBI GI
BLAST score
                   481
                   3.0e-48
E value
Match length
                   142
                   63
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
                   30218
Seq. No.
                   209997 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05268.h1
                   BLASTX
Method -
                   g3006088
NCBI GI
BLAST score
                   183
E value
                   6.0e-14
Match length
                   70
                   49
% identity
                   (AJ222724) SGT protein [Rattus norvegicus]
NCBI Description
                   30219
Seq. No.
                   210012 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05275.h1
                   30220
Seq. No.
                   210014 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy012g09b1
Method
                   BLASTX
                   g3402694
NCBI GI
BLAST score
                   566
                   4.0e-58
E value
                   218
Match length
% identity
                   (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]
NCBI Description
                   30221
Seq. No.
                   210020 1.R1040
Contig ID
5'-most EST
                   fC-gmf1700903761a1
Method
                   BLASTX
NCBI GI
                   q4263791
BLAST score
                   306
                   4.0e-30
E value
Match length
                   108
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
```

thaliana]

NCBI Description

```
30222
Seq. No.
                   210040 1.R1040
Contig ID ·
5'-most EST
                   zhf700\overline{9}61857.h1
Method
                   BLASTX
                   g3810593
NCBI GI
                   285
BLAST score
                   9.0e-26
E value
Match length
                   59
% identity
                   (AC005398) putative sucrose-proton symporter [Arabidopsis
NCBI Description
                   thaliana]
                   30223
Seq. No.
                   210095 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}05408.h1
                   30224
Seq. No.
                   210107 1.R1040
Contig ID
5'-most EST
                   leu701144948.hl
                   30225
Seq. No.
                   210163 1.R1040
Contig ID
                   jC-gmst02400041d08a1---
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2864618
BLAST score
                   424
                   9.0e-42
E value
                   123
Match length
% identity
                    (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   30226
Seq. No.
                   210169 1.R1040
Contig ID
                   jC-gmf\overline{1}02220108c12a1
5'-most EST
                   30227
Seq. No.
                   210206 1.R1040
Contig ID
                   jex700\overline{9}05582.h1
5'-most EST
                   BLASTX
Method
                   q4218122
NCBI GI
                   384
BLAST score
                   7.0e-37
E value
Match length
                   195
                   48
% identity
                    (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                   30228
Seq. No.
                   210210 1.R1040
Contig ID
                    jex700\overline{9}05587.h1
5'-most EST
                   BLASTX
Method
                   q4455171
NCBI GI
                   441
BLAST score
                    4.0e-44
E value
                   96
Match length
                    77
% identity
                    (AL035521) hypothetical protein [Arabidopsis thaliana]
```

```
30229
Seq. No.
                   210222 1.R1040
Contig ID
                   jC-gmf\overline{1}02220140h03d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4510348
BLAST score
                   289
                   7.0e-26
E value
Match length
                   72
% identity
                   67
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   30230
Seq. No.
                   210228 1.R1040
Contig ID
5'-most EST
                   jex700905613.hl
                   30231
Seq. No.
                   210245 1.R1040
Contig ID
                   jex700905630.hl
5'-most EST
                   BLASTX
Method
                   g2367431
NCBI GI
BLAST score
                   224
E value
                   1.0e-18
                   55
Match length
                   76
% identity
                   (AF000403) putative cytochrome P450 [Lotus japonicus]
NCBI Description
Seq. No.
                   30232
                   210269 1.R1040
Contig ID
5'-most EST
                   fua701037858.hl
                   30233
Seq. No.
                   210283 1.R1040
Contig ID
5'-most EST
                   leu701147850.hl
                   30234
Seq. No.
Contig ID
                   210287 1.R1040
5'-most EST
                   jex700905693.hl
Method
                   BLASTX
NCBI GI
                   g927025
BLAST score
                   262
E value
                   2.0e-22
Match length
                   74
% identity
                   (L44134) SPF1-like DNA-binding protein [Cucumis sativus]
NCBI Description
Seq. No.
                   30235
                   210327 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}10291.h1
                   30236
Seq. No.
                   210398 1.R1040
Contig ID
                   zhf700952832.hl
5'-most EST
                   30237
Seq. No.
Contig ID
                   210432 1.R1040
```

pmv700888230.h1

5'-most EST

```
Method
                   BLASTN
NCBI GI
                   q2924653
BLAST score
                   35
E value
                   2.0e-10
Match length
                   107
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   30238
Contig ID
                   210537_1.R1040
5'-most EST
                   uC-gmflminsoy061f12b1
Method
                   BLASTX
                   g4467153
NCBI GI
BLAST score
                   232
E value
                   3.0e-19
Match length
                   118
                   45
% identity
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   30239
Seq. No.
                   210570 1.R1040
Contig ID
5'-most EST
                   jex700<del>9</del>06075.h1
                   30240
Seq. No.
Contig ID
                   210578 1.R1040
5'-most EST
                   epx701105248.hl
Method
                   BLASTX
                   g1848214
NCBI GI
BLAST score
                   298
                   5.0e-27
E value
Match length
                   66
% identity
                   80
                   (Y11210) uracil phosphoribosyltransferase [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   30241
                   210582 1.R1040
Contig ID
5'-most EST
                   jex700906094.hl
                   30242
Seq. No.
Contig ID
                   210636 1.R1040
5'-most EST
                   q5057869
                   30243
Seq. No.
                   210663 1.R1040
Contig ID
5'-most EST
                   k11701212062.h1
                   30244
Seq. No.
                   210678 1.R1040
Contig ID
                   jex700\overline{9}06255.h1
5'-most EST
Seq. No.
                   30245
                   210697 1.R1040
Contig ID
5'-most EST
                   fC-gmro700564904d3
```

BLASTN

Method

```
NCBI GI
                   q1935018
BLAST score
                   150
E value
                   1.0e-78
Match length
                   408
% identity
                   88
NCBI Description
                   V.faba mRNA for sucrose transporter
                   30246
Seq. No.
Contig ID
                   210710 1.R1040
5'-most EST
                   jC-qmst02400025d03a1
Method
                   BLASTX
NCBI GI
                   g2244840
BLAST score
                   253
E value
                   1.0e-21
Match length
                   116
                   47
% identity
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   30247
Seq. No.
Contig ID
                   210747 1.R1040
5'-most EST
                   jex700\overline{9}06370.h1
                   30248
Seq. No.
Contig ID -
                   210764_1.R1040
5'-most EST
                   uC-qmronoir076f12b1
Method
                   BLASTX
                   a2160144
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
Match length
                   128
                   42
% identity
                   (AC000375) Strong similarity to Arabidopsis oligopeptide
NCBI Description
                   transporter (gb_X77503). [Arabidopsis thaliana]
                   30249
Seq. No.
Contig ID
                   210765 1.R1040
5'-most EST
                   rlr700895313.hl
Method
                   BLASTX
                   q2462931
NCBI GI
BLAST score
                   359
                   2.0e-34
E value
Match length
                   89
                   71
% identity
                   (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   30250
Seq. No.
Contig ID
                   210776 1.R1040
5'-most EST
                   jex700\overline{9}06414.h1
                   30251
Seq. No.
                   210786 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}08547.h1
Method
                   BLASTX
                   q3114713
NCBI GI
BLAST score
                   148
```

1.0e-09

E value

```
Match length
                   73
                   48
% identity
                   (AF061346) Edpl protein [Mus musculus]
NCBI Description
                   30252
Seq. No.
                   210813 1.R1040
Contig ID
5'-most EST
                   leu701153394.h1
                   30253
Seq. No.
                   210841 1.R1040
Contig ID
5'-most EST
                   jex700906520.hl
                   30254
Seq. No.
                   210857 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}06549.h1
                   30255
Seq. No.
                   210921 1.R1040
Contig ID
                   jex700\overline{9}06708.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3128477
BLAST score
                   270
E value
                   3.0e-24
                   81
Match length
% identity
                   65
                   (AF062640) metalloproteinase [Arabidopsis thaliana]
NCBI Description
                   30256
Seq. No.
                   210932 1.R1040
Contig ID
5'-most EST
                   g5605826
                   30257
Seq. No.
                   210933_1.R1040
Contig ID
5'-most EST
                   fC-gmf\overline{1}700905073a1
Method
                   BLASTX
NCBI GI
                   g3641836
BLAST score
                   405
E value
                   2.0e-43
Match length
                   141
                   64
% identity
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   30258
Seq. No.
                   210943 1.R1040
Contig ID
5'-most EST
                   uC-gmropic009e05b1
                   30259
Seq. No.
                   210949 1.R1040
Contig ID
                   zhf700964978.hl
5'-most EST
Seq. No.
                   30260
                   210956_1.R1040
Contig ID
5'-most EST
                   jex700906761.hl
                   30261
Seq. No.
```

210998 1.R1040

Contig ID

NCBI Description

```
5'-most EST
                   leu701154452.h1
                   30262
Seq. No.
                   211029 1.R1040
Contig ID
5'-most EST
                   hrw701063013.hl
                   30263
Seq. No.
                   211048 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}08991.h1
Method
                   BLASTX
NCBI GI
                   q4455340
BLAST score
                   249
                   1.0e-21
E value
                   94
Match length
% identity
                   48
NCBI Description
                   (AL035522) putative protein [Arabidopsis thaliana]
                   30264
Seq. No.
Contig ID
                   211055 1.R1040
5'-most EST
                   fC-gmf1700906939a1
Method
                   BLASTX
                   g3915022
NCBI GI
BLAST score
                   411
                   3.0e-40
E value
Match length
                   128
% identity
NCBI Description
                   SUCROSE-PHOSPHATE SYNTHASE 2
                   (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2)
                   >gi 2190350 emb CAA72491 (Y11795) sucrose-phosphate
                   synthase [Craterostigma plantagineum]
Seq. No.
                   30265
Contig ID
                   211082 1.R1040
5'-most EST
                   jex700907578.hl
                   30266
Seq. No.
Contig ID
                   211091 1.R1040
5'-most EST
                   dpv701\overline{1}01879.h1
                   BLASTX
Method
                   g2245012
NCBI GI
BLAST score
                   304
                   8.0e-28
E value
Match length
                   75
% identity
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30267
Seq. No.
Contig ID
                   211094 1.R1040
                   jex700\overline{9}07013.h1
5'-most EST
                   BLASTX
Method
                   g3386611
NCBI GI
                   294
BLAST score
                   6.0e-27
E value
Match length
                   75
% identity
                   63
                   (AC004665) unknown protein [Arabidopsis thaliana]
```

5'-most EST

```
Seq. No.
                   30268
                   211141 1.R1040
Contig ID
5'-most EST
                   jex700907089.hl
                   30269
Seq. No.
                   211145 1.R1040
Contig ID
5'-most EST
                   jC-gmfl02220081f09d1
                   BLASTX
Method
NCBI GI
                   q3335372
BLAST score
                   522
E value
                   6.0e-53
Match length
                   186
                   51
% identity
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30270
Contig ID
                   211215 1.R1040
                   fC-gmle700788247g2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2651300
                   392
BLAST score
E value
                   1.0e-37
Match length
                   170
                   49
% identity
NCBI Description
                   (AC002336) putative initiator tRNA
                   phosphoribosyl-transferase [Arabidopsis thaliana]
                   30271
Seq. No.
Contig ID
                   211237 1.R1040
                   jex700907301.hl
5'-most EST
Method
                   BLASTX
                   g2244866
NCBI GI
                   304
BLAST score
                   5.0e-28
E value
Match length
                   91
                   60
% identity
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   30272
Seq. No.
                   211278_1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}07361.h1
                   30273
Seq. No.
                   211281_1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}07666.h1
                   30274
Seq. No.
Contig ID
                   211282 1.R1040
5'-most EST
                   jex700907564.hl
                   30275
Seq. No.
                   211319 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}41526.h1
                   30276
Seq. No.
                   211326 1.R1040
Contig ID
```

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 $epx701\overline{1}09165.h1$

BLAST score

E value

585

1.0e-60

```
Method
                   BLASTX
NCBI GI
                   q2126113
BLAST score
                   169
E value
                   1.0e-11
Match length
                   116
                   36
% identity
NCBI Description
                   prolyl aminopeptidase (EC 3.4.11.5) - Hafnia alvei
                   >gi_1754489_dbj_BAA09605_ (D61383) prolyl aminopeptidase
                   [Hafnia alvei] >gi_1588323_prf__2208340A Pro aminopeptidase
                   [Hafnia alvei]
                   30277
Seq. No.
                   211346 1.R1040
Contig ID
5'-most EST
                   leu701148125.h1
                   30278
Seq. No.
                   211382 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}09577.h1
Method
                   BLASTX
NCBI GI
                   g4006915
BLAST score
                   332
                   3.0e-31
E value
Match length
                   107
                   61 ----
% identity
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   30279
                   211394 1.R1040
Contig ID
                   jex700\overline{9}07530.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2781433
BLAST score
                   246
                   7.0e-21
E value
Match length
                   131
                   40
% identity
NCBI Description
                   (AF030052) RSW1-like cellulose synthase catalytic subunit
                   [Oryza sativa subsp. japonica]
                   30280
Seq. No.
                   211399 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400076g02a1
Method
                   BLASTX
                   g4115379
NCBI GI
BLAST score
                   277
E value
                   2.0e-24
Match length
                   123
                   54
% identity
NCBI Description
                   (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
                   30281
Seq. No.
                   211442_1.R1040
Contig ID
5'-most EST
                   zsg701118392.hl
Method
                   BLASTX
                   g2911067
NCBI GI
```

```
Match length
                   137
% identity
                   81
                   (AL021960) UV-damaged DNA-binding protein- like
NCBI Description
                   [Arabidopsis thaliana]
                   30282
Seq. No.
                   211471 1.R1040
Contig ID
5'-most EST
                   leu701152212.h1
Method
                   BLASTX
                   g1931652
NCBI GI
BLAST score
                   221
                   9.0e-18
E value
                   188
Match length
% identity
NCBI Description
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
                   [Arabidopsis thaliana]
                   30283
Seq. No.
                   211583 1.R1040
Contig ID
5'-most EST
                   epx701106685.h1
                   30284
Seq. No.
                   211591_1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}45967.h1
Method
                   BLASTX
NCBI GI
                   g2642157
BLAST score
                   201
E value
                   3.0e-19
Match length
                   69
                   70
% identity
                   (AC003000) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   30285
Seq. No.
                   211626_1.R1040
Contig ID
5'-most EST
                   fC-gmro700876145d1
Method
                   BLASTN
                   g1089903
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
Match length
                   128
                   86
% identity
NCBI Description
                   P.sativum mRNA for carboxypeptidase
                   30286
Seq. No.
Contig ID
                   211644 1.R1040
                   zhf700963153.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2655008
BLAST score
                   600
E value
                   3.0e-62
Match length
                   186
% identity
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
                   30287
Seq. No.
```

211656 1.R1040

Contig ID

% identity

45

```
5'-most EST
                   q4313445
Method
                   BLASTN
NCBI GI
                   q287561
BLAST score
                   359
                   0.0e + 00
E value
Match length
                   562
                   91
% identity
                   Vigna radiata auxin-regulated mRNA
NCBI Description
Seq. No.
                   30288
Contig ID
                   211715 1.R1040
5'-most EST
                   jex700908106.hl
                   30289
Seq. No.
Contig ID
                   211732 1.R1040
                   leu701149360.hl
5'-most EST
Method
                   BLASTX
                   g4559368
NCBI GI
BLAST score
                   213
E value
                   2.0e-17
Match length
                   58
                   72
% identity
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30290
                   211817 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}33909.h2
                   BLASTN
Method
                   g2351065
NCBI GI
BLAST score
                   34
E value
                   2.0e-09
Match length
                   82
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   30291
Contig ID
                   211924 1.R1040
5'-most EST
                   leu701150702.h1
                   BLASTX
Method
NCBI GI
                   q4218120
BLAST score
                   167
E value
                   6.0e-12
Match length
                   43
                   77
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
                   30292
Seq. No.
                   211929 1.R1040
Contig ID
5'-most EST
                   gsv701044336.h1
Method
                   BLASTX
                   g3877205
NCBI GI
BLAST score
                   286
E value
                   2.0e-25
Match length
                   112
```

```
NCBI Description (Z70780) similar to lipase [Caenorhabditis elegans]
Seq. No.
                   30293
                   211941 1.R1040
Contig ID
                   jex700\overline{9}08407.h1
5'-most EST
Method
                   BLASTX
                   g2642450
NCBI GI
BLAST score
                   608
E value
                   2.0e-63
Match length
                   140
% identity
                   81
                   (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                   [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
Seq. No.
                   211956 1.R1040
Contig ID
                   zhf700954347.hl
5'-most EST
Seq. No.
                   30295
                   211976 1.R1040
Contig ID
                   fC-qmf\overline{1}700909836a1
5'-most EST
Method
                   BLASTX
                   g3024387 ---
NCBI GI ----
BLAST score
                   544
E value
                   8.0e-56
Match length
                   148
                   67
% identity
                   POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 668998
NCBI Description
                   (U20431) polygalacturonase [Medicago sativa]
Seq. No.
                   211990 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08496.h1
Seq. No.
                   30297
                   211994 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810035f10d1
Seq. No.
Contig ID
                   212002 1.R1040
5'-most EST
                   jex700\overline{9}08480.h1
                   30299
Seq. No.
                   212045 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08548.h1
Method
                   BLASTX
NCBI GI
                   q4512263
BLAST score
                   191
                   1.0e-21
E value
                   74
Match length
% identity
                   (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
NCBI Description
                   30300
Seq. No.
                   212057 1.R1040
Contig ID
5'-most EST
```

uC-qmflminsoy017h03b1

```
BLASTX
Method
NCBI GI
                   g4093155
BLAST score
                   165
E value
                   1.0e-11
Match length
                   103
% identity
                   36
                   (AF088281) phytochrome-associated protein 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30301
                   212062 1.R1040
Contig ID
                   pmv700892882.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q477430
BLAST score
                   438
E value
                   1.0e-43
Match length
                   103
                   82
% identity
NCBI Description
                  nucleolar protein p120 - mouse (fragment)
                   30302
Seq. No.
                   212068 1.R1040
Contig ID
5'-most EST
                   gsv701056516.h1
                   30303
Seq. No.
Contig ID
                   212077 1.R1040
5'-most EST
                   qsv701046554.hl
Method
                   BLASTX
NCBI GI
                   q3335347
BLAST score
                   613
E value
                   1.0e-63
Match length
                   214
% identity
                   55
                   (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                   gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                   gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                   gb_AA042359 come from this gene. [Arabidopsis thaliana]
                   30304
Seq. No.
                   212083 1.R1040
Contig ID
5'-most EST
                   epx701109802.h1
Method
                  BLASTX
                 g3298502
NCBI GI
BLAST score
                   414
E value
                   2.0e-40
Match length
                  157
% identity
                   53
NCBI Description (AB015046) xylulokinase [Homo sapiens]
Seq. No.
                   30305
                   212094 1.R1040
Contig ID
5'-most EST
                  crh700855625.h1
Seq. No.
                  30306
                  212096 1.R1040
Contig ID
                  jex700\overline{9}08622.h1
5'-most EST
```

BLASTX

Method

NCBI Description

```
q1345643
NCBI GI
BLAST score
                   419
                   5.0e-49
E value
                   138
Match length
                   74
% identity
                   FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450
NCBI Description
                   3',5'-hydroxylase Hf2 - garden petunia
>gi_311654_emb_CAA80265_ (Z22544) flavonoid
3',5'-hydroxylase [Petunia x hybrida]
                   >gi 738771 prf 2001426A flavonoid 3',5'-hydroxylase
                   [Petunia x hybrida]
Seq. No.
                   30307
                   212108 1.R1040
Contig ID
5'-most EST
                   pxt700944644.h1
Method
                   BLASTX
                   q1871193
NCBI GI
BLAST score
                   424
                   1.0e-42
E value
Match length
                   163
% identity
                   52
                   (U90439) receptor-like protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana] >gi_2335090 (AC002339) putative receptor-like
                   protein kinase [Arabidopsis thaliana]
                   30308
Seq. No.
                   212118 1.R1040
Contig ID
5'-most EST
                   jex700908656.hl
Seq. No.
                   30309
                   212134 1.R1040
Contig ID
                   zhf700954902.hl
5'-most EST
Seq. No.
                   30310
                   212181 1.R1040
Contig ID
                   jex700<del>9</del>09274.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3687230
BLAST score
                   637
E value
                   1.0e-66
Match length
                   163
% identity
                   70
NCBI Description
                   (AC005169) hypothetical protein [Arabidopsis thaliana]
                   30311
Seq. No.
                   212187 1.R1040
Contig ID
5'-most EST
                   q5510128
Method
                   BLASTX
NCBI GI
                   q4530126
BLAST score
                   227
E value
                   1.0e-18
Match length
                   90 -
% identity
```

[Phaseolus vulgaris]

(AF078082) receptor-like protein kinase homolog RK20-1

```
30312
Seq. No.
                   212193 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08757.h1
                   30313
Seq. No.
                   212197 1.R1040
Contig ID
5'-most EST
                   dpv701098985.h1
Seq. No.
                   30314
                   212218 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy061b07b1
Method
                   BLASTX
NCBI GI
                   q4567279
BLAST score
                   194
E value
                   6.0e-15
Match length
                   95
% identity
                   45
NCBI Description
                   (AC006841) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   30315
                   212225 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir011a01b1
                   30316
Seq. No.
Contig ID
                   212250 1.R1040
5'-most EST
                   jex700908836.hl
                   30317
Seq. No.
                   212251 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08845.h1
                   30318
Seq. No.
                   212253_1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}08848.h1
Method
                   BLASTX
NCBI GI
                   q2738248
BLAST score
                   405
                   6.0e-40
E value
Match length
                   89
% identity
                   88
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                   30319
Seq. No.
                   212285 1.R1040
Contig ID
5'-most EST
                   uC-gmropic016d09b1
Seq. No.
                   30320
                   212311_1.R1040
Contig ID
                   jex700908934.hl
5'-most EST
                   BLASTX
Method
                   g3377517
NCBI GI
BLAST score
                   201
                   2.0e-15
E value
Match length
                   52
```

62

% identity

NCBI Description

```
(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30321
                   212315 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy220g05b1
Seq. No.
                   30322
Contig ID
                   212323 1.R1040
5'-most EST
                   jex700\overline{9}08953.h1
Method
                   BLASTX
NCBI GI
                   q4105698
BLAST score
                   171
E value
                   2.0e-12
Match length
                   66
% identity
                   52
NCBI Description
                   (AF049870) small hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                   30323
Contig ID
                   212331 1.R1040
5'-most EST
                   kl1701214360.hl
Method
                   BLASTX
NCBI GI
                   g4522012
BLAST score
                   546
E value
                   8.0e-56
Match length
                   185
% identity
                   57
                   (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30324
Seq. No.
                   212379 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy158a10b1
                   30325
Seq. No.
                   212408 1.R1040
Contig ID
5'-most EST
                   fC-gmse700755370a2
Seq. No.
                   30326
                   212416 1.R1040
Contig ID
                   jC-gmro02910013e12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252472
BLAST score
                   813
E value
                   3.0e-87
Match length
                   182
% identity
                   85
NCBI Description
                   (297558) argininosuccinate lyase [Arabidopsis thaliana]
Seq. No.
                   30327
Contig ID
                   212437 1.R1040
5'-most EST
                   qsv701\overline{0}56350.h1
Method
                   BLASTX
NCBI GI
                   q1076580
BLAST score
                   223
                   3.0e-18
E value
Match length
                   75
% identity
```

alcohol dehydrogenase homolog ADH3b - tomato

```
cherry, Peptide, 390 aa] [Lycopersicon esculentum]
Seq. No.
                   30328
                   212442 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09113.h1
                   BLASTX
Method
NCBI GI
                   q464900
BLAST score
                   497
E value
                   4.0e-50
Match length
                   127
                   73
% identity
                   PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR
NCBI Description
                   >gi_539008_pir__S39476 kinase-like transmembrane protein
TMKL1 precursor - Arabidopsis thaliana
                   >gi_313190_emb_CAA51385_ (X72863) TMKL1 [Arabidopsis
                thaliana]
                   30329
Seq. No.
                   212458 1.R1040
Contig ID
                   leu701145458.h1
5'-most EST
Method
                   BLASTN
                   g429107 ---
NCBI GI- -
BLAST score
                   126
E value
                   2.0e-64
Match length
                   326
% identity
                   85
                   L.esculentum S-adenosyl-L-methionine synthetase mRNA,
NCBI Description
                   complete CDS
                   30330
Seq. No.
                   212460 1.R1040
Contig ID
                   zhf700960731.hl
5'-most EST
                   30331
Seq. No.
Contig ID
                   212461 1.R1040
                   g5607028
5'-most EST
Seq. No.
                   30332
                   212464 1.R1040
Contig ID
                   zsg701126409.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4530126
BLAST score
                   153
E value
                   8.0e-10
Match length
                   155
% identity
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                    [Phaseolus vulgaris]
                   30333
Seq. No.
Contig ID
                   212530 1.R1040
                   zhf700963094.hl
5'-most EST
Method
                   BLASTX
                   g2739370
NCBI GI
                   334
BLAST score
```

>gi_913446 bbs_160508 (S75487) alcohol dehydrogenase ADH
{EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red

```
2.0e-31
E value
Match length
                   112
                   56
% identity
                   (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   30334
Seq. No.
Contig ID
                   212541 1.R1040
                   zhf700958684.h1
5'-most EST
Seq. No.
                   30335
                   212544 1.R1040
Contig ID
5'-most EST
                   zsg701125485.hl
Seq. No.
                   30336
                   212555 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09294.h1
Method
                   BLASTN
                   g2656030
NCBI GI
BLAST score
                   33
                   4.0e-09
E value
Match length
                   65
% identity
                   88
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUL8-
Seq. No.
                   30337
                   212564 1.R1040
Contig ID
5'-most EST
                   gsv701056257.hl
                   30338
Seq. No.
                   212567 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09318.h1
                   30339
Seq. No.
Contig ID
                   212569 1.R1040
5'-most EST
                   jex700\overline{9}09321.h1
Method
                   BLASTN
NCBI GI
                   q2293111
BLAST score
                   207
E value
                   1.0e-113
Match length
                   378
% identity
                   89
NCBI Description V.faba mRNA for potassium channel
                   30340
Seq. No.
                   212575 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09329.h1
Seq. No.
                   30341
                   212585 1.R1040
Contig ID
5'-most EST
                   fC-qmf1700909057a1
                   BLASTX
Method
NCBI GI
                   q2829204
BLAST score
                   208
E value
                   3.0e-16
Match length
                   81
                   47
% identity
```

```
NCBI Description
                   (AF044204) lipid transfer protein precursor [Gossypium
                   hirsutum]
Seq. No.
                   30342
                   212592 1.R1040
Contig ID
                   jex700\overline{9}09349.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193298
BLAST score
                   178
E value
                   7.0e-13
Match length
                   113
% identity
                   33
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
NCBI Description
                   30343
Seq. No.
                   212605 1.R1040
Contig ID
5'-most EST
                   epx701108145.hl
Seq. No.
                   30344
Contig ID
                   212636 1.R1040
5'-most EST
                   jex700\overline{9}09421.h1
                   BLASTX
Method
NCBI GI
                   g4455316
BLAST score
                   278
E value
                   1.0e-24
Match length
                   76
% identity
                   70
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   30345
Seq. No.
                   212657 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09449.h1
                   30346
Seq. No.
                   212685 1.R1040
Contig ID
5'-most EST
                   hrw701057006.h2
Method
                   BLASTX
                   g3643604
NCBI GI
BLAST score
                   211
E value
                   5.0e-17
Match length
                   102
                   43
% identity
NCBI Description
                   (AC005395) receptor-like protein kinase [Arabidopsis
                   thaliana]
                   30347
Seq. No.
                   212711 1.R1040
Contig ID
                   jex700909530.hl
5'-most EST
                   BLASTN
Method
                   g460088
NCBI GI
BLAST score
                   52
E value
                   2.0e-20
Match length
                   72
% identity
                   93
                   Arabidopsis thaliana Columbia ecotype gl-tubulin (TUBG1)
NCBI Description
```

gene, complete cds

% identity

84

```
30348
Seq. No.
                   212719 1.R1040
Contig ID
5'-most EST
                   jex700\overline{9}09543.h1
                   BLASTX
Method
                   g3249065
NCBI GI
BLAST score
                   396
E value
                   2.0e-44
Match length
                   181
% identity
                   63
NCBI Description
                   (AC004473) Similar to HAK1 gb U22945 high affinity
                   potassium transporter from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
Seq. No.
                   30349
                   212733 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220141q10a1
                   30350
Seq. No.
                   212734 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}13345.h1
                   BLASTX
Method
                   q3212867
NCBI GI
BLAST score
                   272
E value
                   4.0e-24
                   110
Match length
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30351
Seq. No.
                   212749 1.R1040
Contig ID
                   jex700\overline{9}09579.h1
5'-most EST
                   30352
Seq. No.
                   212766 1.R1040
Contig ID
                   zhf700955870.h1
5'-most EST
Seq. No.
                   30353
                   212838 1.R1040
Contig ID
                   fC-qmf1700906093h1
5'-most EST
                   BLASTX
Method
                   g2388565
NCBI GI
BLAST score
                   163
                   6.0e-11
E value
                   71
Match length
% identity
                   42
                   (AC000098) Similar to Prunus pectinesterase (gb X95991).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   30354
                   212845 1.R1040
Contig ID
                   zhf700963860.h1
5'-most EST
Method
                   BLASTN
                   q3702728
NCBI GI
BLAST score
                   46
                   2.0e-16
E value
                   289
Match length
```

```
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   30355
                   212859 1.R1040
Contig ID
                   fC-gmf1700910054a1
5'-most EST
Seq. No.
                   30356
Contig ID
                   212879 1.R1040
5'-most EST
                   zhf700955947.h1
Method
                   BLASTX
NCBI GI
                   q3608134
BLAST score
                   243
E value
                   8.0e-21
Match length
                   88
                   57
% identity
NCBI Description (AC005314) dnaJ-like protein [Arabidopsis thaliana]
                   30357
Seq. No.
Contig ID
                   212882 1.R1040
                   jex700\overline{9}09781.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g18680
BLAST score
                   130
E value
                   4.0e-67
Match length
                   247
                   88
% identity
                   G.max mRNA for mitotic cyclin (S13-7)
NCBI Description
                   30358
Seq. No.
Contig ID
                   212893 1.R1040
5'-most EST
                   jC-gmf102220065f08a1
Method
                   BLASTX
                   g1495802
NCBI GI
BLAST score
                   638
E value
                   1.0e-66
Match length
                   199
% identity
                   61
                   (X96405) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   30359
Seq. No.
Contig ID
                   212893 2.R1040
                   jex700\overline{9}09795.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1495802
BLAST score
                   511
E value
                   6.0e-52
Match length
                   129
% identity
                   71
                   (X96405) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   30360
Seq. No.
Contig ID
                   212932 1.R1040
                   jC-qmf\overline{1}02220065f12d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827548
```

403

BLAST score

Seq. No.

30368

```
E value
                    3.0e-39
 Match length
                    112
 % identity
                    65
 NCBI Description
                    (AL021635) cytochrome P450 - like protein [Arabidopsis
                    thaliana]
 Seq. No.
                    30361
 Contig ID
                    212943 1.R1040
 5'-most EST
                    jex700\overline{9}09885.h1
 Seq. No.
                    30362
 Contig ID
                    212989 1.R1040
 5'-most EST
                    epx701105703.h1
 Seq. No.
                    30363
 Contig ID
                    213002 1.R1040
 5'-most EST
                    jex700909975.h1
 Seq. No.
                    30364
 Contig ID
                    213016 1.R1040
 5'-most EST
                    jex700\overline{9}10001.h1
 Seq. No.
                    30365
 Contig ID
                    213020 1.R1040
 5'-most EST
                    fC-gmf\(\bar{1}\)700907612a1
. Method
                    BLASTX
 NCBI GI
                    g3928519
 BLAST score
                    239
 E value
                    5.0e-23
Match length
                    119
 % identity
 NCBI Description
                    (AB011670) wpk4 protein kinase [Triticum aestivum]
 Seq. No.
                    30366
 Contig ID
                    213029 1.R1040
 5'-most EST
                    hrw701059588.h1
Method
                    BLASTN
NCBI GI
                   g4567193
BLAST score
                    98
E value
                    1.0e-47
Match length
                    434
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T26C19 genomic
                    sequence, complete sequence
Seq. No.
                    30367
Contig ID
                    213043 1.R1040
5'-most EST
                    zhf700952854.h1
Method
                    BLASTX
NCBI GI
                    q2598575
BLAST score
                    436
E value
                    3.0e-43
Match length
                    106
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
```

Seq. No.

Contig ID

```
Contig ID
                   213051 1.R1040
5'-most EST
                   jex700\overline{9}10053.h1
                   BLASTX
Method
NCBI GI
                   q3367576
BLAST score
                   246
                   2.0e-22
E value
                   122
Match length
% identity
                   43
                  (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30369
                   213072 1.R1040
Contig ID
                   k11701209063.hl
5'-most EST
                   30370
Seq. No.
Contig ID
                   213081 1.R1040
5'-most EST
                  gsv701054104.h1
Method
                  BLASTX
NCBI GI
                   g3157945
BLAST score
                   280
E value
                   7.0e-25
Match length
                  111
% identity
                   41
                   (AC002131) Contains similarity to axi 1 gene gb X80301 from
NCBI Description
                  Nicotiana tabacum. [Arabidopsis thaliana]
                   30371
Seq. No.
                   213082 1.R1040
Contig ID
5'-most EST
                   fC-gmf1700907613a1
Method
                  BLASTX
                  g1351945
NCBI GI
BLAST score
                   691
E value
                   9.0e-73
Match length
                  186
% identity
                   56
NCBI Description FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
                  APETALA2 protein [Arabidopsis thaliana]
                   >gi_2464888_emb_CAB16765_ (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
                   30372
Seq. No.
Contig ID
                  213091 1.R1040
5'-most EST
                  zhf700962041.h1
Method
                  BLASTX
                  g1237086
NCBI GI
BLAST score
                  299
E value
                  2.0e-27
Match length
                  109
% identity
                  59
NCBI Description (X96766) ADP-glucose pyrophosphorylase [Pisum sativum]
                  30373
Seq. No.
Contig ID
                  213147 1.R1040
5'-most EST
                  jC-gmf102220056c12a1
                   30374
```

213150 1.R1040

```
5'-most EST
                  zhf700951787.h1
Method
                  BLASTX
                  g2246458
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
Match length
                  41
                  76
% identity
NCBI Description
                   (U81313) S-adenosyl-methionine-sterol-C- methyltransferase
                   [Ricinus communis]
                  30375
Seq. No.
                  213150 2.R1040
Contig ID
5'-most EST
                  jC-qmle01810004e10a1
Method
                  BLASTN
NCBI GI
                  q1399379
BLAST score
                  108
E value
                  1.0e-53
Match length
                  268
% identity
                  85
                  Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase mRNA, complete cds
Seq. No.
                  30376
                  213155 1.R1040
Contig ID
5'-most EST
                  zhf700951794.h1
                  30377
Seq. No.
                  213203 1.R1040
Contig ID
5'-most EST
                  zhf700962818.h1
Seq. No.
                  30378
                  213233 1.R1040
Contig ID
5'-most EST
                   zhf700951901.hl
Method
                  BLASTX
NCBI GI
                  g3335350
BLAST score
                  122
E value
                   3.0e-14
Match length
                  84
% identity
                   51
                   (AC004512) Similar to gb_Z84386 anthranilate
NCBI Description
                  N-hydroxycinnamoyl/benzoyltransferase from Dianthus
                  caryophyllus. [Arabidopsis thaliana]
                  30379
Seq. No.
                  213290 1.R1040
Contig ID
5'-most EST
                  leu701154862.h1
Seq. No.
                  30380
Contig ID
                  213302 1.R1040
5'-most EST
                  jC-gmro02910016b06a1
                  30381
Seq. No.
Contig ID
                  213338 1.R1040
5'-most EST
                   zhf700952049.hl
                  30382
Seq. No.
```

213339 1.R1040

Contig ID

```
5'-most EST
                   zhf700952050.h1
Seq. No.
                   30383
                   213345 1.R1040
Contig ID
                   zhf700952057.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2583128
BLAST score
                   142
E value
                   9.0e-09
Match length
                   75
% identity
                   40
NCBI Description
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
                   30384
Seq. No.
                   213412 1.R1040
Contig ID
5'-most EST
                   zhf700952138.hl
Method
                  BLASTX
NCBI GI
                   g2384675
BLAST score
                   168
E value
                   7.0e-12
Match length
                   65
% identity
                   54
NCBI Description
                   (AF012659) putative potassium transporter AtKT4p
                  [Arabidopsis thaliana]
                   30385
Seq. No.
                   213419 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220115c03a1
                   30386
Seq. No.
Contig ID
                   213439 1.R1040
5'-most EST
                   fua701042188.h1
                   30387
Seq. No.
                   213476_1.R1040
Contig ID
5'-most EST
                   pxt700944312.h1
                   BLASTX
Method
                   g3121917
NCBI GI
BLAST score
                   193
E value
                   6.0e-15
Match length
                   99
                   27
% identity
NCBI Description
                  COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA
                   >gi 1362773 pir A57090 CSA protein - human >gi 975302
                   (U28413) CSA protein [Homo sapiens]
                   >gi_4557467_ref_NP_000073.1_pCKN1_ Cockayne syndrome 1
                  protein
                   30388
Seq. No.
Contig ID
                   213503 1.R1040
5'-most EST
                   zhf700962122.h1
                   30389
Seq. No.
                   213505 1.R1040
Contig ID
                   zhf700952252.h1
5'-most EST
```

30390

Seq. No.

```
213519 1.R1040
Contig ID
5'-most EST
                   zhf700952272.hl
Method
                   BLASTX
NCBI GI
                   g2623248
BLAST score
                   264
E value
                   3.0e-25
Match length
                   93
                   68
% identity
NCBI Description
                   (AF030882) SU1 isoamylase [Zea mays]
Seq. No.
                   30391
                   213533 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy058f04b1
Seq. No.
                   30392
                   213537 1.R1040
Contig ID
                   zhf700952301.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1351945
BLAST score
                   177
E value
                   3.0e-22
Match length
                   107
                   59
% identity
NCBI Description
                  FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
                   APETALA2 protein [Arabidopsis thaliana]
                   >gi_2464888_emb_CAB16765_ (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
                   30393
Seq. No.
                   213598 1.R1040
Contig ID
5'-most EST
                   zhf700952364.h1
Method
                   BLASTN
                   g2330650
NCBI GI
BLAST score
                   49
E value
                   2.0e-18
Match length
                   205
% identity
                   90
NCBI Description
                   Pisum sativum mRNA for topoisomerase II
                   30394
Seq. No.
                   213627 1.R1040
Contig ID
5'-most EST
                   zhf700952402.h1
                   30395
Seq. No.
                   213640 1.R1040
Contig ID
5'-most EST
                   g4313837
                   BLASTX
Method
NCBI GI
                   g3738297
BLAST score
                   487
E value
                   2.0e-49
Match length
                   111
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   30396
Seq. No.
                   213655 1.R1040
Contig ID
```

fua701037671.hl

5'-most EST

Method

NCBI GI

BLASTX

q4468813

```
Seq. No.
                   30397
                   213661 1.R1040
Contig ID
5'-most EST
                   g5606683
Seq. No.
                   30398
Contig ID
                   213669 1.R1040
5'-most EST
                   uC-gmflminsoy120h06b1
Seq. No.
                   30399
                   213679 1.R1040
Contig ID
                   gsv701\overline{0}43845.h1
5'-most EST
Seq. No.
                   30400
                   213700 1.R1040
Contig ID
5'-most EST
                   gsv701053917.hl
Seq. No.
                   30401
                   213709 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy023f05b1
Seq. No.
                   30402
                   213721 1.R1040
Contig ID
5'-most EST-
                   zhf700952524.h1
Method
                   BLASTX
                   g2443881
NCBI GI
BLAST score
                   243
E value
                   2.0e-20
Match length
                   181
% identity
NCBI Description
                    (AC002294) contains beta-transducin motif [Arabidopsis
                   thaliana]
Seq. No.
                   30403
Contig ID
                   213724 1.R1040
5'-most EST
                   uC-gmropic011c08b1
Seq. No.
                   213734 1.R1040
Contig ID
5'-most EST
                   zhf700952545.h1
Seq. No.
                   30405
                   213770 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}54568.h1
Method
                   BLASTX
NCBI GI
                   q3413322
BLAST score
                   501
E value
                   1.0e-50
Match length
                   161
% identity
NCBI Description
                   (Y11118) polygalacturonase [Medicago sativa]
Seq. No.
                   30406
                   213789 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97122.h1
```

NCBI GI

```
BLAST score
                   358
                   3.0e-34
E value
                   81
Match length
                   73
% identity
NCBI Description
                    (AL035601) putative protein [Arabidopsis thaliana]
                   30407
Seq. No.
                   213790 1.R1040
Contig ID
5'-most EST
                   zhf700952630.h1
                   30408
Seq. No.
                   213814 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}52674.h1
Method
                   BLASTX
NCBI GI
                   g2281330
BLAST score
                   333
E value
                    3.0e-31
Match length
                   108
% identity
                   57
NCBI Description
                    (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
Seq. No.
                   213850 1.R1040
Contig ID
5'-most EST---
                   jC-qmf102220061a06a1----
Seq. No.
                   213873 1.R1040
Contig ID
                   zhf700952757.h1
5'-most EST
                   30411
Seq. No.
                   213958 1.R1040
Contig ID
5'-most EST
                   uC-gmropic098d04b1
Method
                   BLASTX
NCBI GI
                   q4138137
BLAST score
                   452
E value
                   6.0e-45
Match length
                   108
% identity
NCBI Description
                    (AJ012796) ss-galactosidase [Lycopersicon esculentum]
Seq. No.
                   30412
                   213963 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220081h02d1
Seq. No.
                   30413
Contig ID
                   213977 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220138g05d1
Seq. No.
                   30414
Contig ID
                   213988 1.R1040
5'-most EST
                   dpv701\overline{0}99482.h1
Seq. No.
                   30415
                   214016 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy053b01b1
Method
                   BLASTX
```

g3928097

NCBI Description

```
BLAST score
                  211
                   1.0e-22
E value
Match length
                  140
                   43
% identity
                   (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  30416
Seq. No.
                  214017 1.R1040
Contig ID
                  zhf700963236.h1
5'-most EST
                  30417
Seq. No.
                  214022 1.R1040
Contig ID
                  qsv701\overline{0}55630.h1
5'-most EST
                  30418
Seq. No.
                  214035 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy017f01b1
                  30419
Seq. No.
                  214057 1.R1040
Contig ID
5'-most EST
                  zhf700953006.h1
Method
                  BLASTX
NCBI GI
                  q2245070 —
BLAST score
                  150
E value
                  2.0e-09
                  167
Match length
% identity
                  28
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30420
                  214099 1.R1040
Contig ID
5'-most EST
                   zhf700953069.h1
Method
                  BLASTX
NCBI GI
                  q3075382
BLAST score
                  320
E value
                   6.0e-30
Match length
                  82
% identity
                  77
NCBI Description
                   (AC002505) putative peroxisome assembly protein PER8
                   [Arabidopsis thaliana] >gi_3075384 (AC004484) putative
                  peroxisome assembly protein PER8 [Arabidopsis thaliana]
Seq. No.
                  30421
                  214157 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir009a11b1
Seq. No.
                  30422
                  214160 1.R1040
Contig ID
5'-most EST
                  zhf700964709.h1
Method
                  BLASTX
NCBI GI
                  q3415115
BLAST score
                  542
E value
                  1.0e-55
Match length
                  131
% identity
                  39
```

(AF081202) villin 2 [Arabidopsis thaliana]

```
30423
Seq. No.
                   214172 1.R1040
Contig ID
                   uC-gmronoir071g02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2911058
BLAST score
                   317
E value
                   8.0e-29
                   145
Match length
                   42
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   30424
Seq. No.
                   214210 1.R1040
Contig ID
                   epx701103943.h1
5'-most EST
                   BLASTX
Method
                   g3980401
NCBI GI
BLAST score
                   189
E value
                   1.0e-20
                   78
Match length
% identity
                   55
NCBI Description
                   (AC004561) putative tropinone reductase [Arabidopsis
                   thaliana]
Seq. No.
                   30425
                   214227 1.R1040
Contig ID
5'-most EST
                   uC-gmropic042a01b1
Seq. No.
                   30426
                   214227 2.R1040
Contig ID
                   k11701\overline{2}06481.h1
5'-most EST
                   30427
Seq. No.
                   214229 1.R1040
Contig ID
5'-most EST
                   zhf700953234.hl
Seq. No.
                   30428
                   214259 1.R1040
Contig ID
5'-most EST
                   iC-qmst02400076e02a1
Method
                   BLASTX
NCBI GI
                   q3201624
BLAST score
                   220
E value
                   1.0e-17
Match length
                   124
                   56
% identity
NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   30429
                   214261 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy020b01b1
                   30430
Seq. No.
                   214263 1.R1040
Contig ID
5'-most EST
                   zhf700953279.h1
                   30431
Seq. No.
```

214278_1.R1040

Contig ID

E value

2.0e-37

```
5'-most EST
                   zhf700953302.h1
Seq. No.
                   30432
                   214281 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810015g10d1
Method
                   BLASTX
                   q4432846
NCBI GI
BLAST score
                   201
E value
                   1.0e-15
Match length
                   70
                   57
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30433
                   214299 1.R1040
Contig ID
                   crh700852282.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2982431
BLAST score
                   176
E value
                   8.0e-13
Match length
                   81
                   47
% identity
NCBI Description
                   (AL022224) leucine rich repeat-like protein [Arabidopsis
                   thalianal
Seq. No.
                   30434
                   214336 1.R1040
Contig ID
5'-most EST
                   zhf700953372.h1
                   30435
Seq. No.
                   214346 1.R1040
Contig ID
5'-most EST
                   zhf700953382.h1
                   30436
Seq. No.
                   214359 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220058e01a1
                   30437
Seq. No.
                   214364 1.R1040
Contig ID
5'-most EST
                   a57530\overline{9}9
Method
                   BLASTX
NCBI GI
                   q3193293
BLAST score
                   386
E value
                   3.0e-37
Match length
                   150
% identity
NCBI Description
                   (AF069298) contains a short region of similarity to another
                   Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                   [Arabidopsis thaliana]
                   30438
Seq. No.
                   214388 1.R1040
Contig ID
                   jC-gmle01810082f04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4325282
BLAST score
                   386
```

```
Match length
                   119
                   66
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
Seq. No.
                   30439
                   214437 1.R1040
Contig ID
                   jC-gmf102220082f01d1
5'-most EST
                   30440
Seq. No.
                   214437 2.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220082g02a1
                   30441
Seq. No.
                   214453 1.R1040
Contig ID
5'-most EST
                   zhf700953514.hl
Seq. No.
                   30442
                   214455 1.R1040
Contig ID
5'-most EST
                   zhf700953516.h1
Method
                   BLASTX
NCBI GI
                   g960289
                   476 ----
BLAST score -
E value
                   4.0e-48
Match length
                   101
% identity
                   89
                   (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
                   30443
Seq. No.
                   214469 1.R1040
Contig ID
                   jC-gmf102220054b08a1
5'-most EST
Seq. No.
                   30444
                   214489 1.R1040
Contig ID
                   uC-qmflminsoy046a06b1
5' ≠most EST
Method
                   BLASTX
                   q3367520
NCBI GI
BLAST score
                   537
E value
                   7.0e-55
                   179
Match length
% identity
                   57
                   (AC004392) Similar to protein kinase APK1A,
NCBI Description
                   tyrosine-serine-threonine kinase gb D12522 from A.
                   thaliana. [Arabidopsis thaliana]
                   30445
Seq. No.
                   214496 1.R1040
Contig ID
                   k11701\overline{2}05657.h1
5'-most EST
Seq. No.
                   30446
                   214500 1.R1040
Contig ID
                   zhf700954982.h1
5'-most EST
                   30447
Seq. No.
```

214500 2.R1040

Contig ID

Method

BLASTX

```
5'-most EST
                   uC-gmropic101h09b1
Seq. No.
                   30448
                   214507 1.R1040
Contig ID
                   zhf700953580.h1
5'-most EST
                   BLASTX
Method
                   g3298550
NCBI GI
BLAST score
                   419
E value
                   4.0e-41
Match length
                   162
% identity
                   52
                   (AC004681) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
                   30449
Seq. No.
                   214526 1.R1040
Contig ID
                   jC-gmf\overline{1}02220136h02d1
5'-most EST
Seq. No.
                   30450
                   214566 1.R1040
Contig ID
5'-most EST
                   zhf700960157.h1
Seq. No.
                   30451
Contig-ID-
                   214623 1.R1040-
5'-most EST
                   k11701210714.h1
Method
                   BLASTX
NCBI GI
                   a3953475
BLAST score
                   275
E value
                   2.0e-24
Match length
                   93
% identity
                   54
NCBI Description
                   (AC002328) F2202.20 [Arabidopsis thaliana]
Seq. No.
                   30452
                   214627 1.R1040
Contig ID
5'-most EST
                   zhf700953726.h1
                   30453
Seq. No.
Contig ID
                   214691_1.R1040
5'-most EST
                   uC-qmrominsoy126e11b1
Method
                   BLASTN
                   g3869069
NCBI GI
BLAST score
                   53
E value
                   1.0e-20
Match length
                   230
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   30454
                   214720 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220143a07a1
                   30455
Seq. No.
                   214744 1.R1040
Contig ID
                   zhf700953878.h1
5'-most EST
```

5'-most EST

```
NCBI GI
                   g4038042
BLAST score
                   477
                   4.0e-48
E value
Match length
                   117
                   79
% identity
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30456
                   214749 1.R1040
Contig ID
                   zhf700953884.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4469024
BLAST score
                   500
E value
                   7.0e-51
Match length
                   110
% identity
                   79
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   214768 1.R1040
Contig ID
5'-most EST
                   zhf700953912.hl
Seq. No.
Contig ID
                   214814 1.R1040
5'-most EST
                   uC-gmrominsoy208g09b1
Seq. No.
                   214848 1.R1040
Contig ID
5'-most EST
                   gsv701045630.hl
Seq. No.
                   30460
                   214859 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}07659.h1
Method
                   BLASTX
NCBI GI
                   q2655098
BLAST score
                   209
E value
                   9.0e-17
Match length
                   54
% identity
NCBI Description
                   (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                   30461
                   214860 1.R1040
Contig ID
5'-most EST
                   zhf700954023.h1
Seq. No.
                   30462
                   214873 1.R1040
Contig ID
5'-most EST
                   hrw701063257.hl
                   30463
Seq. No.
                   214894 1.R1040
Contig ID
5'-most EST
                   zhf700954062.h1
                   30464
Seq. No.
Contig ID
                   214901 1.R1040
```

zhf700954070.hl

% identity

64

```
Method
                   BLASTX
NCBI GI
                   g3928079
                   224
BLAST score
                   3.0e-18
E value
Match length
                   144
% identity
                   40
                  (AC005770) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30465
Seq. No.
                   214922 1.R1040
Contig ID
5'-most EST
                   zhf700954102.h1
Method
                   BLASTX
                   g3168884
NCBI GI
BLAST score
                   171
                   2.0e-12
E value
Match length
                   65
                   48
% identity
                   (AF068716) similar to E. coli thermoresistant gluconokinase
NCBI Description
                   (GB:U18997) [Caenorhabditis elegans]
Seq. No.
                   30466
                   214925 1.R1040
Contig ID
                   zhf700954105.hl
5'-most EST
Method
                   BLASTX
                   q4249409
NCBI GI
BLAST score
                   148
                   1.0e-09
E value
                   59
Match length
% identity
                   (AC006072) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30467
                   214933 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy042b07b1
Method
                   BLASTX
                   q3643598
NCBI GI
BLAST score
                   738
                   2.0e-78
E value
Match length
                   162
% identity
                   (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30468
                   214940 1.R1040
Contig ID
                   zhf700954122.hl
5'-most EST
                   30469
Seq. No.
                   214942 1.R1040
Contig ID
                   zhf700955311.h1
5'-most EST
Method
                  BLASTX
                  g1491615
NCBI GI
BLAST score
                  205
                   2.0e-16
E value
Match length
                  66
```

```
(X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   30470
Seq. No.
                  214943 1.R1040
Contig ID
                   zhf700954126.h1
5'-most EST
Seq. No.
                   30471
                  215022 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810036e05d1
Method
                  BLASTX
NCBI GI
                  g2664210
                   334
BLAST score
E value
                   3.0e - 31
Match length
                   69
% identity
                  87
NCBI Description
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   30472
                   215044_1.R1040
Contig ID
5'-most EST
                  uC-gmropic101g08b1
Seq. No.
                   30473
                   215132 1.R1040
Contiq ID
5'-most EST
                   zhf700954354.h1
Seq. No.
                   30474
                   215173 1.R1040
Contig ID
5'-most EST
                   zhf700954408.hl
                  30475
Seq. No.
                   215221 1.R1040
Contig ID
5'-most EST
                   zhf700954476.h1
                  30476
Seq. No.
Contig ID
                  215223 1.R1040
5'-most EST
                  uC-gmrominsoy126g08b1
                  30477
Seq. No.
                  215249 1.R1040
Contig ID
5'-most EST
                  fua701040622.h1
Seq. No.
                  30478
                  215268 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810078f07a1
Method
                  BLASTX
NCBI GI
                  q3850588
BLAST score
                  525
                  2.0e-53
E value
                  152
Match length
% identity
NCBI Description
                   (AC005278) Contains similarity to gb_AB011110 KIAA0538
                  protein from Homo sapiens brain and to phospholipid-binding
                  domain C2 PF 00168. ESTs gb AA585988 and gb_T04384 come
```

from this gene. [Arabidopsis thaliana]

5'-most EST

```
. 30479
Seq. No.
                   215276 1.R1040
Contig ID
                   leu701145160.hl
5'-most EST
                   30480
Seq. No.
                   215309 1.R1040
Contig ID
5'-most EST
                   zhf700954581.h1
                   30481
Seq. No.
                   215324 1.R1040
Contig ID
5'-most EST
                   kl1701213457.h1
Seq. No.
                   30482
                   215327 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy044c05b1
Method
                   BLASTX
NCBI GI
                   q4204315
BLAST score
                   234
E value
                   3.0e-19
Match length
                   195 .
% identity -
                   30
NCBI Description
                   (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   30483
Contig ID
                   215341 1.R1040
5'-most EST
                   zsq701\overline{1}17642.h1
                   30484
Seq. No.
Contig ID
                   215353 1.R1040
5'-most EST
                   jC-qmle01810016q02a1
Method
                   BLASTX
NCBI GI
                   q1175016
BLAST score
                   143
E value
                   1.0e-08
Match length
                   134
% identity
                   WHITE PROTEIN HOMOLOG >gi_1160186 emb_CAA62631_ (X91249)
NCBI Description
                   white [Homo sapiens]
Seq. No.
                   30485
Contig ID
                   215369 1.R1040
5'-most EST
                   zhf700954654.h1
Seq. No.
                   30486
                   215377 1.R1040
Contig ID
5'-most EST
                   g4313727
Method
                   BLASTX
NCBI GI
                   g3258570
BLAST score
                   172
E value
                   3.0e-12
Match length
                   45
% identity
NCBI Description
                   (U89959) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   30487
                   215396 1.R1040
Contig ID
```

jC-gmst02400029f12a1

NCBI Description

```
30488
Seq. No.
                   215433 1.R1040
Contig ID
                   zhf700954735.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4263722
                   289
BLAST score
E value
                   1.0e-43
Match length
                   101
% identity
                   88
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30489
                   215441 1.R1040
Contig ID
                   k11701\overline{2}12167.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2507229
BLAST score
                   329
E value
                   1.0e-30
Match length
                   93
                   69
% identity
NCBI Description
                   40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
                   PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
                   >gi_423247_pir__A46579 estrogen receptor-binding
                   cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
                   cyclophilin [Bos taurus]
                   30490
Seq. No.
                   215446 1.R1040
Contig ID
5'-most EST
                   fC-gmle7000743383r1
                   30491
Seq. No.
                   215485 1.R1040
Contig ID
5'-most EST
                   zhf700954794.hl
Seq. No.
                   30492
                   215492 1.R1040
Contig ID
                   jC-qmf102220097f08a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   a3982577
BLAST score
                   295
                   4.0e-32
E value
Match length
                   102
% identity
                   (AF023141) histidinol dehydrogenase [Thlaspi goesingense]
NCBI Description
Seq. No.
                   30493
Contig ID
                   215497_1.R1040
5'-most EST
                   uC-gmropic112d12b1
Method
                   BLASTX
                   q4508076
NCBI GI
BLAST score
                   190
                   2.0e-14
E value
Match length
                   96
% identity
```

(AC005882) 55659 [Arabidopsis thaliana]

5'-most EST

```
30494
Seq. No.
                   215509 1.R1040
.Contig ID
5'-most EST
                   zsg701120956.h1
                   30495
Seq. No.
                   215538_1.R1040
Contig ID
5'-most EST
                   zhf700954859.h1
Method
                   BLASTX
NCBI GI
                   q2499535
BLAST score
                   553
                   4.0e-57
E value
Match length
                   114
% identity
                   89
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >qi 595681
NCBI Description
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
Seq. No.
                   30496
                   215547 1.R1040
Contig ID
                   asn701137057.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3776581
BLAST score
                   144
E value
                   3.0e-09
Match length
                   35
% identity
                   71
NCBI Description
                   (AC005388) Similar to Beta integral membrane protein
                   homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   30497
                   215559 1.R1040
Contig ID
5'-most EST
                   leu701153154.h1
                   BLASTX
Method
NCBI GI
                   q1771162
BLAST score
                   365
E value
                   5.0e-35
Match length
                   109
                   66
% identity
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
                   30498
Seq. No.
Contig ID
                   215566 1.R1040
5'-most EST
                   epx701108914.hl
Method
                   BLASTX
NCBI GI
                   q2462826
BLAST score
                   602
E value
                   1.0e-62
Match length
                   182
% identity
NCBI Description
                   (AF000657) unknown protein [Arabidopsis thaliana]
                   30499
Seq. No.
                   215578 1.R1040
Contig ID
```

 $epx701\overline{1}09091.h1$

```
30500
Seq. No.
                   215622 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}54991.h1
Method
                   BLASTX
NCBI GI
                   g2160190
BLAST score
                   277
                   2.0e-48
E value
Match length
                   146
% identity
                   68
NCBI Description
                   (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   30501
                   215673 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220115b09d1
Method
                   BLASTX
                   g2760543
NCBI GI
                   399
BLAST score
E value
                   1.0e-38
Match length
                   83
% identity
                   89
NCBI Description
                   (Z97060) L-galactono-1,4-lactone dehydrogenase [Brassica
                   oleracea]
Seq. No.
                   30502
                   215679 1.R1040
Contig ID
5'-most EST
                   rlr700897214.h1
                   BLASTX
Method
NCBI GI
                   g4512698
BLAST score
                   347
                   6.0e-33
E value
Match length
                   104
% identity
                   66
NCBI Description
                   (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   30503
                   215828 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy035b01b1
Method
                   BLASTX
NCBI GI
                   g2829910
BLAST score
                   224
E value
                   8.0e-22
Match length
                   104
% identity
                   55
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   30504
Seq. No.
                   215834 1.R1040
Contig ID
                   gsv701\overline{0}48383.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1122324
BLAST score
                   235
E value
                   1.0e-129
Match length
                   367
                   91
% identity
NCBI Description P.sativum mRNA for SecA protein
```

```
30505
Seq. No.
                   215857 1.R1040
Contig ID
                   zhf700955308.hl
5'-most EST
                   30506
Seq. No.
Contig ID
                   215886 1.R1040
5'-most EST
                   jC-gmf102220071f04a1
Method
                   BLASTX
                                        : :
NCBI GI
                   g3426037
BLAST score
                   871
                   2.0e-99
E value
                   250
Match length
% identity
                   53
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   30507
Seq. No.
                   215897 1.R1040
Contig ID
                   zhf700955355.hl
5'-most EST
                   30508
Seq. No.
                   215952 1.R1040
Contig ID
                   zhf700964741.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129953
BLAST score
                   155
E value
                   1.0e-10
Match length
                   43
                   63
% identity
                   laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542)
NCBI Description
                   diphenol oxidase [Nicotiana tabacum]
                   30509
Seq. No.
                   215967 1.R1040
Contig ID
5'-most EST
                   q5508898
Method
                   BLASTX
NCBI GI
                   q2252827
BLAST score
                   299
E value
                   5.0e-40
Match length
                   99
% identity
                   (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30510
Contig ID
                   215980 1.R1040
5'-most EST
                   uC-gmropic0001g10b1
Seq. No.
                   30511
                   215994 1.R1040
Contig ID
5'-most EST
                   uC-gmropic059h04b1
Method
                   BLASTX
NCBI GI
                   q4544446
BLAST score
                   288
E value
                   9.0e-26
                   109
Match length
% identity
                   58
```

```
NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]
                   30512
Seq. No.
                   215997 1.R1040
Contig ID
5'-most EST
                   leu701145993.h1
Method
                   BLASTX
NCBI GI
                   g2342685
                   336
BLAST score
                   2.0e-31
E value
                   126
Match length
% identity
                   52
                   (AC000106) Contains similarity to Rhodococcus amidase
NCBI Description
                   (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   30513
                   215997 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220061a09a1
Method
                   BLASTX
NCBI GI
                   g2342685
BLAST score
                   231
E value
                   4.0e-19
                   147
Match length
                   37
% identity
                   (AC000106) Contains similarity to Rhodococcus amidase
NCBI Description
                   (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]
                   30514
Seq. No.
                   216033 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910072e02a1
Method
                   BLASTX
                   q3776559
NCBI GI
BLAST score
                   671
E value
                   1.0e-70
Match length
                   151
% identity
                   (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                   30515
Seq. No.
                   216037 1.R1040
Contig ID
                   zhf700955536.h1
5'-most EST
Seq. No.
                   30516
                   216060 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy017a05b1
                   30517
Seq. No.
                   216101 1.R1040
Contig ID
5'-most EST
                   uC-qmropic065c05b1
                   30518
Seq. No.
                   216111 1.R1040
Contig ID
```

zhf700955632.h1

5'-most EST

```
BLASTX
Method
NCBI GI
                   g3135254
BLAST score
                   704
                   3.0e-74
E value
Match length
                   278
% identity
                   50
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
                   30519
Seq. No.
                   216112 1.R1040
Contig ID
5'-most EST
                  pxt700944059.h1
Method
                   BLASTX
NCBI GI
                   q2760839
BLAST score
                   417
                   1.0e-40
E value
                   175
Match length
% identity
                   47
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30520
                   216131 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy112e02b1
                   BLASTX *
Method
NCBI GI
                  g2252843
BLAST score
                   482
                   1.0e-48
E value
                   147
Match length
                                                                       98 L -
                   62
% identity
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
                   30521
Seq. No.
                   216137 1.R1040
Contig ID
                   zhf700\overline{9}55669.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q1239962
BLAST score
                   38
                   4.0e-12
E value
                   62
Match length
                   90
% identity
NCBI Description A.majus mRNA for MADS-box protein (DEFH72)
                   30522
Seq. No.
                   216144 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}55668.h1
Seq. No.
                   30523
                   216209 1.R1040
Contig ID
                   zsq701119566.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3256848
BLAST score
                   175
                   8.0e-13
E value
                   100
Match length
                   40
% identity
                   (AP000002) 219aa long hypothetical protein [Pyrococcus
NCBI Description
```

horikoshii]

```
30524
Seq. No.
Contig ID
                   216211 1.R1040
5'-most EST
                   zhf700\overline{9}55970.h1
Seq. No.
                   30525
Contig ID
                   216228 1.R1040
                   crh700850117.h1
5'-most EST
                   30526
Seq. No.
                   216245 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}08209.h1
Method
                   BLASTX
NCBI GI
                   g3386604
BLAST score
                   264
E value
                   8.0e-23
Match length
                   147
% identity
                   36
NCBI Description
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
                   30527
Seq. No.
                   216279 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810089e12a1
                   30528 -
Seq. No.
                   216288 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}55848.h1
Method
                   BLASTX
NCBI GI
                   g2914703
BLAST score
                   355
E value
                   1.0e-33
Match length
                   142
                   52
% identity
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                   30529
                   216315 1.R1040
Contig ID
5'-most EST
                   zhf700955880.h1
Seq. No.
                   30530
                   216321 1.R1040
Contig ID
5'-most EST
                   zhf700955887.h1
Seq. No.
                   30531
                   216322 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810060h09a1
                   30532
Seq. No.
                   216441 1.R1040
Contig ID
                   zhf700\overline{9}56027.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4558556
BLAST score
                   390
E value
                   5.0e-38
Match length
                   110
% identity
                   66
                   (AC007138) predicted protein of unknown function
NCBI Description
```

[Arabidopsis thaliana]

```
30533
Seq. No.
                  216450 1.R1040
Contig ID
5'-most EST
                  zhf700956039.hl
Seq. No.
                  30534
                  216483 1.R1040
Contig ID
                  zhf700956079.h1
5'-most EST
                  30535
Seq. No.
                  216492 1.R1040
Contig ID
                  jC-qmf102220102c08a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4006913
BLAST score
                  450
                  1.0e-44
E value
Match length
                  127
                  72
% identity
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30536
                  216529 1.R1040
Contig ID
5'-most EST
                  zhf700956142.h1
Method
                  BLASTX
NCBI GI
                  g1708971
BLAST score
                  226
E value
                  8.0e-19
Match length
                  98
% identity
                  49
                  (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                  (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                  >gi 421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                  black cherry >gi 288116 emb CAA51194 (X72617)
                  mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                  (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                  serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
                  [Prunus serotina]
                  30537
Seq. No.
                  216530 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy024h03b1
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  414
E value
                  8.0e-41
Match length
                  106
% identity
                  66
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  30538
Seq. No.
                  216546 1.R1040
Contig ID
                  zhf700956164.h1
5'-most EST
                  30539
Seq. No.
                  216559 1.R1040
Contig ID
5'-most EST
                  zhf700956452.h1
                  BLASTX
Method
```

5'-most EST Method

```
NCBI GI
                  g431154
BLAST score
                  201
                   5.0e-16
E value
Match length
                   68
% identity
                  59
NCBI Description
                   (D21813) ORF [Lilium longiflorum]
Seq. No.
                  30540
                  216563 1.R1040
Contig ID
                  fua701038569.h1
5'-most EST
                  30541
Seq. No.
                  216632 1.R1040
Contig ID
                  zhf700958851.h1
5'-most EST
                  BLASTX
Method
                  g1408473
NCBI GI
BLAST score
                  224
E value
                  9.0e-19
Match length.
                  55
                  73
% identity
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                  thaliana]
                  30542
Seq. No.
                  216634 1.R1040
Contig ID
5'-most EST
                  k11701203845.hl
                  30543
Seq. No.
                  216679 1.R1040
Contig ID
5'-most EST
                  leu701146301.hl
Method
                  BLASTX
                  g3395585
NCBI GI
BLAST score
                  156
E value
                  1.0e-10
Match length
                  67
% identity
                   (AL031179) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  30544
Seq. No.
                  216690 1.R1040
Contig ID
5'-most EST
                  kl1701204502.h2
Method
                  BLASTX
NCBI GI
                  g2245077
BLAST score
                  327
E value
                   9.0e-31
Match length
                  92
% identity
                  72
NCBI Description
                   (297343) glucanase homolog [Arabidopsis thaliana]
Seq. No.
                  216777 1.R1040
Contig ID
                  zhf700956512.h1
5'-most EST
Seq. No.
                  30546
                  216780 1.R1040
Contig ID
```

jC-qmf102220144e02a1

BLASTX

Contig ID

```
NCBI GI
                   g4337196
BLAST score
                   595
                   1.0e-61
E value
Match length
                   171
                   71
% identity
                   (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
                   30547
Seq. No.
                   216783 1.R1040
Contig ID
5'-most EST
                   zhf700956558.h1
                   BLASTX
Method
NCBI GI
                   q2944178
BLAST score
                   147
                   3.0e-17
E value
Match length
                   82
% identity
NCBI Description
                   (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
                   thaliana]
Seq. No.
                   30548
                   216801 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810026d03a1
Method
                   BLASTX
NCBI GI
                   g4567095
BLAST score
                   691
E value
                   6.0e-73
Match length
                   160
% identity
                   80
NCBI Description
                   (AF129516) fertilization-independent endosperm protein
                   [Arabidopsis thaliana]
                   30549
Seq. No.
                   216810 1.R1040
Contig ID
5'-most EST
                   zhf700956567.h1
Method
                   BLASTX
NCBI GI
                   g3337352
BLAST score
                   156
                   2.0e-17
E value
Match length
                   86
% identity
                   57
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
                   30550
Seq. No.
Contig ID
                   216830 1.R1040
                   zhf700956605.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1209756
BLAST score
                   1039
E value
                   1.0e-113
Match length
                   279
% identity
                   72
                   (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
Seq. No.
                   30551
                   216888 1.R1040
```

```
5'-most EST
                   zhf700956689.h1
                   30552
Seq. No.
                   216910 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}07525.h1
                   30553
Seq. No.
                   216952 1.R1040
Contig ID
                   zhf700956793.hl
5'-most EST
                   30554
Seq. No.
                   216958 1.R1040
Contig ID
                   uC-qmflminsoy016d12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4336426
BLAST score
                   548
E value
                   2.0e-56
Match length
                   127
% identity
                   77
                   (AF090835) Ca2+-dependent protein kinase [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   30555
                   216970 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910037f12a1
                   30556
Seq. No.
                   216970 2.R1040
Contig ID
5'-most EST
                   q56061\overline{5}9
Seq. No.
                   30557
                   217019 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}56924.h1
                   30558
Seq. No.
Contig ID
                   217035 1.R1040
                   jC-gmle01810028e12d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2262116
BLAST score
                   196
                   4.0e-15
E value
Match length
                   117
                   37
% identity
NCBI Description
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
                   30559
Seq. No.
Contig ID
                   217045 1.R1040
5'-most EST
                   zhf700956981.h1
Seq. No.
                   30560
                   217052 1.R1040
Contig ID
5'-most EST
                   zhf700956992.h1
                   30561
Seq. No.
                   217082 1.R1040
Contig ID
5'-most EST
                   zhf700957045.h1
```

BLASTX

Method

Contig ID 5'-most EST

```
NCBI GI
                   g4415933
BLAST score
                   462
E value
                   3.0e-46
Match length
                   123
% identity
NCBI Description
                   (AC006418) putative cellular apoptosis susceptibility
                  protein [Arabidopsis thaliana]
                  >gi 4559390 gb AAD23050.1 AC006526 15 (AC006526) putative
                   cellular apoptosis susceptibility protein [Arabidopsis
                   thaliana]
                   30562
Seq. No.
                   217104 1.R1040
Contig ID
5'-most EST
                  zhf700957082.h1
                   30563
Seq. No.
Contig ID
                  217118 1.R1040
5'-most EST
                  uC-gmflminsoy055c12b1
Method
                  BLASTX
NCBI GI
                  g2494116
BLAST score
                   865
                   3.0e-93
E value
Match length
                  215
% identity
                   78
                   (AC002376) Similar to Synechocystis hypothetical protein
NCBI Description
                   (gb D90915). [Arabidopsis thaliana]
                   30564
Seq. No.
                  217126 1.R1040
Contig ID
5'-most EST
                   zhf700957121.h1
Method
                  BLASTX
NCBI GI
                  g2213624
BLAST score
                   481
E value
                   4.0e-48
                  252
Match length
% identity
                   44
                   (AC000103) F21J9.16 [Arabidopsis thaliana]
NCBI Description
                   30565
Seq. No.
                  217128 1.R1040
Contig ID
5'-most EST
                  gsv701055604.hl
                  30566
Seq. No.
                  217129 1.R1040
Contig ID
5'-most EST
                  zhf700958162.h1
Method
                  BLASTX
NCBI GI
                  g2245108
BLAST score
                  143
E value
                   4.0e-09
                  28
Match length
% identity
                  89
                  (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30567
```

217149 1.R1040

zhf700957171.h1

```
Seq. No.
                   30568
                   217170 1.R1040
Contig ID
5'-most EST
                   jC-gmr002800027c07a1
Method
                   BLASTX
NCBI GI
                   g4567197
BLAST score
                   225
E value
                   2.0e-18
Match length
                   91
                   56
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                   30569
Seq. No.
                   217188 1.R1040
Contiq ID
                   fua701040949.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3396079
BLAST score
                   198
E value
                   1.0e-15
Match length
                   83
                   47
% identity
NCBI Description
                   (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase
                   [Arabidopsis thaliana]
                  - 30570
Seq. No.
                   217189 1.R1040
Contig ID
5'-most EST
                   leu701151606.h1
Method
                   BLASTX
NCBI GI
                   q4006924
BLAST score
                   684
E value
                   3.0e-72
                   155
Match length
% identity
                   75
NCBI Description
                   (Z99708) beta-galactosidase like protein [Arabidopsis
                   thalianal
Seq. No.
                   30571
                   217191 1.R1040
Contig ID
5'-most EST
                   zsq701120810.hl
Seq. No.
                   217192 1.R1040
Contig ID
5'-most EST
                   uC-gmropic055a03b1
                   30573
Seq. No.
                   217240 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy047b05b1
Method
                   BLASTX
NCBI GI
                   g2213590
BLAST score
                   477
E value
                   9.0e-48
                  188
Match length
% identity
                   49
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
                   30574
Seq. No.
                   217284 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}56235.h1
```

Contig ID

```
Seq. No.
                   30575
                   217306 1.R1040
Contig ID
                   zhf700957456.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2911075
BLAST score
                   336
E value
                   1.0e-31
Match length
                   81
                   83
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   30576
Seq. No.
                   217348 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400026a08d1
                   30577
Seq. No.
                   217438 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy169h05b1
Method
                   BLASTX
                   g3378491
NCBI GI
BLAST score
                   159
E value
                   1.0e-10
Match length
                   48
% identity
                   (AJ007578) pRIB5 protein [Ribes nigrum]
NCBI Description
Seq. No.
                   217441 1.R1040
Contig ID
5'-most EST
                   uC-gmropic090c04b1
Seq. No.
                   217452 1.R1040
Contig ID
5'-most EST
                   uC-gmropic070c10b1
Method
                   BLASTX
NCBI GI
                   g3337361
BLAST score
                   661
E value
                   2.0e-69
Match length
                   179
% identity
NCBI Description
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                   30580
Seq. No.
                   217459 1.R1040
Contig ID
                   zhf700957744.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g544006
BLAST score
                   181
E value
                   1.0e-13
Match length
                   59
% identity
                   58
                  ACIDIC ENDOCHITINASE PRECURSOR >gi 322686_pir__ S31763
NCBI Description
                   chitinase (EC 3.2.1.14) - chickpea >gi_17942_emb_CAA49998_
                   (X70660) chitinase [Cicer arietinum]
                   30581
Seq. No.
```

217476_1.R1040

Contig ID 5'-most EST

```
5'-most EST
                   zhf700957764.h1
Method
                   BLASTX
NCBI GI
                   g4454035
BLAST score
                   278
E value
                   2.0e-24
Match length
                   94
% identity
NCBI Description
                   (AL035394) polyprenyltransferase like protein [Arabidopsis
                   thaliana]
                   30582
Seq. No.
                   217498 1.R1040
Contig ID
                   zhf700957796.h1
5'-most EST
                   30583
Seq. No.
                   217536 1.R1040
Contig ID
                   zhf700\overline{9}57857.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2623245
BLAST score
                   111
E value
                   1.0e-55
Match length
                   206
                   89
% identity
NCBI Description Pisum sativum poly(A) polymerase mRNA, nuclear gene
                   encoding chloroplast protein, complete cds
                   30584
Seq. No.
                   217545 1.R1040
Contig ID
                   uC-gmflminsoy083e05b1
5'-most EST
Method
                   BLASTX
                   g2623299
NCBI GI
BLAST score
                   89
E value
                   1.0e-09
Match length
                   80
% identity
NCBI Description
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   217571 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy054f09b1
Seq. No.
                   217579 1.R1040
Contig ID
                   zhf700957923.h1
5'-most EST
Seq. No.
                   30587
                   217591 1.R1040
Contig ID
                   zhf700957939.h1
5'-most EST
                   30588
Seq. No.
                   217607 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy059b01b1
Seq. No.
                   30589
                   217633 1.R1040
```

pxt700945371.h1

Seq. No.

30598

```
30590
 Seq. No.
                    217641 1.R1040
 Contig ID
                    zhf700958020.h1
 5'-most EST
                    BLASTX
Method
NCBI GI
                    g4539435
BLAST score
                    496
 E value
                    2.0e-50
                    103
Match length
 % identity
                    83
                    (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    217718 1.R1040
 Contig ID
 5'-most EST
                    uC-gmflminsoy063h05b1
 Seq. No.
                    217723 1.R1040
 Contig ID
 5'-most EST
                    zhf700958142.hl
                    30593
 Seq. No.
                    217726 1.R1040
 Contig ID
 5'-most EST
                    asn701142016.hl
                    30594 --- ---
- Seq. No. ---
                    217787 1.R1040
 Contig ID
 5'-most EST
                    uC-qmropic042d12b1
Seq. No.
                    30595
                    217791 1.R1040
 Contig ID
 5'-most EST
                    g4260307
 Method
                    BLASTX
NCBI GI
                    q4006864
BLAST score
                    241
E value
                    1.0e-20
Match length
                    101
 % identity
NCBI Description (299707) nucleoporin-like protein [Arabidopsis thaliana]
                    30596
Seq. No.
                    217865 1.R1040
 Contig ID
 5'-most EST
                    jC-gmf102220143h08a1
 Method
                    BLASTX
NCBI GI
                    g728868
BLAST score
                    223
E value
                    3.0e-18
Match length
                    75
 % identity
                    59
                    ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                    >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                    protein [Brassica napus]
                    30597
Seq. No.
                    217866 1.R1040
Contig ID
 5'-most EST
                    g4260349
```

```
217895 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220068c05d1
                  30599
Seq. No.
                  217957_1.R1040
Contig ID
5'-most EST
                  jC-gmro02910011g08a1
Seq. No.
                  30600
                  217969 1.R1040
Contig ID
5'-most EST
                  leu701151263.h1
                  30601
Seq. No.
                  217977 1.R1040
Contig ID
                  zsg701\overline{1}26152.h1
5'-most EST
                  30602
Seq. No.
                  217984 1.R1040
Contig ID
5'-most EST
                  zhf700958486.h1
                  30603
Seq. No.
                  218000 1.R1040
Contig ID
5'-most EST
                  pxt700945957.h1
Method
                  BLASTX
                  NCBI GI
BLAST score
                  638
E value
                  1.0e-66
                  180
Match length
% identity
                  60
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                  30604
Seq. No.
                  218014 1.R1040
Contig ID
                  zhf700961801.hl
5'-most EST
Seq. No.
                  30605
                  218021 1.R1040
Contig ID
                  zhf700958541.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4191789
BLAST score
                  218
E value
                  9.0e-18
Match length
                  83
% identity
                  (AC005917) putative transmembrane transport protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  30606
                  218022 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400068q07d1
Method
                  BLASTN
NCBI GI
                  q4519194
BLAST score
                  50
E value
                  5.0e-19
Match length
                  118
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MHM17, complete sequence

```
30607
Seq. No.
                    218067 1.R1040
Contig ID
                    fua701042740.hl
5'-most EST
                    30608
Seq. No.
                    218077 1.R1040
Contig ID
                    zhf700\overline{9}58626.h1
5'-most EST
                    30609
Seq. No.
                    218084 1.R1040
Contig ID
                    zhf700\overline{9}58634.h1
5'-most EST
                    30610
Seq. No.
                    218112 1.R1040
Contig ID
                    zhf700959017.hl
5'-most EST
Seq. No.
                    30611
                    218118 1.R1040
Contig ID
5'-most EST
                    zhf700958705.hl
Seq. No.
                    30612
                    218163 1.R1040
Contig ID
5'-most EST
                    jC-gmf102220114g03d1
                    30613
Seq. No.
                    218232 1.R1040
Contig ID
                    zhf700\overline{9}58874.h1
5'-most EST
Seq. No.
                    30614
                    218272 1.R1040
Contig ID
                    zhf700958932.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g4371293
BLAST score
                    162
E value
                    4.0e-11
Match length
                    132
% identity
                    34
NCBI Description
                    (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    30615
                    218304 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}55031.h1
                    30616
Seq. No.
                    218350 1.R1040
Contig ID
5'-most EST
                    zhf700959050.h1
                    30617
Seq. No.
                    218384 1.R1040
Contig ID
5'-most EST
                    asn701138736.hl
Seq. No.
                    30618
                    218391 1.R1040
Contig ID
                    k11701\overline{2}08301.h1
5'-most EST
Method
                   BLASTX
```

g4098647

NCBI GI

Method

BLASTX

```
467
BLAST score
                   3.0e-47
E value
                   90
Match length
                   92
% identity
                   (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30619
                   218446 1.R1040
Contig ID
                   k11701\overline{2}08553.h1
5'-most EST
                   BLASTX
Method
                   q3176714
NCBI GI
BLAST score
                   389
E value
                   7.0e-46
                   121
Match length
                   74
% identity
                   (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                   effector [Arabidopsis thaliana]
Seq. No.
                 ....30620
                   218459 1.R1040
Contig ID
5'-most EST
                   kl1701207149.hl
Method
                   BLASTX
NCBI GI
                   g2245378
BLAST score
                   407
E value
                   1.0e-39
                   204
Match length
% identity
                   50
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30621
                   218467 1.R1040
Contig ID
                   zhf700959231.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2894567
BLAST score
                   370
E value
                   2.0e-35
Match length
                   150
% identity
                   50
                   (AL021890) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   218497 1.R1040
Contig ID
                   kl1701204387.h2
5'-most EST
Seq. No.
                   218504 1.R1040
Contig ID
                   zhf700959281.h1
5'-most EST
Seq. No.
                   30624
                   218524 1.R1040
Contig ID
                   zhf700959307.hl
5'-most EST
Seq. No.
                   30625
                   218549 1.R1040
Contig ID
                   zhf700959333.hl
5'-most EST
```

5'-most EST

```
NCBI GI
                  g4454467
BLAST score
                  240 .
E value
                  1.0e-20
Match length
                  87
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  30626
Seq. No.
                  218558_1.R1040
Contig ID
                  epx701109743.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4128133
                  254
BLAST score
                  6.0e-22
E value
                  87
Match length
% identity
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                  30627
Seq. No.
                  218583 1.R1040
Contig ID
5'-most EST
                  pxt700946231.hl
Method
                  BLASTX
NCBI GI
                  q4455338
BLAST score
                  289
E value
                  6.0e-26
Match length
                  144
                  47
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                  30628
Seq. No.
                  218591 1.R1040
Contig ID
5'-most EST
                  g5175438
Method
                  BLASTX
NCBI GI
                  g1665817
BLAST score
                  152
E value
                  1.0e-09
Match length
                  108
% identity
                  35
                  (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                   (S59316) [Homo sapiens]
                  30629
Seq. No.
                  218682 1.R1040
Contig ID
5'-most EST
                  zhf700959510.h1
Seq. No.
                  30630
                  218694 1.R1040
Contig ID
5'-most EST
                  zhf700959525.h1
                  30631
Seq. No.
                  218789 1.R1040
Contig ID
                  zhf700959683.h1
5'-most EST
                  30632
Seq. No.
                  218809 1.R1040
Contig ID
```

zhf700959715.h1

Contig ID

```
Seq. No.
                   30633
Contig ID
                   218864 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220065d12d1
Seq. No.
                   30634
Contig ID
                   218891 1.R1040
5'-most EST
                   epx701106945.hl
Seq. No.
                   30635
                   218931 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy007e06b1
Seq. No.
                   30636
                   218945 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy241g07b1
Method
                   BLASTX
NCBI GI
                   g2072986
BLAST score
                   684
                   5.0e-72
E value
Match length
                   182
% identity
                   73
NCBI Description
                   (U95142) putative G-protein-coupled receptor [Arabidopsis
                   thaliana] >gi 2072988 (U95143) putative G-protein-coupled
                   receptor [Arabidopsis thaliana]
                   30637
Seq. No.
                   219009 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810071a01a1
Method
                   BLASTX
NCBI GI
                   q100226
BLAST score
                   229
E value
                   7.0e-19
Match length
                   103
% identity
                   38
NCBI Description
                   hypothetical protein - tomato >gi 19275 emb CAA78112
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                   30638
                   219031 1.R1040
Contig ID
5'-most EST
                   g4396000
Method
                   BLASTX
NCBI GI
                   g1707016
BLAST score
                   157
E value
                   2.0e-10
Match length
                   47
% identity
                   (U78721) cadmium-induced protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   30639
Seq. No.
                   219034 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014e01a1
Seq. No.
                   30640
```

219048_1.R1040

```
5'-most EST
                  jC-gmst02400032d01a1
                  BLASTX
Method
                  g4056421
NCBI GI
BLAST score
                  834
                  1.0e-89
E value
Match length
                  183
% identity
                  81
                  (AC005322) Similar to gb Z30094 basic transcripion factor
NCBI Description
                  2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes
                  from this gene. [Arabidopsis thaliana]
                  30641
Seq. No.
                  219064 1.R1040
Contig ID
                  uC-gmrominsoy224g05b1
5'-most EST
                  BLASTX
Method
                  g4559384
NCBI GI
BLAST score
                  146
                  5.0e-09
E value
Match length
                  112
% identity
                  32
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                  30642
Seq. No.
                  219139 1.R1040 ----
Contig ID
                  jC-qmf102220103e11a1
5'-most EST
                  30643
Seq. No.
                  219147 1.R1040
Contig ID
                  uC-gmflminsoy008d02b1
5'-most EST
                  30644
Seq. No.
                  219153 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810010d12a1
Method
                  BLASTX
                  g4006867
NCBI GI
BLAST score
                  168
E value
                  1.0e-11
Match length
                  72
                  43
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                  30645
Seq. No.
                  219168 1.R1040
Contig ID
5'-most EST
                  g55092\overline{2}2
                  30646
Seq. No.
                  219233 1.R1040
Contig ID
                  zhf700960282.h1
5'-most EST
                  30647
Seq. No.
                  219249 1.R1040
Contig ID
5'-most EST
                  rlr700898788.hl
                  30648
Seq. No.
                  219259 1.R1040
Contig ID
```

leu701147216.hl

5'-most EST

Contig ID

```
30649
Seq. No.
                   219277 1.R1040
Contig ID
                   zhf700\overline{9}60342.h1
5'-most EST
                   30650
Seq. No.
                   219284 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400025a03a1
Method
                   BLASTX
NCBI GI
                   g2832241
BLAST score
                   505
                   3.0e-51
E value
Match length
                   145
                   50
% identity
                   (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
NCBI Description
                   thaliana]
                   30651
Seq. No.
                   219302 1.R1040
Contig ID
5'-most EST
                   zhf700960376.h1
                   30652
Seq. No.
                   219326 1.R1040
Contig ID
                   leu701155385.h1
5'-most EST
Seq. No.
                   30653
                   219332 1.R1040
Contig ID
                   asn701134881.h2
5'-most EST
Seq. No.
                   30654
                   219338 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810047e03a1
Method
                   BLASTX
NCBI GI
                   g2113914
BLAST score
                   149
E value
                   1.0e-09
Match length
                   81
% identity
                   21
                   (Z95554) rpsA [Mycobacterium tuberculosis]
NCBI Description
Seq. No.
                   30655
                   219413 1.R1040
Contig ID
5'-most EST
                   zhf700960602.h1
Method
                   BLASTX
NCBI GI
                   g2661676
BLAST score
                   161
E value
                   8.0e-11
Match length
                   100
% identity
                   (AL009199) hypothetical ATP/GTP binding protein
NCBI Description
                   [Streptomyces coelicolor]
Seq. No.
                   219413 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220114e02d1
Seq. No.
```

219483_1.R1040

5'-most EST

```
5'-most EST
                  zhf700960719.h1
Method
                  BLASTX
NCBI GI
                  q3608127
BLAST score
                  319
E value
                  3.0e-29
Match length
                  66
% identity
NCBI Description
                  (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  219487 1.R1040
5'-most EST
                  hrw701058931.hl
                  30659
Seq. No.
                  219489 1.R1040
Contig ID
5'-most EST
                  zhf700960845.hl
Method
                  BLASTX
NCBI GI
                  q3367537
BLAST score
                  172
                  9.0e-19
E value
Match length
                  63
% identity
NCBI Description
                  (ACO04392) Contains similarity to ANK repeat region of
                  Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi 485107
                  from Caenorhabditis elegans cosmid gb U00049. This gene is
                  continued from unannotated gene on BAC F19K23 gb_AC000375.
                  [Arabid
                  30660
Seq. No.
                  219632 1.R1040
Contig ID
                  zhf700960978.h1
5'-most EST
                  30661
Seq. No.
                  219675 1.R1040
Contig ID
5'-most EST
                  asn701136803.hl
                  30662
Seq. No.
Contig ID
                  219695 1.R1040
5'-most EST
                  zhf700\overline{9}61072.h1
                  BLASTX
Method
NCBI GI
                  g3142303
BLAST score
                  299
                  4.0e-27
E value
Match length
                  114
% identity
                  61
NCBI Description
                  (AC002411) Strong similarity to MRP-like ABC transporter
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb_L49379 from Rattus norvegicus.
                  [Arabidopsis thaliana]
                  30663
Seq. No.
                  219726 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220064b01d1
Seq. No.
                  30664
Contig ID
                  219730 1.R1040
```

 $jC-gmf\overline{1}02220112c05d1$

```
Method
                  BLASTX
NCBI GI
                  q2315983
BLAST score
                  180
                  5.0e-13
E value
Match length
                  148
% identity
                  35
                  (U82087) calmodulin-like domain protein kinase [Tortula
NCBI Description
                  30665
Seq. No.
Contig ID
                  219741 1.R1040
5'-most EST
                  zhf700964314.h1
                  30666
Seq. No.
                  219785 1.R1040
Contig ID
5'-most EST
                  jC-qmf\(\overline{1}\)02220113e03a1
Method
                  BLASTX
NCBI GI
                  q2244996
BLAST score
                  439
E value
                  1.0e-43
Match length
                  117
                  31
% identity
NCBI Description (Z97341) similarity to a membrane-associated salt-inducible
               protein [Arabidopsis thaliana]
Seq. No.
                  30667
                  219792 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy306d05b1
                  30668
Seq. No.
                  219800_1.R1040
Contig ID
                  zsg701129832.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g100226
BLAST score
                  355
                  5.0e-34
E value
Match length
                  97
                  71
% identity
NCBI Description
                  hypothetical protein - tomato >gi 19275 emb CAA78112_
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf_ 1909366A Leu zipper protein
                  [Lycopersicon esculentum]
                  30669
Seq. No.
Contig ID
                  219825 1.R1040
5'-most EST
                  jC-gmst02400043c08d1
                  30670
Seq. No.
                  219868 1.R1040
Contig ID
5'-most EST
                  g5058245
Method
                  BLASTX
                  g3786004
NCBI GI
BLAST score
                  267
                  1.0e-27
E value
Match length
                  92
% identity
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
```

E value

7.0e-24

```
Seq. No.
                   30671 .
Contig ID
                   219916 2.R1040
5'-most EST
                   leu701\overline{1}53836.h1
Method
                   BLASTX
NCBI GI
                   q2905893
BLAST score
                   183
E value
                   6.0e-14
Match length
                   58
% identity
NCBI Description
                  (U66424) fimbrin-like protein [Arabidopsis thaliana]
                   30672
Seq. No.
Contig ID
                   219934 1.R1040
5'-most EST
                   uC-gmflminsoy100c12b1
Method
                   BLASTX
                   g4006913
NCBI GI
BLAST score
                   388
E value
                   1.0e-37
Match length
                   100
% identity
                   80
NCBI Description
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
                   Seq. No.
                   219936 1.R1040
Contig ID
                   k11701215367.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2656028
BLAST score
                   47
E value
                   3.0e-17
Match length
                   107
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNF13
                   30674
Seq. No.
                   219939 1.R1040
Contig ID
5'-most EST
                   zhf700961477.h1
Method
                   BLASTX
NCBI GI
                   g3935187
BLAST score
                   515
                   2.0e-52
E value
Match length
                  138
% identity
NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]
                   30675
Seq. No.
                   219982 1.R1040
Contig ID
5'-most EST
                  zhf700961553.h1
Seq. No.
                   30676
                  220022 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400070a11a1
                  BLASTX
Method
NCBI GI
                  g1749686
BLAST score
                  274
```

E value

1.0e-34

```
Match length
                   180
% identity
                   36
                   (D89239) similar to Saccharomyces cerevisiae unknown, EMBL
NCBI Description
                   Accession Number Z68194 [Schizosaccharomyces pombe]
Seq. No.
Contig ID
                   220038 1.R1040
5'-most EST
                   pmv700890656.hl
                   30678
Seq. No.
                   220070 1.R1040
Contig ID
5'-most EST
                   leu701144949.hl
                   BLASTX
Method
NCBI GI
                   g1778145
BLAST score
                   415
E value
                   8.0e-41
                   123
Match length
% identity
                   67
                   (U66402) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor [Nicotiana tabacum]
                   30679
Seq. No.
                   220205 1.R1040
Contig ID
5'-most-EST-
                   zhf700965015.h1
Method
                   BLASTX
NCBI GI
                   q4263822
BLAST score
                   167
E value
                   9.0e-12
Match length
                   84
% identity
NCBI Description
                   (AC006067) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   30680
Seq. No.
                   220246 2.R1040
Contig ID
5'-most EST
                   asn701134689.h2
Seq. No.
                   30681
                   220248 1.R1040
Contig ID
                   zhf700961933.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501011
BLAST score
                   445
E value
                   3.0e-44
Match length
                   147
% identity
                   57
                   ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
NCBI Description
                   >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA
synthetase [Synechocystis sp.]
Seq. No.
                   30682
                   220254 1.R1040
Contig ID
5'-most EST
                   zhf700961942.hl
Method
                   BLASTX
NCBI GI
                   g2266985
BLAST score
                   220
```

5'-most EST

```
Match length
                   94
                   82
% identity
                   (Y13943) METRS [Arabidopsis thaliana]
NCBI Description
                   30683
Seq. No.
Contig ID
                   220310 1.R1040
5'-most EST
                   uC-gmflminsoy031c01b1
Method
                   BLASTX
NCBI GI
                   g4415942
BLAST score
                   364
                   9.0e-35
E value
Match length
                   134
% identity
                   54
NCBI Description
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
                   30684
Seq. No.
                   220319 1.R1040
Contig ID
                   fua701039125.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832629
BLAST score
                   497
E value
                   5.0e-50
                   174
Match length
                   53--
% identity -
                   (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                   thaliana]
                   30685
Seq. No.
                   220344 2.R1040
Contig ID
5'-most EST
                   pxt700945686.h1
                   30686
Seq. No.
                   220353 1.R1040
Contig ID
                   zhf700\overline{9}62060.h1
5'-most EST
Seq. No.
                   30687
                   220379 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}01245.h1
                   30688
Seq. No.
                   220424 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400013a01a1
Method
                   BLASTX
NCBI GI
                   g4220534
BLAST score
                   404
E value
                   2.0e-39
Match length
                   125
% identity
                   67
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   30689
Seq. No.
                   220427 1.R1040
Contig ID
                   zhf700\overline{9}62154.h1
5'-most EST
                   30690
Seq. No.
                   220432 1.R1040
Contig ID
```

jC-gmro02910039g11d1

```
30691
Seq. No.
Contig ID
                   220438 1.R1040
                  zhf700962171.h1
5'-most EST
Seq. No.
                  30692
                  220448_1.R1040
Contig ID
                  zhf700\overline{9}62183.h1
5'-most EST
                  30693
Seq. No.
                  220454 1.R1040
Contig ID
                  zhf700962463.h1
5'-most EST
                  30694
Seq. No.
                  220489 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810094f02a1
Method
                  BLASTX
NCBI GI
                  g2497542
BLAST score
                  393
E value
                  9.0e-53
Match length
                  164
% identity
                   67
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                  ->gi_629696_pir__S44287_pyruvate kinase, plastid - common
                  tobacco >qi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  30695
                  220501 1.R1040
Contig ID
5'-most EST
                  pmv700891893.hl
                  30696
Seq. No.
                  220508 1.R1040
Contig ID
                  zhf700962260.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g126306
BLAST score
                  352
E value
                  3.0e-33
Match length
                  179
% identity
NCBI Description
                  TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, GASTRIC)
                  >gi_106904_pir__S07145 triacylglycerol lipase (EC 3.1.1.3)
                  precursor, gastric - human >gi_758063_emb_CAA29413_
                   (X05997) gastric lipase precursor [Homo sapiens]
Seq. No.
                  30697
                  220535 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy119e02b1
Method
                  BLASTX
NCBI GI
                  q3096930
BLAST score
                  353
E value
                  3.0e-33
Match length
                  88
% identity
NCBI Description
                   (AL023094) Homeodomain - like protein [Arabidopsis
```

thaliana]

.

NCBI GI

```
Seq. No.
                   30698
Contig ID
                   220551 1.R1040
5'-most EST
                   zhf700962319.hl
Method
                   BLASTX
NCBI GI
                   g2642448
BLAST score
                   204
E value
                   4.0e-16
Match length
                   114
% identity
NCBI Description
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
                   >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   30699
Seq. No.
                   220610 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}49810.h1
Method
                   BLASTX
NCBI GI
                   g3549652
BLAST score
                   477
                   3.0e-48
E value
Match length
                   104
                   88
% identity
NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis
                   thaliana]
                   30700
Seq. No.
                   220629 1.R1040
Contig ID
5'-most EST
                   lus701015830.hl
                   30701
Seq. No.
Contig ID
                   220642 1.R1040
5'-most EST
                   uC-gmropic032e05b1
                   30702
Seq. No.
                   220667 1.R1040
Contig ID
                   zhf700\overline{9}62475.h1
5'-most EST
                   30703
Seq. No.
                   220721 1.R1040
Contiq ID
                   zhf700962540.h1
5'-most EST
Method
                   BLASTX
                   g2655098
NCBI GI
BLAST score
                   263
E value
                   5.0e-23
Match length
                   98
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
                   30704
Seq. No.
                   220723 1.R1040
Contig ID
5'-most EST
                   fua701038983.hl
                   30705
Seq. No.
                   220747 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}62571.h1
Method
                   BLASTX
```

g861299

```
BLAST score
                   248
                   2.0e-21
E value
                  107
Match length
                   47
% identity
NCBI Description
                   (U28742) highly similar to alpha-adaptin (rat and mouse)
                   [Caenorhabditis elegans]
                   30706
Seq. No.
                   220765 1.R1040
Contig ID
                  dpv701096980.hl
5'-most EST
Seq. No.
                  30707
                  220766 1.R1040
Contig ID
                  epx701\overline{1}10249.h1
5'-most EST
                  30708
Seq. No.
Contig ID
                  220819 1.R1040
5'-most EST
                  jC-gmst02400015h12a1
                  30709 - 1
Seq. No.
                  220859 1.R1040
Contig ID
5'-most EST
                  gsv701045933.hl
Seq. No.
                  30710
                  220860 1.R1040
Contig ID
5'-most EST
                  zhf700962718.h1
                  30711
Seq. No.
                  220918 1.R1040
Contig ID
5'-most EST
                  zhf700962796.h1
                  30712
Seq. No.
                  220919 1.R1040
Contig ID
5'-most EST
                  zhf700962801.h1
Method
                  BLASTX
NCBI GI
                  q3135274
BLAST score
                  169
                  3.0e-12
E value
Match length
                   48
% identity
                   (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  30713
Seq. No.
Contig ID
                  220930 1.R1040
                  asn701138573.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1881268
BLAST score
                  190
                  2.0e-14
E value
Match length
                  104
                  40
% identity
                   (AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG.
NCBI Description
                   [Bacillus subtilis] >gi_2632758_emb_CAB12265 (Z99106)
                  similar to ATP-dependent RNA helicase [Bacillus subtilis]
```

30714

Seq. No.

BLAST score

33

```
220955 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir007g06b1
Seq. No.
                  30715
Contig ID
                  220981 1.R1040
5'-most EST
                  g5058284
Method
                  BLASTX
NCBI GI
                  g1709347
BLAST score
                  198
E value
                  2.0e-28
Match length
                  135
% identity
                  47
                  SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE
NCBI Description
                  KINASE 2) >gi 348245 (L20321) protein serine/threonine
                  kinase [Homo sapiens] >gi_4507277_ref_NP_003148.1_pSTK2_
                  serine/threonine kinase
                  30716
Seq. No.
                  221054 1.R1040
Contig ID
5'-most EST
                  leu701149692.hl
Method
                  BLASTX
                  g3335359
NCBI GI
BLAST score
                  213
                  6.0e-17
E value
                  97
Match length
                  43
% identity
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  30717
                  221056 1.R1040
Contig ID
                  zhf700962968.h1
5'-most EST
Seq. No.
                  30718
                  221077 1.R1040
Contig ID
                  zhf700962990.h1
5'-most EST
                  30719
Seq. No.
                  221083 1.R1040
Contig ID
5'-most EST
                  fjg700968335.h1
                  30720
Seq. No.
                  221133 1.R1040
Contig ID
                  zhf700963053.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4099835
BLAST score
                  212
E value
                  6.0e-20
Match length
                  72
% identity
                  (U90266) bifunctional nuclease [Zinnia elegans]
NCBI Description
Seq. No.
                  30721
                  221199 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy088d07b1
Method
                  BLASTN
NCBI GI
                  g3873174
```

Seq. No.

30726

```
E value
                   7.0e-09
Match length
                   129
% identity
                   81
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   30722
                   221220 1.R1040
Contig ID
                   zhf700964947.h1
5'-most EST
Method •
                   BLASTX
NCBI GI
                   g1086249
BLAST score
                   338
                   4.0e-32
E value
                   90
Match length
                   70
% identity
NCBI Description
                   subtilisin-like protease - Alnus glutinosa
                   >gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease
                   [Alnus glutinosa]
Seq. No.
                   30723
                   221222 1.R1040
Contig ID
                   zhf700\overline{9}63158.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539460
BLAST score
                   166
E value
                   1.0e-11
                   108
Match length
% identity
NCBI Description
                   (AL049500) putative protein [Arabidopsis thaliana]
                   30724
Seq. No.
                   221242_1.R1040
Contig ID
5'-most EST
                   zhf700963180.hl
Method
                   BLASTX
NCBI GI
                   q1711512
BLAST score
                   311
E value
                   1.0e-28
                   59
Match length
                   95
% identity
                   SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
NCBI Description
                   >gi_1076577_pir__S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288__
                   (Z34527) 54-kD signal recognition particle (SRP) specific
                   protein [Lycopersicon esculentum]
Seq. No.
                   30725
                   221353 1.R1040
Contig ID
5'-most EST
                   pxt700941791.h1
Method
                   BLASTX
NCBI GI
                   g1707019
BLAST score
                   216
E value
                   1.0e-17
Match length
                   114
% identity
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
```

5'-most EST

```
221360 1.R1040
   Contig ID
   5'-most EST
                     zhf700\overline{9}63625.h1
                     30727
   Seq. No.
   Contig ID
                     221367 1.R1040
   5'-most EST
                     zhf700963334.h1
                     30728
   Seq. No.
                     221370 1.R1040
   Contig ID
                     jC-qmle01810093h12d1
   5'-most EST
   Method
                     BLASTX
   NCBI GI
                     g1841468
   BLAST score
                     339
                     8.0e-32
   E value
  Match length
                     87
   % identity
   NCBI Description
                      (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
                     30729
   Seq. No.
                     221434 1.R1040
   Contig ID
                     zhf700963418.h1
   5'-most EST
                     30730
   Seq. No.
                  - 221469 1.R1040 -- --
  Contig ID
                     zhf700963457.h1
   5'-most EST
                     BLASTX
   Method
                     g1778015
   NCBI GI
   BLAST score
                     554
   E value
                      9.0e-57
   Match length
                     217
                      53
   % identity
                      (U59508) osmotic stress-induced proline dehydrogenase
   NCBI Description
                      [Arabidopsis thaliana]
   Seq. No.
                     30731
                     221472 1.R1040
   Contig ID
5'-most EST
                     'uC-gmflminsoy028b06b1
                     30732
   Seq. No.
                     221487 1.R1040
   Contig ID
   5'-most EST
                     uC-gmropic073g07b1
   Seq. No.
                     30733
                     221501 1.R1040
   Contig ID
   5'-most EST
                     zhf700963596.h1
   Method
                     BLASTX
                     g2213884
   NCBI GI
   BLAST score
                     259
                     2.0e-22
   E value
   Match length
                     91
                     57
   % identity
                      (AF004166) 2-isopropylmalate synthase [Lycopersicon
   NCBI Description
                     pennellii]
                     30734
   Seq. No.
                     221566 1.R1040
   Contig ID
```

zhf700963591.h1

E value

9.0e-12

```
30735
Seq. No.
                   221576 1.R1040
Contig ID
                   g56066<del>6</del>6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3004564
BLAST score
                   193
                   1.0e-14
E value
Match length
                   79
                   52
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   30736
Seq. No.
                   221590 1.R1040
Contig ID
5'-most EST
                   epx701106304.hl
                   BLASTX
Method
NCBI GI
                   g3269289
BLAST score
                   152
E value
                   4.0e-10
Match length
                   50
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30737
                   221624 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220084f12a1
                   BLASTX
Method
NCBI GI
                   g2842496
BLAST score
                   147
                   2.0e-09
E value
Match length
                   32
% identity
                   (ALO21749) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30738
                   221631 1.R1040
Contig ID
                   zhf700964218.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2979544
BLAST score
                   238
                   7.0e-20
E value
                   96
Match length
                   47
% identity
                   (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30739
                   221687 1.R1040
Contig ID
5'-most EST
                   zhf700963743.h1
                   30740
Seq. No.
                   221730 1.R1040
Contig ID
                   zhf700963803.h1
5'-most EST
Method
                   BLASTX
                   g4220461
NCBI GI
BLAST score
                   169
```

```
Match length
                  114
                  37
% identity
                  (AC006216) ESTs gb T75642 and gb AA650997 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
Seq. No.
                  30741
                  221741 1.R1040
Contig ID
5'-most EST
                  leu701156407.h1
Seq. No.
                  30742
Contig ID
                  221754 1.R1040
                  uC-gmrominsoy061f11b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g556421
BLAST score
                  53
E value
                  6.0e-21
Match length
                  113
                  87
% identity
NCBI Description
                  Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
                  mRNA, complete cds
                  30743
Seq. No.
                  221773 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810084d05a1
Method
                  BLASTX
NCBI GI
                  q4249412
BLAST score
                  582
E value
                  3.0e-60
                  146
Match length
                  76
% identity
NCBI Description (AC006072) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30744
Contig ID
                  221801 1.R1040
                  zhf700963882.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2252836
BLAST score
                  355
E value
                  5.0e-34
Match length
                  95
                  77
% identity
NCBI Description
                  (AF013293) contains weak similarity to S. cerevisiae BOB1
                  protein (PIR:S45444) [Arabidopsis thaliana]
Seq. No.
                  30745
                  221828 1.R1040
Contig ID
5'-most EST
                  zhf700963921.h1
Method
                  BLASTX
NCBI GI
                  q4206209
BLAST score
                  320
E value
                  5.0e-30
Match length
                  74
% identity
                  (AF071527) putative glucan synthase component [Arabidopsis
NCBI Description
                  thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative
```

glucan synthase component [Arabidopsis thaliana]

E value

8.0e-26

```
30746
Seq. No.
Contig ID
                  221845 1.R1040
5'-most EST
                  uC-gmropic099h12b1
                  BLASTX
Method
NCBI GI
                  q2285885
BLAST score
                  516
                  1.0e-52
E value
Match length
                  118
% identity
                  84
NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]
Seq. No.
                  30747
Contig ID
                  221845 2.R1040
                  jsh701\overline{0}63802.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2285885
BLAST score
                  407
                   4.0e-40
E value
Match length
                  97
                  79
% identity
NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]
                  30748
Seq. No.
Contig ID ----
               ---221873 1.R1040 ---
                  uC-gmflminsoy077h05b1
5'-most EST
                  30749
Seq. No.
Contig ID
                  221884 1.R1040
5'-most EST
                  dpv701102641.h1
                  30750
Seq. No.
                  221915 1.R1040
Contig ID
                  zhf700964031.h1
5'-most EST
Seq. No.
                  30751
                  221943 1.R1040
Contig ID
                  zhf700\overline{9}64063.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2252840
BLAST score
                  456
                  3.0e-45
E value
                  202
Match length
                  44
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
                  30752
Seq. No.
                  221950 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy077g11b1
                  30753
Seq. No.
                  222002 1.R1040
Contig ID
                  fua701043085.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3250679
BLAST score
                  282
```

Contig ID

```
Match length
                   86
% identity
                    64
                    (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30754
Contig ID
                    222071 1.R1040
5'-most EST
                   uC-gmronoir030d08b1
                   30755
Seq. No.
                   222081 1.R1040
Contig ID
5'-most EST
                   zhf700964239.h1
                   30756
Seq. No.
                   222132 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220108d01d1
Seq. No.
                   30757
Contig ID
                   222148 1.R1040
                   zhf700964326.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2108252
BLAST score
                   343
E value
                   2.0e-32
                   123 - -
Match length "
% identity
                    (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_
                    (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   30758
Seq. No.
                   222167 1.R1040
Contig ID
5'-most EST
                   fua701040929.hl
                   30759
Seq. No.
                   222211 1.R1040
Contig ID
5'-most EST
                   zhf700964402.h1
Seq. No.
                   30760
                   222220 1.R1040
Contig ID
5'-most EST
                   zsg701127981.hl
Method
                   BLASTX
NCBI GI
                   g629602
BLAST score
                    476
E value
                   5.0e-92
                   302
Match length
                   58
% identity
                   probable imbibition protein - wild cabbage
NCBI Description
                   >gi 488787 emb CAA55893 (X79330) putative imbibition
                   protein [Brassica oleracea]
                   30761
Seq. No.
                   222252 1.R1040
Contig ID
5'-most EST
                   zhf700964451.h1
Seq. No.
                   30762
```

222263 1.R1040

```
5'-most EST
                   zhf700964464.hl
                   30763
Seq. No.
                   222273 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}23360.h1
Seq. No.
                   30764
                   222292 1.R1040
Contig ID
                   zhf700964501.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3540181
BLAST score
                   561
E value
                   7.0e-76
Match length
                   203
                   70
% identity
NCBI Description
                   (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   30765
                   222300 1.R1040
Contig ID
5'-most EST
                   uC-gmropic104h05b1
Method
                   BLASTN
NCBI GI
                   g2330650
BLAST score
                   141
E value ---
                   2.0e-73
                   377
Match length
                   84
% identity
NCBI Description Pisum sativum mRNA for topoisomerase II
Seq. No.
                   30766
                   222338 1.R1040
Contig ID
5'-most EST
                   zhf700964559.hl
                   BLASTN
Method
NCBI GI
                   g3786500
BLAST score
                   33
-E value
                   4.0e-09
                   59
Match length
                   3
% identity
NCBI Description
                   Caenorhabditis elegans cosmid T06A4
Seq. No.
                   30767
                   222412 1.R1040
Contig ID
5'-most EST
                   zhf700964650.h1
Method
                   BLASTX
NCBI GI
                   g2642448
BLAST score
                   161
E value
                   6.0e-11
Match length
                   131
% identity
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   30768
Seq. No.
                   222417 1.R1040
Contig ID
5'-most EST
                   zhf700964656.h1
```

BLAST score

```
222493 1.R1040
Contig ID
                   asj700967309.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g728868
                   197
BLAST score
                   2.0e-15
E value
Match length
                   52
                   69
% identity
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                   >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                   protein [Brassica napus]
                   30770
Seq. No.
                   222514 1.R1040
Contig ID
                   zhf700964776.hl
5'-most EST
Method
                   BLASTX
                   g2921340
NCBI GI
BLAST score
                   668
                   7.0e-70
E value
                   201
Match length
% identity
                   66
                   (AF034134) MYB-like DNA-binding domain protein [Gossypium
NCBI Description
                   hirsutum]
                   30771
Seq. No.
                   222527 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}56718.h1
Seq. No.
                   30772
                   222546 1.R1040
Contig ID
                   zhf700\overline{9}64815.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3811347
BLAST score
                   163
E value
                   1.0e-11
Match length
                   62
% identity
                   47
                   (AF065215) cytosolic phospholipase A2 beta [Homo sapiens]
NCBI Description
Seq. No.
                   30773
                   222548 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810082b01a1
Method
                   BLASTX
NCBI GI
                   g3337366
BLAST score
                   339
E value
                   1.0e-31
                   122
Match length
                   26
% identity
                   (AC004481) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   30774
                   222569 1.R1040
Contig ID
                   jC-gmf102220060c12d1
5'-most EST
Method
                   BLASTX
                   q960289
NCBI GI
```

```
2.0e-40
E value
Match length
                   104
% identity
                   74
                   (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
Seq. No.
                   30775
Contig ID
                   222674 1.R1040
                   zhf700964974.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2739385
BLAST score
                   246
E value
                   5.0e-21
Match length
                   75
% identity
                   (AC002505) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30776
                   222699 1.R1040
Contig ID
5'-most EST
                   zhf700\overline{9}65008.h1
                   30777
Seq. No.
                   222702 1.R1040---
Contig ID
                   uC-gmrominsoy100b02b1
5'-most EST
                   30778
Seq. No.
                   222753 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy036h05b1
                   30779
Seq. No.
                   222809 1.R1040
Contig ID
                   zhf700965140.hl
5'-most EST
Seq. No.
                   30780
                   222817 1.R1040
Contig ID
                   epx701107471.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1172633
BLAST score
                   485
E value
                   7.0e-49
Match length
                   135
                   67
% identity
                   PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5
NCBI Description
                   family signature; PROSITE; PS00847; disruption leads to
                   early lethal phenotype; similar to MCM2/3/5 family, most
                   similar to YBR1441 [Arabidopsis thaliana]
                   30781
Seq. No.
                   222827 1.R1040
Contig ID
                   zhf700965161.hl
5'-most EST
                   BLASTX
Method
                   g4572671
NCBI GI
BLAST score
                   216
E value
                   2.0e-17
Match length
                   75
```

56

% identity

```
(AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                    [Arabidopsis thaliana]
                    30782
Seq. No.
                    222830 1.R1040
Contig ID
                    jC-gmf\overline{1}02220126d11a1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q3341693
BLAST score
                    151
                    6.0e-10
E value
                    88
Match length
% identity
                    38
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
                    30783
Seq. No.
                    222830 2.R1040
Contig ID
5'-most EST
                    zhf700965166.hl
                    30784
Seq. No.
                    222843 1.R1040
Contig ID
                    zhf700\overline{9}65182.h1
5'-most EST
                    30785
Seq. No.
                   222845-1.R1040--
Contig-ID ---
                    zhf700\overline{9}65184.h1
5'-most EST
Method
                    BLASTN
NCBI GI
                    g2654107
BLAST score
                    280
E value
                    1.0e-156
Match length
                    528
                    88
% identity
NCBI Description
                   Pisum sativum cytosine-5 DNA methyltransferase mRNA,
                    complete cds
Seq. No.
                    30786
                    222853 1.R1040
Contig ID
5'-most EST
                    zhf700965201.h1
Method
                    BLASTX
NCBI GI
                    q3953457
BLAST score
                    187
E value
                    5.0e-14
                   72
Match length
% identity
                    50
NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]
Seq. No.
                    30787
                    222876 1.R1040
Contig ID
                    zhf700\overline{9}65225.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3024898
BLAST score
                    400
E value
                    4.0e-39
Match length
                   109
% identity
                    69
                   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                   HELICASE KIAA0224 (HA4657) >gi 1504028 dbj BAA13213
```

(D86977) similar to putative ATP-dependent RNA helicase

Contig ID

30793

223039 1.R1040

```
(AF038391) pre-mRNA splicing factor [Homo sapiens]
                  30788
Seq. No.
                  222891 1.R1040
Contig ID
5'-most EST
                  fC-gmro700565636z3
Method
                  BLASTX
NCBI GI
                  g2924516
                  761
BLAST score
                  2.0e-99
E value
                  234
Match length
                  52
% identity
NCBI Description
                   (AL022023) WD-40 repeat protein (MSI3) [Arabidopsis
                  thaliana]
                  30789
Seq. No.
                  222891 2.R1040
Contig ID
                   fC-gmro700565636r2
5'-most EST
Method
                  BLASTX
                  q3122389
NCBI GI
BLAST score
                  198
E value
                   9.0e-16
                  53
Match length
                  79
% identity -
                  WD-40 REPEAT PROTEIN MSI3 >gi 2394233 (AF016848) WD-40
NCBI Description
                  repeat protein [Arabidopsis thaliana]
                   30790
Seq. No.
                  222912 1.R1040
Contig ID
                   zhf700965271.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3165536
BLAST score
                  358
E value
                   2.0e-34
Match length
                  83
% identity
                   (AF067608) similar to DEAD-box helicases (Pfam: DEAD.hmm,
NCBI Description
                   score: 262.89) (Pfam: helicase_C.hmm, score: 76.21)
                   [Caenorhabditis elegans]
Seq. No.
                   30791
                  222925 1.R1040
Contig ID
5'-most EST
                  g5678025
                  30792
Seq. No.
Contig ID
                  222980 1.R1040
5'-most EST
                  all700863157.hl
Method
                  BLASTX
NCBI GI
                  g2739002
BLAST score
                  172
E value
                  1.0e-12
Match length
                  81
% identity
                  37
                   (AF022460) CYP83Dlp [Glycine max]
NCBI Description
```

KO3H1.2 of C.elegans(S41025) [Homo sapiens] >gi 3123906

```
5'-most EST
                   jC-gmst02400072b08d1
Method
                   BLASTX
NCBI GI
                   g3874495
BLAST score
                   242
                   2.0e-20
E value
Match length
                   70
% identity
                   66
                   (Z92826) predicted using Genefinder; cDNA EST EMBL:C09402
NCBI Description
                   comes from this gene [Caenorhabditis elegans]
                   30794
Seq. No.
                   223177 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810006b08d1
                   BLASTX
Method
NCBI GI
                   g4106395
BLAST score
                   348
                   7.0e-33
E value
Match length
                   118
% identity
                   58
NCBI Description
                   (AF073744) raffinose synthase [Cucumis sativus]
Seq. No.
                   30795
                   223253 1.R1040
Contig ID
5'-most EST--
                   pmv700889558:h1
Seq. No.
                   30796
                   223334 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}52196.h1
Method
                   BLASTX
NCBI GI
                   q461735
BLAST score
                   496
                   2.0e-50
E value
Match length
                   103
% identity
                   97
NCBI Description
                   MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
                   >gi_478785_pir__S29315 chaperonin 60 - cucurbit
>gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                   30797
                   223368 1.R1040
Contig ID
5'-most EST
                   g4105688
Method
                   BLASTX
NCBI GI
                   g3790677
BLAST score
                   249
E value
                   8.0e-35
Match length
                   307
% identity
                   (AF099002) similar to human 5'-nucleotidase (SW:P49902)
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   30798
                   223373 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910006a09a1
Seq. No.
                   30799
```

223463 1.R1040

Contig ID

```
5'-most EST
                   kl1701214569.hl
Seq. No.
                   30800
                   223518 1.R1040
Contig ID
5'-most EST
                   pxt700942813.hl
Method
                   BLASTX
NCBI GI
                   g2980773
BLAST score
                   148
                   1.0e-09
E value
Match length
                   57
% identity
NCBI Description
                   (AL022198) putative protein [Arabidopsis thaliana]
                   30801
Seq. No.
                   223520 1.R1040
Contig ID
5'-most EST
                   crh700850473.h1
Method
                   BLASTX
NCBI GI
                   g2160163
BLAST score
                   270
E value
                   5.0e-24
                   70
Match length
% identity
                   45
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   30802
Seq. No.
                   223612 2.R1040
Contig ID
5'-most EST
                   pxt700942360.h1
Seq. No.
                   30803
                   223620 1.R1040
Contig ID
5'-most EST
                   crh700850690.hl
Method
                   BLASTN
NCBI GI
                   g4220643
BLAST score
                   35
E value
                   4.0e-10
Match length
                   51
                   92
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD22, complete sequence [Arabidopsis thaliana]
                   30804
Seq. No.
                   223624 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910062f05a1
Seq. No.
                   30805
                   223633 1.R1040
Contig ID
5'-most EST
                   zsg701124347.h1
                   30806
Seq. No.
                   223730 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy095a06b1
Method
                   BLASTX
NCBI GI
                   g2244799
BLAST score
                   430
E value
                   3.0e-42
Match length
                   191
```

46

% identity

```
NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
                    30807
Seq. No.
                    223748 1.R1040
  Contig ID
  5'-most EST
                    crh700850888.h1
  Method
                    BLASTX
  NCBI GI
                    q3334489
  BLAST score
                    208
  E value
                    9.0e-17
 Match length
                    67
  % identity
                    60
                    DNA-DIRECTED RNA POLYMERASE I 190 KD POLYPEPTIDE
  NCBI Description
                    >gi 82799 pir__JS0080 DNA-directed RNA polymerase (EC
                    2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces
                    pombe) >gi 173433 (M37411) RNA polymerase I largest subunit
                     [Schizosaccharomyces pombe] >gi_2832886_emb_CAA16827_
                     (AL021730) dna-directed rna polymerase i 190 kd subunit
                    [Schizosaccharomyces pombe]
                    30808
  Seq. No.
                    223759 1.R1040
  Contig ID
  5'-most EST
                    zsg701\overline{1}24765.h1
  Seq. No :-
                    -30809
                    223827 1.R1040
  Contig ID
  5'-most EST
                    crh700851110.h1
                    30810
  Seq. No.
                    223833 1.R1040
  Contig ID
  5'-most EST
                    crh700851118.hl
                    30811
  Seq. No.
                    223874 1.R1040
  Contig ID
                    crh700\overline{8}51178.h1
  5'-most EST
                    30812
  Seq. No.
                    223880 1.R1040
  Contig ID
  5'-most EST
                    crh700851184.h1
                    30813
  Seq. No.
                    223889 1.R1040
  Contig ID
  5'-most EST
                    crh700851202.h1
                    30814
  Seq. No.
  Contig ID
                    223893 1.R1040
  5'-most EST
                    jC-gmro02800034c08a1
                    30815
  Seq. No.
                    223931 1.R1040
  Contig ID
  5'-most EST
                    crh700\overline{8}51424.h1
 Method
                    BLASTX
                    g3377805
 NCBI GI
  BLAST score
                    168
                    4.0e-17
  E value
 Match length
                    73
  % identity
 NCBI Description (AF075597) contains similarity to several apoptosis or
```

Match length

% identity

175 83

```
>gi 3912928 gb AAC78712.1 (AF001308) putative zinc finger
                  protein [Arabidopsis thaliana]
                   30816
Seq. No.
                   224061 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810022f06d1
Seq. No.
                   30817
                  224107 1.R1040
Contig ID
                  crh700851516.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3913425
BLAST score
                   635
                   2.0e-66
E value
                   144
Match length
% identity
                   88
                   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   30818
                   224227 1.R1040
Contig ID
5'-most EST
                   kl1701215344.hl
Method
                  BLASTX
NCBI GI
                   q4454048
BLAST score
                   285
E value
                   2.0e-25
Match length
                   142
% identity
                   44
NCBI Description
                   (AL035394) putative protein [Arabidopsis thaliana]
                   30819
Seq. No.
                   224272 1.R1040
Contig ID
5'-most EST
                   crh700851772.hl
Method
                  BLASTX
NCBI GI
                   q3757515
BLAST score
                   510
E value
                   7.0e-52
Match length
                   146
% identity
NCBI Description
                   (AC005167) hypothetical protein [Arabidopsis thaliana]
                   30820
Seq. No.
                   224315 1.R1040
Contig ID
5'-most EST
                   crh700851837.h1
Seq. No.
                   30821
                   224329 1.R1040
Contig ID
5'-most EST
                  crh700851896.hl
                  BLASTN
Method
NCBI GI
                  a4519195
BLAST score
                  59
E value
                  1.0e-24
```

programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana]

% identity

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  30822
Contig ID
                  224343 1.R1040
                  fC-qmse700851887f1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4164145
BLAST score
                  451
E value
                  7.0e-45
Match length
                  158
% identity
                  54
NCBI Description (AB012205) gibberelin 3beta-hydroxylase [Lactuca sativa]
                  30823
Seq. No.
Contig ID
                  224366 1.R1040
5'-most EST
                  crh700856137.hl
Method
                  BLASTX
NCBI GI
                  g3004555
BLAST score
                  317
E value
                  3.0e-29
Match length
                  136
% identity
NCBI Description
                  (AC003673) similar to salt inducible protein [Arabidopsis
                  thaliana]
Seq. No.
                  30824
Contig ID
                  224375 1.R1040
5'-most EST
                  crh700852006.hl
Method
                  BLASTN
                  g2104682
NCBI GI
BLAST score
                  81
E value
                  8.0e-38
                  245
Match length
% identity
NCBI Description V.faba mRNA for putative transciption factor (2861bp)
Seq. No.
                  30825
                  224379 1.R1040
Contig ID
5'-most EST
                  fC-qmse700851947f1
Method
                  BLASTX
NCBI GI
                  q2652938
BLAST score
                  521
E value
                  4.0e-53
Match length
                  132
% identity
                  47
NCBI Description (247554) orf [Zea mays]
Seq. No.
                  30826
                  224413 1.R1040
Contig ID
5'-most EST
                  gsv701049938.hl
Method
                  BLASTX
NCBI GI
                  g3183347
BLAST score
                  249
E value
                  8.0e-21
Match length
                  178
```

NCBI GI

E value

BLAST score

Match length

NCBI Description HYPOTHETICAL 48.5 KD PROTEIN C23C11.04C IN CHROMOSOME I >gi_2330768_emb_CAB11157_ (Z98559) SPAC23C11.04c; len:421aa, similar eg. to C. elegans Q19683, F21D5.5, (250aa), fasta scores, opt:395, E():1.1e-32, (41.7% identity in 223 aa overlap)also similar eg. to YMR156C, YM31 YEAST, Q03796, hypothetical 27.4 kd 30827 Seq. No. 224473 1.R1040 Contig ID 5'-most EST pxt700943889.h1 Seq. No. 30828 Contig ID 224498 1.R1040 crh700852121.hl 5'-most EST Seq. No. 30829 224510 1.R1040 Contig ID 5'-most EST crh700852272.h1 Seq. No. 224522 1.R1040 Contig ID 5'-most EST fua701037333.hl Seq. No. Contig ID 224546 1.R1040 5'-most EST uC-gmflminsoy043d11b1 Method BLASTX NCBI GI g1130682 BLAST score 498 1.0e-50 E value 118 Match length 77 % identity NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum] 30832 Seq. No. 224569 1.R1040 Contig ID 5'-most EST kl1701206318.hl Seq. No. 30833 224580 1.R1040 Contig ID fC-gmse700852258f1 5'-most EST Method BLASTX NCBI GI q3980380 BLAST score 493 E value 4.0e-59 Match length 151 % identity NCBI Description (AC004561) putative enolase [Arabidopsis thaliana] Seq. No. 30834 224600 1.R1040 Contig ID 5'-most EST crh700852284.h1 Method BLASTX

g4263791

3.0e-51

504

30844

```
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30835
Contig ID
                   224708 1.R1040
5'-most EST
                  epx701109365.h1
Seq. No.
                   30836
Contig ID
                   224713 1.R1040
5'-most EST
                  fC-qmse700852469f1
Method
                  BLASTX
NCBI GI
                  g2497752
BLAST score
                   320
E value
                   1.0e-29
Match length
                  116
% identity
                   53
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                  >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                   30837
                  224742 1.R1040
Contig ID
5'-most EST
                  r1r700\overline{9}01185.h1
Seq. No.
                   30838
Contig ID
                  224744 1.R1040
5'-most EST
                  uC-gmropic016a07b1
Seq. No.
                   30839
                  224806 1.R1040
Contig ID
5'-most EST
                  crh700852610.h1
Seq. No.
                  30840
                  224846_1.R1040
Contig ID
5'-most EST
                  fC-gmro700844279d3
                  30841
Seq. No.
                  224900 1.R1040
Contig ID
5'-most EST
                  leu701155145.h1
Method
                  BLASTX
NCBI GI
                  g3080375
BLAST score
                  496
E value
                  3.0e-50
Match length
                  124
% identity
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]
Seq. No.
                  30842
                  224907 1.R1040
Contig ID
5'-most EST
                  crh700852746.h1
                  30843
Seq. No.
Contig ID
                  224964_1.R1040
5'-most EST
                  fC-gmse700839629g1
```

Method

BLASTN

```
Contig ID
                   224998 1.R1040
5'-most EST
                   uC-gmrominsoy315b09b1
Seq. No.
                   30845
Contig ID
                   225100 1.R1040
                   fC-gmse700852993a1
5'-most EST
                   BLASTX
Method
                   g2245136
NCBI GI
BLAST score
                   503
E value
                   4.0e-51
Match length
                   111
% identity
                   74
                   (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   30846
                   225200 1.R1040
Contig ID
5'-most EST
                   kl1701207083.h1
Method
                   BLASTX
NCBI GI
                   q4538928
BLAST score
                   156
E value
                   2.0e-10
Match length
                   37
% identity
NCBI Description
                  (AL049483) putative protein [Arabidopsis thaliana]
Seq. No.
                   30847
Contig ID
                   225226 1.R1040
5'-most EST
                   pmv700888944.h1
                   30848
Seq. No.
Contig ID
                   225254 1.R1040
5'-most EST
                   qsv701\overline{0}52672.h1
                   30849
Seq. No.
Contig ID
                   225292 1.R1040
5'-most EST
                   crh700853334.h1
Method
                   BLASTX
NCBI GI
                   g2244986
BLAST score
                   257
E value
                   2.0e-22
Match length
                   94
% identity
NCBI Description
                  (Z97340) FCA gamma [Arabidopsis thaliana]
Seq. No.
Contig ID
                   225297 1.R1040
5'-most EST
                  crh700853339.hl
Seq. No.
Contig ID
                   225363 1.R1040
5'-most EST
                  crh700853454.h1
Seq. No.
Contig ID
                   225390 1.R1040
5'-most EST
                  crh700853504.h1
```

Contig ID

5'-most EST

```
NCBI GI
                   g2330648
BLAST score
                   154
E value
                   5.0e-81
Match length
                   321
% identity
NCBI Description
                   Pisum sativum mRNA for topoisomerase I
                   30853
Seq. No.
Contig ID
                   225444 1.R1040
5'-most EST
                   asn701142024.h1
                   30854
Seq. No.
                   225466 1.R1040
Contig ID
5'-most EST
                   fC-gmse700853718a1
                   BLASTX
Method
NCBI GI
                   q3860250
BLAST score
                   213
                   7.0e-17
E value
Match length
                   67
% identity
                   63
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   30855
                   225530 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400051a07d1
Seq. No.
                   30856
                   225584 1.R1040
Contig ID
5'-most EST
                   crh700853988.h1
Method
                   BLASTX
                   q2129662
NCBI GI
BLAST score
                   202
E value
                   1.0e-21
Match length
                   75
                   75
% identity
NCBI Description
                  ovule-specific homeotic protein homolog A20 - Arabidopsis
                   thaliana >gi 1881536 (U37589) A20 [Arabidopsis thaliana]
Seq. No.
                   30857
                   225642 1.R1040
Contig ID
5'-most EST
                   crh700854105.hl
Seq. No.
                   30858
                   225674_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810067e07d1
Method
                   BLASTX
NCBI GI
                   q3819699
BLAST score
                  259
E value
                   3.0e-22
                  109
Match length
% identity
                   52
NCBI Description
                  (AJ009609) BnMAP4K alpha2 [Brassica napus]
Seq. No.
                   30859
```

225722 1.R1040

uC-gmropic070e11b1

```
30860
Seq. No.
Contig ID
                   225738 1.R1040
5'-most EST
                   crh700854306.h1
                   30861
Seq. No.
                   225747 1.R1040
Contig ID
                   crh700\overline{8}54318.h1
5'-most EST
Seq. No.
                   30862
                   225787 1.R1040
Contig ID
                   crh700854410.hl
5'-most EST
Seq. No.
                   30863
Contig ID
                   225837 1.R1040
5'-most EST
                   fC-qmse700854493a1
Method
                   BLASTX
NCBI GI
                   q4098647
BLAST score
                   382
E value
                   9.0e-37
Match length
                   94
% identity
NCBI Description
                   (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
                   thaliana] -----
Seq. No.
                   30864
Contig ID
                   225845 1.R1040
5'-most EST
                   crh700854505.h1
Seq. No.
                   30865
                   225882 1.R1040
Contig ID
5'-most EST
                   crh700854563.h1
                   30866
Seq. No.
                   225890 1.R1040
Contig ID
5'-most EST
                   leu701156924.h1
Method
                   BLASTX
NCBI GI
                   g4454018
BLAST score
                   224
                   3.0e-18
E value
Match length
                   101
% identity
NCBI Description
                  (AL035396) SRG1-like protein [Arabidopsis thaliana]
                   30867
Seq. No.
Contig ID
                   225892 1.R1040
5'-most EST
                   jC-qmf\overline{1}02220144d07a1
Seq. No.
                   30868
Contig ID
                   225920 1.R1040
5'-most EST
                   crh700854630.hl
                   30869
Seq. No.
Contig ID
                   226016 1.R1040
5'-most EST
                   g4291148
```

E value

6.0e-58

```
Contig ID
                   226018 1.R1040
5'-most EST
                   gsv701\overline{0}54582.h1
Method
                   BLASTX
NCBI GI
                   g688423
BLAST score
                   122
E value
                   3.0e-11
                   90
Match length
% identity
                   41
                   (D26453) tumor-related protein [Nicotiana glauca X
NCBI Description
                   Nicotiana langsdorffii]
                   30871
Seq. No.
                   226047 1.R1040
Contig ID
5'-most EST
                   leu701155547.h1
Seq. No.
                   30872
Contig ID
                   226056_1.R1040
5'-most EST
                   crh700854933.h1
                   30873
Seq. No.
                   226077 1.R1040
Contig ID
5'-most EST
                   g5606449
                   30874 -- -- ----
Seq. No.
                   226077 2.R1040
Contig ID
5'-most EST
                   gsv701046666.hl
                   30875
Seq. No.
                   226092 1.R1040
Contig ID
5'-most EST
                   crh700855006.h1
Seq. No.
                   30876
                   226104 1.R1040
Contig ID
5'-most EST
                   crh700855024.h1
                   30877
Seq. No.
                   226218 1.R1040
Contig ID
5'-most EST
                   crh700855435.h1
Seq. No.
                   30878
                   226277 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}06295.h1
                   BLASTX
Method
NCBI GI
                   g4325342
BLAST score
                   238
                   3.0e-20
E value
Match length
                   89
% identity
                  (AF128393) No definition line found [Arabidopsis thaliana]
NCBI Description
                   30879
Seq. No.
Contig ID
                   226372 1.R1040
5'-most EST
                   fC-gmse700855772a1
Method
                   BLASTX
NCBI GI
                   g3822223
BLAST score
                   562
```

5'-most EST

```
142
Match length
% identity
                  73
NCBI Description
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  30880
                  226380 1.R1040
Contig ID
                  crh700855811.h1
5'-most EST
Seq. No.
                  30881
Contig ID
                  226414 1.R1040
5'-most EST
                  gsv701056785.h1
                  30882
Seq. No.
                  226476 1.R1040
Contig ID
5'-most EST
                  crh700856007.h1
Seq. No.
                  30883
                  226506 1.R1040
Contig ID
5'-most EST
                  crh700856088.h1
                  BLASTX
Method
NCBI GI
                  q4468984
BLAST score
                  323
                  7.0e-30 -- - -----
E value
                  107
Match length
% identity
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  30884
Contig ID
                  226510 1.R1040
5'-most EST
                  jC-gmro02800042c09d1
Seq. No.
                  30885
                  226524 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810002e05d1
Method
                  BLASTX
                  q4056493
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
Match length
                  56
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30886
                  226561 1.R1040
Contig ID
5'-most EST
                  jC-qmf102220068e03a1
Method
                  BLASTX
NCBI GI
                  q2281090
BLAST score
                  437
                  2.0e-43
E value
                  114
Match length
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30887
Contig ID
                  226756 1.R1040
```

jC-gmst02400067d10d1

BLAST score

```
Seq. No.
                  30888
Contig ID
                  226773 1.R1040
5'-most EST
                  uC-gmropic105h06b1
Seq. No.
                  30889
Contig ID
                  226783 1.R1040
5'-most EST
                  jC-gmle01810046b08d1
                  30890
Seq. No.
                  226821 1.R1040
Contig ID
5'-most EST
                  g5752647
Seq. No.
                  30891
                  226858 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400073f08a1
Method
                  BLASTX
NCBI GI
                  g3395440
BLAST score
                  392
                  2.0e-43
E value
Match length
                  138
% identity
                  65
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                  30892
Seq. No.
                  226866 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy065b03b1
Method
                  BLASTX
NCBI GI
                  g2623296
BLAST score
                  367
                  5.0e-35
E value
Match length
                  150
                  52
% identity
NCBI Description
                 (AC002409) hypothetical protein [Arabidopsis thaliana]
                  30893
Seq. No.
Contig ID
                  226877 1.R1040
5'-most EST
                  jC-gmst02400023c07a1
                  30894
Seq. No.
                  226881 1.R1040
Contig ID
                  pmv700888211.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2435522
BLAST score
                  537
E value
                  4.0e-55
Match length
                  127
% identity
NCBI Description
                   (AF024504) contains similarity to other AMP-binding enzymes
                   [Arabidopsis thaliana]
                  30895
Seq. No.
                  226885 1.R1040
Contig ID
5'-most EST
                  pmv700888216.h1
Method
                  BLASTX
NCBI GI
                  q4263795
```

```
E value
                   5.0e-12
Match length
                   58
% identity
NCBI Description
                   (AC006068) putative glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   30896
                   226934 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400033g10d1
Method
                   BLASTX
NCBI GI
                   g1711618
BLAST score
                   263
E value
                   2.0e-36
Match length
                   132
% identity
                   61
                   LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir S51765
NCBI Description
                   low affinity sulphate transporter - Stylosanthes hamata
                   >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
transporter [Stylosanthes hamata]
Seq. No.
                   30897
                   226960 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810053e09a1
Method -
                   BLASTX
                   g4335734
NCBI GI
BLAST score
                   362
E value
                   3.0e - 34
Match length
                   185
% identity
                   42
NCBI Description
                   (AC006248) putative calmodulin [Arabidopsis thaliana]
                   30898
Seq. No.
                   226961 1.R1040
Contig ID
5'-most EST
                   pmv700888312.hl
                   30899
Seq. No.
                   226967 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400025f05a1
Method
                   BLASTX
NCBI GI
                   g4220462
                   903
BLAST score
E value
                   1.0e-97
Match length
                   211
% identity
NCBI Description
                   (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                   and bZIP PF 00170 domains. [Arabidopsis thaliana]
                   30900
Seq. No.
Contig ID
                   226977 1.R1040
                   pmv700890884.h1
5'-most EST
Seq. No.
                   30901
                   226981 1.R1040
Contig ID
5'-most EST
                   pmv700888336.h1
```

Contig ID

```
Contig ID
                   227026 1.R1040
 5'-most EST
                   pmv700892102.h1
                   30903
 Seq. No.
                   227040 2.R1040
Contig ID
 5'-most EST
                   pmv700888509.h1
 Seq. No.
                   30904
                   227045 1.R1040
Contig ID
                   pmv700888414.hl
 5'-most EST
                   30905
 Seq. No.
                   227057 1.R1040
Contig ID
 5'-most EST
                   q4284686
Method
                   BLASTX
                   g1755192
NCBI GI
BLAST score
                   201
                   5.0e-26
E value
Match length
                   95
 % identity
                   66
                   (U75207) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   30906
Seq. No.
                   227060 1.R1040
Contig ID
 5'-most EST
                   uC-gmropic018d03b1
     30907
Seq. No.
                   227081 1.R1040
Contig ID
                   jsh701\overline{0}69769.h1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g1703376
BLAST score
                   297
E value
                   3.0e-27
Match length
                   67
 % identity
                   85
NCBI Description
                   ADP-RIBOSYLATION FACTOR 1 >qi 480121 pir S36453
                   ADP-ribosylation factor 1 - potato >gi 396808 emb_CAA52468
                   (X74461) ADP-ribosylation factor 1 [Solanum tuberosum]
                   30908
Seq. No.
                   227097 1.R1040
 Contig ID
                   pmv700888489.h1
 5'-most EST
                 ·· 30909
Seq. No.
                   227101 1.R1040
Contig ID
 5'-most EST
                   pmv700888494.h1
Method
                   BLASTN
NCBI GI
                   g429107
BLAST score
                   100
E value
                   4.0e-49
                   248
Match length
% identity
                   85
                   L.esculentum S-adenosyl-L-methionine synthetase mRNA,
NCBI Description
                   complete CDS
Seq. No.
                   30910
                   227192 1.R1040
```

```
5'-most EST
                   jC-gmf102220089a09d1
                   30911
Seq. No.
                   227194 1.R1040
Contig ID
5'-most EST
                   leu701155561.h1
Seq. No.
                   30912
                   227202_1.R1040
Contig ID
5'-most EST
                   jC-gmst02400034g02d2
                   30913
Seq. No.
Contig ID
                   227289 1.R1040
5'-most EST
                   pmv700888746.h1
                   30914
Seq. No.
                   227328 1.R1040
Contig ID
5'-most EST
                   pmv700888821.hl
Method
                   BLASTX
NCBI GI
                   g4249411
BLAST score
                   210
E value
                   1.0e-16
Match length
                   42
% identity
NCBI Description
                    (AC006072) unknown protein [Arabidopsis thaliana]
                   30915
Seq. No.
                   227329 1.R1040
Contig ID
5'-most EST
                   pmv700888822.h1
Seq. No.
                   30916
                   227360 1.R1040
Contig ID
                   leu701154547.h1
5'-most EST
Seq. No.
                   30917
                   227369 1.R1040
Contig ID
5'-most EST
                   uC-gmropic007h11b1
Method
                   BLASTX
NCBI GI
                   g1076315
BLAST score
                   172
E value
                   3.0e-12
                   101
Match length
                   40
% identity
                   cytochrome P450 - Arabidopsis thaliana
NCBI Description
                   >gi_853719_emb_CAA60793_ (X87367) CYP90 protein
[Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
                   CYP90 protein [Arabidopsis thaliana]
Seq. No.
                   30918
                   227373 1.R1040
Contig ID
5'-most EST
                   pmv700888873.h1
Seq. No.
                   30919
                   227387 1.R1040
Contig ID
5'-most EST
                   rlr700896045.hl
                   30920
Seq. No.
```

227421 1.R1040

Contig ID

BLAST score

```
5'-most EST
                   pmv700888935.h1
Method
                   BLASTX
NCBI GI
                   g4539369
BLAST score
                   189
E value
                   4.0e-14
Match length
                   65
% identity
                   (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   227423 1.R1040
5'-most EST
                   jC-gmle01810031a08d1
Seq. No.
                   30922
                   227431 1.R1040
Contig ID
5'-most EST
                   uC-gmropic034h09b1
Method
                   BLASTX
NCBI GI
                   g3548802
BLAST score
                   502
E value
                   6.0e-51
Match length
                   146
% identity
                   63
NCBI Description
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
                   >gi 4335769 gb AAD17446 (AC006284) putative axil protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   30923
Seq. No.
Contig ID
                   227446 1.R1040
5'-most EST
                   pmv700888964.h1
                   BLASTX
Method
NCBI GI
                   g3522956
BLAST score
                   238
E value
                   2.0e-22
Match length
                   88
% identity
                   (AC004411) putative pectinacetylesterase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   30924
Seq. No.
Contig ID
                   227451 1.R1040
5'-most EST
                   fC-gmro700869490f2
Method
                   BLASTX
NCBI GI
                   g1703318
BLAST score
                   483
E value
                   2.0e-48
Match length
                   119
                   77
% identity
                  ANNEXIN-LIKE PROTEIN RJ4 >gi 1362037 pir S56674 annexin
NCBI Description
                   homolog RJ4 (clone RJ4) - garden strawberry (fragment)
                   >gi 643076 (U19941) annexin [Fragaria x ananassa]
                   30925
Seq. No.
                   227452 1.R1040
Contig ID
5'-most EST
                   pmv700888972.h1
Method
                   BLASTX
                   g2494231
NCBI GI
```

```
E value
                   7.0e-14
Match length
                   89
                   47
% identity
NCBI Description
                   TRANSCRIPTION FACTOR E2F5 (E2F-5) >qi 2137276 pir 148338
                  E2F-5 - mouse >gi 806572 emb CAA60508 (X86925) E2F-5 [Mus
                  musculus]
                   30926
Seq. No.
Contig ID
                   227471 1.R1040
5'-most EST
                  pxt700944495.h1
                   30927
Seq. No.
                   227472 1.R1040
Contig ID
5'-most EST
                  pmv700888994.h1
Seq. No.
                   30928
                   227528 1.R1040
Contig ID
5'-most EST
                  pxt700942665.h1
Method
                  BLASTX
                  q1420936
NCBI GI
BLAST score
                  1002
E value
                  1.0e-109
                  237
Match length
% identity
                  76
                   (U61396) Vigna unguiculata aspartic proteinase mRNA,
NCBI Description
                  complete cds. [Vigna unguiculata]
Seq. No.
                  30929
                  227532 1.R1040
Contig ID
5'-most EST
                  asn701134848.h2
Method
                  BLASTX
NCBI GI
                  g3386605
BLAST score
                  168
                   5.0e-22
E value
Match length
                  86',
                   57
% identity
NCBI Description
                   (AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  30930
                  227551 1.R1040
Contig ID
5'-most EST
                  pmv700889088.h1
Seq. No.
                  30931
Contig ID
                  227554 1.R1040
                  pxt700941410.h1
5'-most EST
Seq. No.
                  30932
                  227589 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810049a08d1
                  30933
Seq. No.
                  227602 1.R1040
Contig ID
5'-most EST
                  pmv700889151.h1
Method
                  BLASTX
                  g1742955
NCBI GI
BLAST score
                  667
```

4.0e-70

E value

```
202
Match length
 % identity
                    67
 NCBI Description
                    (271446) CLC-b chloride channel protein [Arabidopsis
                    30934
 Seq. No.
 Contig ID
                    227643 1.R1040
 5'-most EST
                    rlr700898408.h1
Method
                   BLASTX
 NCBI GI
                    g584861
 BLAST score
                    159
 E value
                    7.0e-11
Match length
                    57
 % identity
                   CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)
 NCBI Description
                   >gi_480396_pir__S36806 cytochrome P450 71A2 - eggplant
                   >gi 408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum
                   melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome
                    P-450EG4 [Solanum melongena]
                    30935
 Seq. No.
 Contig ID
                    227697 1.R1040
                   jC-gms\overline{t}02400036e11d2
 5'-most EST
 Seq. No.
                    30936
                    227708 1.R1040
 Contig ID
 5'-most EST
                   jC-gmst02400006f10d1
 Seq. No.
                    30937
 Contig ID
                    227723 1.R1040
 5'-most EST
                    fC-gmro700869757f5
Method
                   BLASTX
 NCBI GI
                   g2511693
 BLAST score
                    608
 E value
                    6.0e-63
Match length
                   170
 % identity
                    62
 NCBI Description
                    (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
 Seq. No.
                    227731 1.R1040
 Contig ID
 5'-most EST
                   k11701\overline{2}14248.h1
 Seq. No.
                   30939
                   227737 1.R1040
 Contig ID
 5'-most EST
                   uC-gmrominsoy247f08b1
 Seq. No.
                   30940
 Contig ID
                   227742 1.R1040
 5'-most EST
                   pmv700889626.h1
 Seq. No.
                   30941
                   227747 1.R1040
 Contig ID
 5'-most EST
                   pmv700893691.hl
Method
                   BLASTX
NCBI GI
                   q3892057
```

252

BLAST score

Contig ID 5'-most EST

```
4.0e-22
E value
Match length
                   69
% identity
                   32
NCBI Description
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   30942
Contig ID
                   227769 1.R1040
5'-most EST
                   pmv700889360.hl
Method
                   BLASTX
NCBI GI
                   g3258569
BLAST score
                   465
E value
                   1.0e-46
Match length
                   121
% identity
                   79
NCBI Description
                   (U89959) Similar to yeast general negative regulator of
                   transcription subunit 1 [Arabidopsis thaliana]
Seq. No.
                   30943
Contig ID
                   227797 1.R1040
5'-most EST
                   pmv700889393.h1
Method
                   BLASTX
NCBI GI
                   q3327271
BLAST score
                   231
E value --
                  3.0e-19
Match length
                   100
% identity
NCBI Description
                  (AB016000) PKn2 [Ipomoea nil]
                   30944
Seq. No.
Contig ID
                   227918 1.R1040
5'-most EST
                   q4300792
Seq. No.
                   30945
Contig ID
                   227960 1.R1040
5'-most EST
                   jC-qmro02910047b01a1
Method
                   BLASTX
NCBI GI
                   g4490300
BLAST score
                   430
E value
                   2.0e-42
Match length
                   121
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   30946
Seq. No.
Contig ID
                   227989 1.R1040
5'-most EST
                  pxt700940986.h1
Method
                   BLASTX
NCBI GI
                   g1360090
BLAST score
                   300
E value
                   2.0e-27
Match length
                  106
% identity
NCBI Description
                   (X95576) C1C-Nt1 [Nicotiana tabacum]
                   30947
Seq. No.
```

228004 1.R1040

leu701154017.h1

30956

```
30948
Seq. No.
                   228031 1.R1040
Contig ID
5'-most EST
                   fC-gmro700870127f3
Method
                   BLASTX
NCBI GI
                  g3269291
BLAST score
                   417
                   8.0e-41
E value
Match length
                   181
                   49
% identity
NCBI Description
                   (AL030978) putative receptor protein kinase [Arabidopsis
                  thaliana]
                   30949
Seq. No.
                   228040 1.R1040
Contig ID
5'-most EST
                  gsv701054529.h1
Seq. No.
                   30950
Contig ID
                   228042 1.R1040
5'-most EST
                   fC-gmro700870195a4
Method
                  BLASTX
NCBI GI
                  g2853078
BLAST score
                  147
E value -
                   4.0e-09
Match length
                  161
                  19
% identity
                   (AL021768) TMV resistance protein N-like [Arabidopsis
NCBI Description
                  thaliana]
                   30951
Seq. No.
                   228046 1.R1040
Contig ID
                  pmv700889742.h1
5'-most EST
Method
                  BLASTX
                  g2914698
NCBI GI
                   388
BLAST score
E value
                   8.0e-40
                  190
Match length
% identity
                   45
                   (AC003974) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30952
Seq. No.
Contig ID
                   228054 1.R1040
5'-most EST
                  dkc700968025.h1
                   30953
Seq. No.
                   228054 2.R1040
Contiq ID
5'-most EST
                  jsh701064341.hl
Seq. No.
                  30954
                  228054 3.R1040
Contig ID
5'-most EST
                  pxt700942158.h1
                  30955
Seq. No.
Contig ID
                  228064 1.R1040
5'-most EST
                  hrw701063230.hl
```

e ()

E value

4.0e-30

```
Contig ID
                  228066 1.R1040
5'-most EST
                  pmv700889774.h1
                  30957
Seq. No.
Contig ID
                  228121 1.R1040
5'-most EST
                  epx701106844.hl
                  BLASTX
Method
NCBI GI
                  q3695019
BLAST score
                  287
                   6.0e-26
E value
Match length
                  97
% identity
                  57
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  30958
Contig ID
                  228141 1.R1040
5'-most EST
                  jC-gmle01810063e05a1
Seq. No.
                  30959
Contig ID
                  228145 1.R1040
5'-most EST
                  fC-gmle700870650f3
                  BLASTX
Method
NCBI GI
                  g2129698
BLAST score
                  669
                  2.0e-93
E value
Match length
                  219
                  79
% identity
NCBI Description
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 1054633 emb CAA63387 (X92728) protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  30960
                  228152 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400005g06a1
Seq. No.
                  30961
                  228155 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910004e07a1
                  30962
Seq. No.
                  228157 1.R1040
Contig ID
5'-most EST
                  pmv700889894.hl
Method
                  BLASTX
NCBI GI
                  g3935181
BLAST score
                  184
                  4.0e-20
E value
Match length
                  60
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                  30963
Seq. No.
                  228167 1.R1040
Contig ID
5'-most EST
                  pmv700889912.h1
                  BLASTX
Method
NCBI GI
                  g2832661
BLAST score
                  323
```

Contig ID

```
Match length
                  116
% identity
                  59
NCBI Description
                  (AL021710) pherophorin - like protein [Arabidopsis
                  30964
Seq. No.
Contig ID
                  228182 1.R1040
5'-most EST
                  pmv700889931.h1
                  30965
Seq. No.
Contig ID
                  228189 1.R1040
5'-most EST
                  pxt700943687.h1
                  30966
Seq. No.
                  228211 1.R1040
Contig ID
5'-most EST
                  fua701037866.hl
Seq. No.
                  30967
                  228351 1.R1040
Contig ID
                  r1r700899917.h1
5'-most EST
Seq. No.
                  30968
                  228353 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy043h09b1
Method
                  BLASTX
NCBI GI
                  g2498329
BLAST score
                  435
E value
                  4.0e-43
Match length
                  139
% identity
                  63
                  PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571
NCBI Description
                  pattern-formation protein GNOM - Arabidopsis thaliana
                  >gi 1209633 (U36433) GNOM gene product [Arabidopsis
                  thaliana] >gi 1335997 (U56140) similar to the Saccharomyces
                  cerevisiae Sec7 protein, GenBank Accession Number J03918
                  [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the
                  Saccharomyces cerevisiae Sec7 protein, GenBank Accession
                  Number J03918 [Arabidopsis thaliana]
                  30969
Seq. No.
                  228366 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy035g07b1
Seq. No.
                  30970
                  228375 1.R1040
Contig ID
5'-most EST
                  uC-gmropic045h04b1
Method
                  BLASTX
NCBI GI
                  q3695059
BLAST score
                  531
E value
                  3.0e-54
Match length
                  155
% identity
                  (AF064787) rac GTPase activating protein 1 [Lotus
NCBI Description
                  japonicus]
Seq. No.
                  30971
```

228393 1.R1040

```
uC-gmrominsoy277g05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4218120
BLAST score
                  231
E value
                   5.0e-19
Match length
                   144
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  30972
Contig ID
                  228398 1.R1040
5'-most EST
                  jC-qmst02400044f01a1
Method
                  BLASTX
NCBI GI
                  g1350783
BLAST score
                   667
E value
                  8.0e-70
Match length
                   321
% identity
                   48
                  RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                  >gi_282883_pir__S27756 receptor-like protein kinase
                  precursor - Arabidopsis thaliana >qi 166850 (M84660)
                  receptor-like protein kinase [Arabidopsis thaliana]
                  >gi 2842492 emb CAA16889 (AL021749) receptor-like protein
                  kinase 5 precursor (RLK5) [Arabidopsis thaliana]
Seq. No.
                  30973
Contig ID
                  228435 1.R1040
5'-most EST
                  fC-gmle700871051f3
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  379
E value
                  9.0e-37
Match length
                  93
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  30974
Seq. No.
                  228442 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400047d09a1
Seq. No.
                  30975
Contig ID
                  228471 1.R1040
                  pmv700892204.hl
5'-most EST
                  30976
Seq. No.
                  228489 1.R1040
Contig ID
5'-most EST
                  pmv700892264.h1
Method
                  BLASTX
                  g4115563
NCBI GI
BLAST score
                  268
                  2.0e-26
E value
Match length
                  82
% identity
                  71
                  (AB013598) UDP-glucose:anthocyanin 5-0-glucosyltransferase
NCBI Description
```

[Verbena x hybrida]

BLAST score

```
30977
Seq. No.
                   228491 1.R1040
Contig ID
5'-most EST
                   pmv700890335.h1
Method
                   BLASTX
                   g3258575
NCBI GI
BLAST score
                   225
                   2.0e-22
E value
                   79
Match length
                   71
% identity
NCBI Description
                   (U89959) Hypothetical protein [Arabidopsis thaliana]
                   30978
Seq. No.
                   228499 1.R1040
Contig ID
                   pmv700892214.h1
5'-most EST
Seq. No.
                   30979
                   228503 1.R1040
Contig ID
5'-most EST
                   pmv700892258.h1
                   30980
Seq. No.
                   228506 1.R1040
Contig ID
5'-most EST
                   pmv700890392.h1
                   30981
Seq. No.
                   228509 1.R1040
Contig ID
5'-most EST
                   k11701203832.h1
                   30982
Seq. No.
                   228524 1.R1040
Contig ID
5'-most EST
                   pmv700892272.h1
                   BLASTX
Method
                   g1865677
NCBI GI
BLAST score
                   326
                   8.0e-31
E value
                  74
Match length
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   30983
Seq. No.
                   228578 1.R1040
Contig ID
5'-most EST
                   gsv701052775.h1
                   BLASTX
Method
NCBI GI
                   g2578818
BLAST score
                   168
                   7.0e-12
E value
                   75
Match length
% identity
NCBI Description
                   (AB000121) TBPIP [Mus musculus]
                   30984
Seq. No.
                   228691 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400011b05d1
Method
                   BLASTX
NCBI GI
                   g3327178
```

% identity

```
E value
                   3.0e-18
Match length
                   139
% identity
NCBI Description
                   (AB014582) KIAA0682 protein [Homo sapiens]
Seq. No.
Contig ID
                   228736 1.R1040
5'-most EST
                   pmv700890653.hl
                   30986
Seq. No.
Contig ID
                   228747 1.R1040
5'-most EST
                   uC-gmflminsoy030g05b1
Method
                   BLASTX
NCBI GI
                   g4522005
BLAST score
                   193
E value
                   1.0e-19
Match length
                   125
% identity
                   43
                   (AC007069) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   30987
                   228774 1.R1040
Contig ID
5'-most EST
                   pmv700890711.h1
                   30988
Seq. No.
Contig ID
                   228780 1.R1040
5'-most EST
                   jC-gmle01810022d12d1
Seq. No.
                   30989
Contig ID
                   228784 1.R1040
5'-most EST
                   jC-gmst02400054e12a1
                   30990
Seq. No.
Contig ID
                   228875 1.R1040
5'-most EST
                   uC-gmropic059g07b1
Seq. No.
                   30991
Contig ID
                   228929 1.R1040
5'-most EST
                   uC-gmropic059h02b1
Method
                   BLASTX
NCBI GI
                   q3695019
BLAST score
                   277
E value
                   1.0e-24
Match length
                   101
% identity
NCBI Description
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   30992
Contig ID
                   228979 1.R1040
5'-most EST
                   fC-gmf1700898910f1
Method
                   BLASTX
NCBI GI
                   g629722
BLAST score
                   227
E value
                   2.0e-18
Match length
                   188
```

5'-most EST

Seq. No.

Contig ID

```
NCBI Description
                   finger protein pcp1 - potato >gi 563623 emb CAA57772
                   (X82328) putative DNA/RNA binding protein [Solanum
                   tuberosum]
                   30993
Seq. No.
Contig ID
                   229088 1.R1040
5'-most EST
                   fC-gmro7000749140r1
                   30994
Seq. No.
                   229101 1.R1040
Contig ID
5'-most EST
                   pmv700891126.h1
Seq. No.
                   30995
                   229117 1.R1040
Contig ID
                   uC-gmropic025h05b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2104534
                   596
BLAST score
E value
                   5.0e-62
Match length
                   129
% identity
                   84
                   (AF001308) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   30996
Seq. No.
                   229131 1.R1040
Contiq ID
                   k11701\overline{2}13809.h1
5'-most EST
Seq. No.
                   30997
                   229150 1.R1040
Contig ID
5'-most EST
                   zsg701124540.h1
Method
                   BLASTX
NCBI GI
                   q3880026
BLAST score
                   277
                   1.0e-25
E value
Match length
                   101
% identity
                   55
                   (Z75550) Similarity with Schizosaccharomyces hypothetical
NCBI Description
                   gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from
                   this gene [Caenorhabditis elegans]
                   30998
Seq. No.
                   229155 1.R1040
Contig ID
                   asn701\overline{1}33270.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3763933
BLAST score
                   715
E value
                   1.0e-75
Match length
                   187
% identity
                   85
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   30999
Seq. No.
                   229165 1.R1040
Contig ID
```

pmv700891209.h1

229271 1.R1040

```
5'-most EST
                   g4284566
                   31001
Seq. No.
Contig ID
                   229294 1.R1040
5'-most EST
                   pmv700891358.h1
Method
                   BLASTX
                   g2827528
NCBI GI
BLAST score
                   333
                   6.0e-31
E value
                   108
Match length
% identity
                   64
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   31002
Seq. No.
                   229303 1.R1040
Contig ID
5'-most EST
                   kl1701202962.hl
Method
                   BLASTX
NCBI GI
                   g1747310
BLAST score
                   158
                   2.0e-17
E value
                   73
Match length
                   73
% identity
                  (D58424) Myb-like DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   31003
Seq. No.
                   229314 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}18417.h1
                   31004
Seq. No.
Contig ID
                   229330 1.R1040
5'-most EST
                   dpv701\overline{1}01822.h1
                   31005
Seq. No.
                   229365 1.R1040
Contig ID
5'-most EST
                   pmv700891445.hl
                   BLASTX
Method
NCBI GI
                   g2098709
BLAST score
                   426
                   4.0e-42
E value
                   118
Match length
                   68
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
Seq. No.
                   31006
                   229382 1.R1040
Contig ID
5'-most EST
                   pmv700891466.h1
                   BLASTX
Method
NCBI GI
                   g3184285
BLAST score
                   143
                   5.0e-09
E value
                   49
Match length
% identity
                  (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31007
```

229425 1.R1040

Contig ID

., % (

```
5'-most EST
                  dpv701100873.h1
                  BLASTX
Method
NCBI GI
                  q4115384
BLAST score
                   459
E value
                   4.0e-46
Match length
                  106
% identity
                   79
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  31008
Seq. No.
Contig ID
                  229445 1.R1040
                  pmv700891569.h1
5'-most EST
Method -
                  BLASTX
NCBI GI
                  g3786021
BLAST score
                  191
E value
                  1.0e-14
Match length
                   66
                  58
% identity
NCBI Description
                 (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  31009
                  229465 1.R1040
Contig ID
5'-most EST
                  fC-gmle700872274f7
Method
                  BLASTX
NCBI GI
                  g2760839
BLAST score
                  756
E value
                   4.0e-86
Match length
                  252
% identity
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31010
                  229503 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400001b07a1
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  286
E value
                  6.0e-26
Match length
                  64
                  72
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  31011
Seq. No.
Contig ID
                  229607 1.R1040
5'-most EST
                  jC-gmro02910024g02d1
Seq. No.
                  31012
                  229643 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910048b02a1
Method
                  BLASTX
NCBI GI
                  g3360289
BLAST score
                  164
                  3.0e-11
E value
Match length
                  54
% identity
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase
```

```
1 [Zea mays]
                   31013
Seq. No.
                   229657 1.R1040
Contig ID
5'-most EST
                   hrw701061016.h1
Seq. No.
                   31014
Contig ID
                   229658 1.R1040
5'-most EST
                   fC-gmle700873056f3
Method
                   BLASTX
NCBI GI
                   g2795809
BLAST score
                   319
                   3.0e-29
E value
Match length
                   64
% identity
                   (AC003674) putative expansin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31015
                   229664_1.R1040
Contig ID
5'-most EST
                   uC-gmropic096a08b1
Method
                   BLASTX
NCBI GI
                   q4539314
BLAST score
                   193
E value
                   2.0e-14
                   89
Match length
                   51
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31016
                   229704 1.R1040
Contig ID
                   pmv700891910.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1850545
BLAST score
                   34
E value
                   2.0e-09
Match length
                   115
                   89
% identity
                   Arabidopsis thaliana syntaxin related protein AtVam3p
NCBI Description
                   (AtVAM3) mRNA, complete cds
                   31017
Seq. No.
                   229839 1.R1040
Contig ID
5'-most EST
                   fC-gmle700873194f3
Method
                   BLASTX
NCBI GI
                   q1350783
BLAST score
                   400
E value
                   6.0e-39
Match length
                   149
% identity
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                   >gi 282883 pir S27756 receptor-like protein kinase
                   precursor - Arabidopsis thaliana >gi_166850 (M84660)
                   receptor-like protein kinase [Arabidopsis thaliana]
                   >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein
kinase 5 precursor (RLK5) [Arabidopsis thaliana]
```

```
229855 1.R1040
Contig ID
                   r1r700\overline{8}96085.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1946360
BLAST score
                   249
E value
                   1.0e-21
Match length
                   84
% identity
                   57
NCBI Description
                   (U93215) elicitor response element binding protein WRKY3
                   isolog [Arabidopsis thaliana]
Seq. No.
                   31019
Contig ID
                   229856 1.R1040
5'-most EST
                   asn701\overline{1}30917.h1
Seq. No.
                   31020
Contig ID
                   229905 1.R1040
5'-most EST
                   kl1701213279.hl
Seq. No.
                   31021
                   229939 1.R1040
Contig ID
5'-most EST
                   pmv700892206.hl
Seq. No.
                   31022
                   229947 1.R1040
Contig ID
5'-most EST
                   pmv700892225.hl
Seq. No.
                   31023
                   229952 1.R1040
Contig ID
5'-most EST
                   pmv700892231.h1
Seq. No.
                   31024
Contig ID
                   230015 1.R1040
5'-most EST
                   pmv700892338.h1
Seq. No.
                   31025
                   230039 1.R1040
Contig ID
5'-most EST
                  pmv700892367.h1
                   31026
Seq. No.
                   230045_1.R1040
Contig ID
5'-most EST
                   hrw701058029.hl
Seq. No.
                   31027
                   230056 1.R1040
Contig ID
5'-most EST
                  pmv700892390.h1
Seq. No.
                   31028
Contig ID
                   230060 1.R1040
5'-most EST
                  pmv700892395.h1
                   31029
Seq. No.
                   230085 1.R1040
Contig ID
5'-most EST
                   fC-gmle700873426f3
Method
                   BLASTX
                   g729775
NCBI GI
```

288

BLAST score-

Seq. No.

```
E value
                  2.0e-25
Match length
                  99
% identity
                  57
NCBI Description
                  HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION
                  FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)
                  >gi 100264 pir S25481 heat shock transcription factor 8 -
                  Peruvian tomato >gi 19492 emb CAA47869 (X67600) heat shock
                  transcription factor 8 [Lycopersicon peruvianum]
                  31030
Seq. No.
Contig ID
                  230087 1.R1040
5'-most EST
                  leu701154633.h1
Method
                  BLASTX
NCBI GI
                  g3386609
BLAST score
                  385
E value
                  2.0e-37
Match length
                  106
% identity
                  70
NCBI Description
                  (AC004665) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  31031
                  230100 1.R1040
Contig ID
5'-most EST
                  pmv700892449.h1
Method
                  BLASTX
NCBI GI
                  g4432857
BLAST score
                  285
E value
                  3.0e-25
Match length
                  159
                  38
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  31032
                  230108 1.R1040
Contig ID
5'-most EST
                  pmv700892457.h1
Seq. No.
                  31033
Contig ID
                  230110 1.R1040
5'-most EST
                  jC-gmle01810062h09d1
Seq. No.
                  31034
                  230129 1.R1040
Contig ID
5'-most EST
                  fua701043214.h1
Seq. No.
                  31035
                  230150 1.R1040
Contig ID
5'-most EST
                  pmv700892549.h1
Seq. No.
                  31036
                  230189 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400002b06a1
Seq. No.
                  31037
Contig ID
                  230231 1.R1040
5'-most EST
                  pmv700892623.h1
```

```
Contig ID
                   230253 2.R1040
5'-most EST
                   jC-gmst02400020c12a1
Method
                   BLASTX
NCBI GI
                   q3757521
BLAST score
                   268
E value
                   2.0e-23
Match length
                   98
% identity
NCBI Description
                   (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31039
Contig ID
                   230258 1.R1040
5'-most EST
                   pmv700892661.h1
                   31040
Seq. No.
Contig ID
                   230264 1.R1040
5'-most EST
                   pmv700892668.h1
Method
                   BLASTX
NCBI GI
                   q1730133
BLAST score
                   158
                   4.0e-10
E value
Match length
                   87
% identity
                   ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE
NCBI Description
                   3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
                   (ELAM-1 LIGAND FUCOSYLTRANSFERASE) >gi_105261_pir__A40976
                   alpha(1,3)-fucosyltransferase (EC 2.4.\overline{1}.-) - \overline{\text{human}}
                   >gi 1236720 (M65030) alpha(1,3)-fucosyltransferase [Homo
                   sapiens]
                   31041
Seq. No.
                   230319 1.R1040
Contig ID
5'-most EST
                   pmv700892794.h1
                   31042
Seq. No.
                   230343 2.R1040
Contig ID
5'-most EST
                   qsv701048887.hl
                   31043
Seq. No.
                   230382 1.R1040
Contig ID
                   pmv700892877.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3434969
BLAST score
                   168
                   2.0e-11
E value
Match length
                   107
% identity
                   44
NCBI Description
                   (AB008104) ethylene responsive element binding factor 2
                   [Arabidopsis thaliana]
                   31044
Seq. No.
Contig ID
                   230410 1.R1040
5'-most EST
                   pmv700892924.h1
Method
                   BLASTX
NCBI GI
                   g2191193
BLAST score
                   183
```

Method

BLASTX

```
Match length
                   153
% identity
                   29
NCBI Description
                   (AF007271) contain similarity to type 1 inositol
                   1,4,5-triphosphate receptors [Arabidopsis thaliana]
Seq. No.
Contig ID
                   230429 2.R1040
5'-most EST
                   jC-qmf102220131e01d1
Method
                   BLASTX
NCBI GI
                   q4006831
BLAST score
                   165
E value
                   3.0e-11
Match length
                   82
% identity
                   (AC005970) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31046
Contig ID
                   230430 1.R1040
5'-most EST
                   fC-gmle700877271f1
Method
                   BLASTX
NCBI GI
                   g2961358
BLAST score
                   231
E value
                   3.0e-19
Match length
                   105
                   48
% identity
                   (AL022140) serine/threonine protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   31047
Seq. No.
                   230467 1.R1040
Contig ID
                   pmv700894827.h1
5'-most EST
Seq. No.
                   31048
Contig ID
                   230484 1.R1040
                   gsv701048525.hl
5'-most EST
                   31049
Seq. No.
                   230496 1.R1040
Contig ID
                   leu701148894.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2160694
BLAST score
                   666
E value
                   3.0e-70
Match length
                   138
% identity
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31050
                   230500 1.R1040
Contig ID
                   asn701\overline{1}41708.h1
5'-most EST
                   31051
Seq. No.
Contig ID
                   230507 1.R1040
                   pmv700893055.h1
5'-most EST
```

Seq. No.

```
NCBI GI
                   q2618698
BLAST score
                   324
E value
                   4.0e-32
Match length
                   104
% identity
                   61
NCBI Description
                   (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31052
                   230521 1.R1040
Contig ID
5'-most EST
                   pmv700893071.h1
Seq. No.
                   31053
                   230522 1.R1040
Contig ID
5'-most EST
                   pmv700893072.h1
Seq. No.
                   31054
                   230527 1.R1040
Contig ID
5'-most EST
                   pmv700893083.h1
                   31055
Seq. No.
                   230545 1.R1040
Contig ID
5'-most EST
                   pmv700893117.h1
Method
                   BLASTX
                   g3334200
NCBI GI
                   390
BLAST score
                   4.0e-38
E value
Match length
                   94
% identity
                   GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE
NCBI Description
                   DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
                   >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor
                   [Solanum tuberosum]
Seq. No.
                   31056
                   230550 1.R1040
Contig ID
5'-most EST
                   zsg701122283.h1
                   31057
Seq. No.
Contig ID
                   230635 1.R1040
                   r1r700\overline{8}96343.h1
5'-most EST
                   31058
Seq. No.
                   230690 1.R1040
Contig ID
5'-most EST
                   g42826<del>3</del>7
Method
                   BLASTX
NCBI GI
                   g1346792
BLAST score
                   186
E value
                   7.0e-14
Match length
                   119
% identity
                   36
NCBI Description
                   DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE 49 KD SUBUNIT) (P49)
                   >gi_631124 pir S45630 DNA primase chain p48 - human
                   >gi_510406 emb CAA52377 (X74330) DNA primase (subunit p48)
                   [Homo sapiens] >gi 4506051 ref NP 000937.1 pPRIM1 primase,
                   polypeptide 1 (49k\overline{D})
```

Match length

```
230692 1.R1040
Contig ID
5'-most EST
                   pmv700893312.h1
Method
                   BLASTX
NCBI GI
                   g2911073
BLAST score
                   440
                   1.0e-43
E value
                   108
Match length
                   77
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   31060
Seq. No.
                   230743 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}05938.h1
Method
                   BLASTX
NCBI GI
                   g4220514
BLAST score
                   359
E value
                   5.0e - 34
Match length
                   115
% identity
NCBI Description
                   (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   230759 1.R1040
5'-most EST
                   uC-gmrominsoy142f10b1
Seq. No.
Contig ID
                   230783 1.R1040
5'-most EST
                   jC-gmf102220080a08a1
Seq. No.
                   230792 1.R1040
Contig ID
5'-most EST
                   pmv700893471.hl
                   31064
Seq. No.
                   230814 1.R1040
Contig ID
5'-most EST
                   pmv700893535.h1
    30 L
Seq. No.
                   31065
                   230818 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810009b11d1
Seq. No.
Contig ID
                   230875 1.R1040
5'-most EST
                   jC-qmf\overline{1}02220062d09a1
Seq. No.
Contig ID
                   230886 1.R1040
5'-most EST
                   pmv700893608.h1
                   31068
Seq. No.
                   231037 1.R1040
Contig ID -
5'-most EST
                   jC-gmle01810025d02a1
Method
                   BLASTX
NCBI GI
                   q3928084
BLAST score
                   316
E value
                   5.0e-29
```

Contig ID

```
% identity
NCBI Description
                   (AC005770) retrotransposon-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   31069
Contig ID
                   231050 1.R1040
5'-most EST
                   k11701\overline{2}13823.h1
                   BLASTX
Method
                   g2245066
NCBI GI
BLAST score
                   245
                   5.0e-21
E value
Match length
                   108
% identity
                   48
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   31070
Seq. No.
Contig ID
                   231057 1.R1040
5'-most EST
                   pmv700893864.hl
Seq. No.
                   31071
                   231103 1.R1040
Contig ID
5'-most EST
                   pxt700942790.hl
                   BLASTX
Method
NCBI GI
                   g2114104
BLAST score
                   653
E value
                   2.0e-68
Match length
                   167
                   70
% identity
                   (AB003590) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                   >gi_2114106_dbj_BAA20085_ (AB003591) sulfate transporter
                   [Arabidopsis thaliana]
Seq. No.
                   31072
Contig ID
                   231134 1.R1040
5'-most EST
                   gsv701\overline{0}45634.h1
Method
                   BLASTX
NCBI GI
                   q4455340
BLAST score
                   281
E value
                   2.0e-25
                   70
Match length
% identity
NCBI Description
                  (AL035522) putative protein [Arabidopsis thaliana]
                   31073
Seq. No.
Contig ID
                   231164 1.R1040
5'-most EST
                   jC-qmro02800031b11a1
                   31074
Seq. No.
                   231329 1.R1040
Contig ID
5'-most EST
                   pmv700894208.h1
                   31075
Seq. No.
                   231330 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}62070.h1
Seq. No.
                   31076
```

231337 1.R1040

```
5'-most EST
                   pmv700894217.h1
Method
                   BLASTX
NCBI GI
                   g1730630
BLAST score
                   298
E value
                   6.0e-27
Match length
                   164
% identity
                   41
                   HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III
NCBI Description
                   >gi 458956 (U00031) similar to cytoplasmic domain of
                   synaptobrevin [Caenorhabditis elegans]
                   31077
Seq. No.
                   231353 1.R1040
Contig ID
5'-most EST
                   fua701\overline{0}41207.h1
Seq. No.
                   31078
                   231383 1.R1040
Contig ID
5'-most EST
                   pmv700894269.h1
                   31079
Seq. No.
Contig ID
                   231396 1.R1040
5'-most EST
                   uC-gmflminsoy082f10b1
                   31080
Seq. No.
                   231404 1.R1040
Contig ID
5'-most EST
                   pmv700894293.h1
Seq. No.
                   31081
                   231435 1.R1040
Contig ID
5'-most EST
                   pmv700894335.h1
                   BLASTX
Method
NCBI GI
                   g3063469
BLAST score
                   185
E value
                   9.0e-14
Match length
                   127
% identity
                   40
                   (AC003981) F22013.31 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31082
                   231458 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400055f11d1
Seq. No.
                   31083
Contig ID
                   231476 1.R1040
5'-most EST
                   k11701\overline{2}02873.h1
                   31084
Seq. No.
Contig ID
                   231494 1.R1040
5'-most EST
                   jC-gmst02400053h06d1
Method
                   BLASTN
NCBI GI
                   g2293111
BLAST score
                   100
E value
                   7.0e-49
Match length
                   284
% identity
                   86
```

NCBI Description V.faba mRNA for potassium channel

```
31085
Seq. No.
                  231495 1.R1040
Contig ID
5'-most EST
                  asn701138631.h1
Method
                  BLASTX
NCBI GI
                  g3367519
BLAST score
                  197
                   3.0e-23
E value
Match length
                  82
% identity
NCBI Description
                   (AC004392) Contains similarity to gb U51898
                  Ca2+-independent phospholipase A2 from Rattus norvegicus.
                   [Arabidopsis thaliana]
Seq. No.
                   31086
Contig ID
                  231498 1.R1040
5'-most EST
                  jC-qmst02400052h08a1
Method
                  BLASTX
NCBI GI
                  g2894600
BLAST score
                  268
E value
                  2.0e-23
Match length
                  117
% identity
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                  31087
Seq. No.
Contig ID
                  231506 1.R1040
5'-most EST
                  uC-gmflminsoy046g09b1
Method
                  BLASTX
NCBI GI
                  q3142295
BLAST score
                  335
E value
                   3.0e-31
Match length
                   98
% identity
NCBI Description
                   (AC002411) Strong similarity to phosphoribosylanthranilate
                  transferase qb D86180 from Pisum sativum. [Arabidopsis
                  thaliana]
Seq. No.
                  31088
Contig ID
                  231540 1.R1040
5'-most EST
                  pmv700894468.hl
Seq. No.
                  31089
Contig ID
                  231568 1.R1040
5'-most EST
                  zsq701127162.h1
Method
                  BLASTN
NCBI GI
                  q3860320
BLAST score
                  83
E value
                  1.0e-38
Match length
                  190
% identity
                  87
                  Cicer arietinum mRNA for beta-galactosidase, clone
NCBI Description
                  CanBGal-5
Seq. No.
                  31090
Contig ID
                  231568 2.R1040
```

 $r1r700\overline{9}01926.h1$

BLASTN

5'-most EST Method

```
g3860320
NCBI GI
BLAST score
                   253
E value
                   1.0e-140
Match length
                   648
% identity
                   85
                  Cicer arietinum mRNA for beta-galactosidase, clone
NCBI Description
                   CanBGal-5
Seq. No.
                   31091
Contig ID
                   231588 1.R1040
5'-most EST
                   pmv700894539.h1
Seq. No.
                   31092
Contig ID
                   231639 1.R1040
5'-most EST
                   jC-qmst02400061h01a1
Method
                   BLASTX
                   q4567304
NCBI GI
BLAST score
                   340
                   9.0e-32
E value
Match length
                   183
% identity
NCBI Description
                   (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                   231691 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy007g03b1
                   31094
Seq. No.
                   231761 1.R1040
Contig ID
5'-most EST
                   pmv700894763.hl
Seq. No.
                   31095
Contig ID
                   231800 1.R1040
5'-most EST
                   r1r700896970.h1
Method
                   BLASTX
NCBI GI
                   q3128210
BLAST score
                   316
                                           , î.,
                   4.0e-54
E value
                   198
Match length
% identity
                   (AC004077) putative cytochrome P450 protein [Arabidopsis
NCBI Description
                   thaliana] >gi 3337378 (AC004481) putative cytochrome P450
                   protein [Arabidopsis thaliana]
                   31096
Seq. No.
                   231803 1.R1040
Contig ID
5'-most EST
                  q4304935
Seq. No.
                   31097
                   231810 1.R1040
Contig ID
                   asn701133583.h2
5'-most EST
                  BLASTN
Method
                   g1223915
NCBI GI
BLAST score
                   203
E value
                   1.0e-110
                   255
Match length
```

95

% identity

5'-most EST

Method

```
NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds
                   31098
Seq. No.
Contig ID
                   231856 1.R1040
5'-most EST.
                   pmv700894885.h1
Method
                   BLASTX
                   g4455284
NCBI GI
BLAST score
                   410
                   4.0e-40
E value
                   112 .
Match length
% identity
                   69
NCBI Description
                   (AL035527) beta-glucosidase-like protein [Arabidopsis
                   thaliana]
                   31099
Seq. No.
Contig ID
                   231857 1.R1040
5'-most EST
                   uC-gmrominsoy229c05b1
Seq. No.
                   31100
                   231881_1.R1040
Contig ID
5'-most EST
                  pmv700894927.h1
Seq. No.
                   31101
                   231887 1.R1040
Contig ID
5'-most EST
                  pmv700894938.h1
Seq. No.
                   31102
Contig ID
                   231981 1.R1040
5'-most EST
                  pmv700895087.h1
Method
                  BLASTN
NCBI GI
                   g22738
BLAST score
                   147
E value
                   4.0e-77
Match length
                   259
% identity
                   94
NCBI Description
                  G.max mitochondrial atpA
Seq. No.
                   31103
Contig ID
                   231984 1.R1040
5'-most EST
                  pmv700895091.h1
                   31104
Seq. No.
                  232044 1.R1040
Contig ID
5'-most EST
                  pmv700895173.hl
Method
                  BLASTX
NCBI GI
                  g2160156
BLAST score
                  578
E value
                  8.0e-60
                  145
Match length
% identity
NCBI Description
                   (ACO00132) Strong similarity to S. pombe leucyl-tRNA
                  synthetase (gb Z73100). [Arabidopsis thaliana]
Seq. No.
                  31105
                  232062 1.R1040
Contig ID
```

pmv700895196.h1

BLASTX

```
NCBI GI
                   g4508068
BLAST score
                   390
                   1.0e-37
E value
                   142
Match length
                   58
% identity
NCBI Description
                   (AC005882) 3063 [Arabidopsis thaliana]
Seq. No.
                   31106
                   232119 1.R1040
Contig ID
5'-most EST
                   uC-gmropic006c04b1
Seq. No.
                   31107
                   232120 1.R1040
Contig ID
5'-most EST
                   zsq701127724.h1
Method
                   BLASTN
NCBI GI
                   g2924733
BLAST score
                   46
E value
                   1.0e-16
                   230
Match length
                   80
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31108
                   232159 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy188g02b1
Method
                   BLASTX
NCBI GI
                   g4468985
BLAST score
                   152
E value
                   9.0e-10
Match length
                   60
% identity
NCBI Description
                   (AL035605) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31109
                   232207 1.R1040
Contig ID
5'-most EST
                   rry700808389.hl
                   BLASTX
Method
NCBI GI
                   g4249404
BLAST score
                   295
                   6.0e-27
E value
Match length
                   89
% identity
                   64
                   (AC006072) putative nuclear protein SA-1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31110
                   232221 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}55274.h1
Seq. No.
                   31111
                   232294 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910023e01d1
                   BLASTX
Method
                   g3080420
NCBI GI
BLAST score
                   751
```

Method

BLASTX

```
Match length
                   171
                   82
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31112
                   232321 1.R1040
Contig ID
5'-most EST
                   g4313762
Method
                   BLASTX
NCBI GI
                   g2460200
BLAST score
                   375
E value
                   8.0e-36
Match length
                   147
% identity
                   54
NCBI Description
                   (AF020833) eukaryotic translation initiation factor 3
                   subunit [Homo sapiens]
Seq. No.
                   31113
Contig ID
                   232321 2.R1040
5'-most EST
                   uC-gmrominsoy180f04b1
Seq. No.
                   31114
                   232377 1.R1040
Contig ID
5'-most EST
                   uC-gmropic058d02b1
Method
                   BLASTX
NCBI GI
                   g2501011
BLAST score
                   495
E value
                   5.0e-50
Match length
                   159
% identity
                   56
                   ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
NCBI Description
                   >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA
synthetase [Synechocystis sp.]
Seq. No.
                   31115
                   232381 1.R1040
Contig ID
5'-most EST
                   pxt700941004.hl
Seq. No.
                   31116
                   232394 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir043h04b1
Method
                   BLASTX
NCBI GI
                   g1407705
BLAST score
                   721
E value
                   2.0e-76
Match length
                   158
                   79
% identity
NCBI Description
                   (U60202) lipoxygenase [Solanum tuberosum]
Seq. No.
                   31117
                   232397 1.R1040
Contig ID
5'-most EST
                   zsg701122060.hl
Seq. No.
                   31118
                   232422_1.R1040
Contig ID
5'-most EST
                   pxt700941055.h1
```

```
NCBI GI
                   g2501231
BLAST score
                   392
                   2.0e-47
E value
Match length
                   118
% identity
                   76
NCBI Description
                  HYPOTHETICAL 38.1 KD PROTEIN >gi 99505 pir S24930
                   hypothetical protein - pink corydalis
                   >qi 18258 emb CAA45139 (X63595) protein of unknown
                   function [Corydalis sempervirens] >gi 444333 prf 1906382A
                   pCSC71 protein [Corydalis sempervirens]
Seq. No.
                   31119
Contig ID
                   232443 1.R1040
5'-most EST
                   jC-gmro02910006a02d1
Seq. No.
                   31120
Contig ID
                   232474 1.R1040
5'-most EST
                  pxt700941117.h1
Method
                  BLASTX
NCBI GI
                   q4406819
BLAST score
                   549
E value
                   3.0e-56
Match length
                  155
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31121
                   232503 1.R1040
Contig ID
5'-most EST
                  pxt700941149.hl
Seq. No.
                   31122
Contig ID
                   232518 1.R1040
5'-most EST
                  k11701\overline{2}11586.h1
Seq. No.
                   31123
Contig ID
                  232519 1.R1040
5'-most EST
                   leu701148185.h1
                  BLASTN
Method '
NCBI GI
                  g3688527
BLAST score
                  185
                   1.0e-99
E value
Match length
                  512
% identity
                  84
NCBI Description Pisum sativum mRNA for TPE4A thiol-protease
Seq. No.
                   31124
                  232560 1.R1040
Contig ID
5'-most EST
                  zsq701\overline{1}28408.h1
Method
                  BLASTX
NCBI GI
                  g2285885
BLAST score
                  327
                   9.0e-31
E value
                  90
Match length
% identity
NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]
```

31125

Seq. No.

```
Contig ID
                    232565 1.R1040
  5'-most EST
                    pxt700941226.hl
  Method
                    BLASTX
  NCBI GI
                    q3236235
  BLAST score
                    215
  E value
                    3.0e-17
  Match length
                    79
  % identity
  NCBI Description
                    (AC004684) unknown protein [Arabidopsis thaliana]
                    >qi 4056501 (AC005896) unknown protein [Arabidopsis
                    thaliana]
                    31126
  Seq. No.
  Contig ID
                    232574 1.R1040
  5'-most EST
                    jC-gmle01810078d12d1
 Method
                    BLASTN
  NCBI GI
                    q169956
  BLAST score
                    91
                    2.0e-43
  E value
 Match length
                    280
  % identity
                    90
 NCBI Description
                    Glycine max G-box binding factor (GBF1) mRNA, complete cds
                    31127
  Seq. No.
                    232634 1.R1040
 Contig ID
  5'-most EST
                    g4305763
Method
                    BLASTX
                    g4510381
 NCBI GI
 BLAST score
                    203
 E value
                    8.0e-16
 Match length
                    98
  % identity
                    45
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    31128
                    232640 1.R1040
 Contig ID
  5'-most EST
                    jC-qmst02400028e04a1
 Method
                    BLASTX
 NCBI GI
                    g3046815
 BLAST score
                    162
 E value
                    3.0e-11
 Match length
                    118
  % identity
 NCBI Description
                   (AL021687) cytochrome P450 [Arabidopsis thaliana]
  Seq. No.
                    31129
                    232656 1.R1040
 Contig ID
  5'-most EST
                    pxt700941358.hl
 Seq. No.
                    31130
                    232738 1.R1040
 Contig ID
                    jC-gmf\overline{1}02220102e12a1
 5'-most EST
                    31131
 Seq. No.
 Contig ID
                    232777 1.R1040
```

 $g42926\overline{5}3$

5'-most EST

```
Seq. No.
                  31132
                  232787 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir033h06b1
Method
                  BLASTX
NCBI GI
                  q3033375
BLAST score
                  546
E value
                  7.0e-56
Match length
                  190
% identity
NCBI Description
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
                  31133
Seq. No.
Contig ID
                  232794 1.R1040
5'-most EST
                  jC-gmle01810066c12a1
                  31134
Seq. No.
Contig ID
                  232814 1.R1040
5'-most EST
                  pxt700942401.h1
                  BLASTX
Method
NCBI GI
                  q3176686
BLAST score
                  394
                  1.0e-38
E value
                  89
Match length
% identity
                  82
                  (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                  HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                  [Arabidopsis thaliana]
Seq. No.
                  31135
                  232849 1.R1040
Contig ID
5'-most EST
                  pxt700941795.hl
Seq. No.
                  31136
                  232888 1.R1040
Contig ID
5'-most EST
                  uC-gmropic074d08b1
Method
                  BLASTN
NCBI GI
                  g4159703
BLAST score
                  34
                  1.0e-09
E value
                  58
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  31137
                  232892 1.R1040
Contig ID
5'-most EST
                  epx701109856.hl
Seq. No.
                  31138
                  232954 1.R1040
Contig ID
5'-most EST
                  pxt700942963.h1
                  BLASTX
Method
NCBI GI
                  q4539404
BLAST score
                  343
                  6.0e-32
E value
```

127

Match length

BLAST score

```
% identity
 NCBI Description
                    (AL049524) putative protein [Arabidopsis thaliana]
 Seq. No.
 Contig ID
                    232976 1.R1040
 5'-most EST
                    k11701\overline{2}06489.h1
                    BLASTX
 Method
 NCBI GI
                    a1169128
 BLAST score
                    284
                    9.0e-26
 E value
 Match length
                    87
                    62
 % identity
                    SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789)
 NCBI Description
                    protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                    protein kinase [Arabidopsis thaliana]
 Seq. No.
                    31140
 Contig ID
                    232995 1.R1040
 5'-most EST
                    uC-gmrominsoy262b07b1
                    31141
 Seq. No.
 Contig ID
                    233012 1.R1040
                    leu701151389.hl
 5'-most EST
                    31142
 Seq. No.
                   233044 1.R1040
 Contig ID
 5'-most EST
                    uC-gmflminsoy012f10b1
 Method
                    BLASTX
 NCBI GI
                    g3687833
 BLAST score
                    317
                    2.0e-30
 E value
 Match length
                    90
 % identity
 NCBI Description (AF069737) notchless [Xenopus laevis]
 Seq. No.
                    31143
 Contig ID
                    233047 1.R1040
                    pxt700942390.h1
 5'-most EST
 Seq. No.
                    31144
                    233103 1.R1040
 Contig ID
 5'-most EST
                    pxt700945970.h1
 Method
                    BLASTX
 NCBI GI
                    g3426048
                    221
 BLAST score
 E value
                    2.0e-18
 Match length
                    88
 % identity
                    (AC005168) putative hydroxymethylglutaryl-CoA lyase
 NCBI Description
                    precursor [Arabidopsis thaliana]
 Seq. No.
                    31145
                    233110 1.R1040
 Contig ID
 5'-most EST
                    gsv701\overline{0}46923.h1
 Method
                    BLASTX
 NCBI GI
                    g4522004
```

Match length

```
3.0e-19
E value
Match length
                   53
                   77
% identity
                   (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31146
Contig ID
                   233177 1.R1040
5'-most EST
                   jC-qmro02910037d08d1
                  BLASTX
Method
NCBI GI
                   q1049022
BLAST score
                   207
                   4.0e-16
E value
                   96
Match length
% identity
NCBI Description
                  (U25696) transcription factor SaMADS A [Sinapis alba]
                   31147
Seq. No.
                 233203 2.R1040
Contig ID
                  pxt700942656.h1
5'-most EST
                   31148
Seq. No.
                   233291 1.R1040
Contig ID
                  pxt700942779.h1
5'-most EST
                   31149
Seq. No.
                   233324 1.R1040
Contig ID
5'-most EST
                   g4289918
Method
                   BLASTN
                   g4388714
NCBI GI
BLAST score
                   36
                   2.0e-10
E value
Match length
                   40
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC F5K7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31150
                   233406 1.R1040
Contig ID
5'-most EST
                   pxt700942954.hl
Seq. No.
                   31151
Contig ID
                   233424 1.R1040
5'-most EST
                   leu701156434.hl
Seq. No.
                   31152
                   233429 1.R1040
Contig ID
5'-most EST
                  q55101\overline{6}3
Seq. No.
                   31153
                   233434 1.R1040
Contig ID
5'-most EST
                   pxt700942995.hl
Method
                   BLASTX
NCBI GI
                   q4467108
BLAST score
                   359
                   1.0e-34
E value
                   75
```

5'-most EST

```
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                  233447 1.R1040
5'-most EST
                  zsg701121850.h1
                  BLASTX
Method
NCBI GI
                  q3738339
BLAST score
                  698
                  7.0e-74
E value
Match length
                  157
                  85
% identity
                  (AC005170) putative kinase [Arabidopsis thaliana]
NCBI Description
                  31155
Seq. No.
Contig ID
                  233460 1.R1040
5'-most EST
                  pxt700943027.hl
Seq. No.
                  31156
                  233463 1.R1040
Contig ID
                  pxt700943031.h1
5'-most EST
Seq. No.
                  31157
                  233497 1.R1040
Contig ID
5'-most EST
                  g4313707
                  BLASTX
Method
NCBI GI
                  g3924596
BLAST score
                  716
E value
                  5.0e-76
Match length
                  140
% identity
                  97
NCBI Description
                   (AF069442) putative phospho-ser/thr phosphatase
                   [Arabidopsis thaliana]
                  31158
Seq. No.
Contig ID
                  233600 1.R1040
5'-most EST
                  jC-gmst02400027e10a1
Seq. No.
                  31159
Contig ID
                  233619 1.R1040
5'-most EST
                  pxt700943247.hl
                  BLASTN
Method
NCBI GI
                  g1752733
BLAST score
                  95
E value
                  4.0e-46
Match length
                  258
% identity
NCBI Description
                  Glycine max mRNA for beta-glucan-elicitor receptor,
                  complete cds
                  31160
Seq. No.
                  233644 1.R1040
Contig ID
5'-most EST
                  pxt700943279.h1
Seq. No.
                  31161
                  233691_1.R1040
Contig ID
```

uC-gmropic021g02b1

```
BLASTX
Method
 NCBI GI
                    g3025447
                   175
 BLAST score
                    2.0e-12
 E value
                   116
 Match length
                    29
 % identity
 NCBI Description (ACO04528) R32184_3 [Homo sapiens]
 Seq. No.
                    31162
                    233776 1.R1040
 Contig ID
                   pxt700943441.hl
 5'-most EST
                   BLASTN
 Method
 NCBI GI
                    q603870
 BLAST score
                    36
 E value
                    1.0e-10
                    99
 Match length
                    89
 % identity
 NCBI Description
                   P.hybrida mRNA for MAP/ERK kinase
 Seq. No.
                    31163
                    233810 1.R1040
 Contig ID
 5'-most EST
                    jC-gmro02800041g06a1
                   BLASTX
 Method
 NCBI GI
                    g3193316
 BLAST score
                    328
 E value
                    6.0e-44
 Match length
                    138
 % identity
                    68
                    (AF069299) contains similarity to nucleotide sugar
 NCBI Description
                    epimerases [Arabidopsis thaliana]
 Seq. No.
                    31164
                    233811 1.R1040
 Contig ID
                    g50575\overline{5}1
 5'-most EST
 Method
                   BLASTN
 NCBI GI
                    g4336435
 BLAST score
                   83
 E value
                    1.0e-38
                    207
 Match length
 % identity
                    85
                   Lotus japonicus protein phosphatase type 2C (PP2C2) mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    31165
 Contig ID
                    233849 1.R1040
                    jC-gmfl02220114f05d1
 5'-most EST
 Seq. No.
                    31166
                    233865 1.R1040
 Contig ID
 5'-most EST
                   pxt700944432.hl
                    31167
 Seq. No.
                    233890 1.R1040
 Contig ID
 5'-most EST
                   pxt700943586.h1
 Seq. No.
                    31168
                   233891 1.R1040
 Contig ID
```

Contig ID

```
5'-most EST
                   leu701151322.h1
                  BLASTN
Method
                   g3046856
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
                   45
Match length
                   96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI22, complete sequence [Arabidopsis thaliana]
                   31169
Seq. No.
                   233892 1.R1040
Contig ID
                  pxt700943588.h1
5'-most EST
                   31170
Seq. No.
                  233947 1.R1040
Contig ID
5'-most EST
                  pxt700943659.h1
                   31171
Seq. No.
                   233982 1.R1040
Contig ID
5'-most EST
                  pxt700943708.hl
Method
                  BLASTX
NCBI GI
                  g2832300
BLAST score
                   430
E value
                   2.0e-42
                  114
Match length
                   70
% identity
                   (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                  roseus]
Seq. No.
                   31172
                   233985 1.R1040
Contig ID
                  pxt700943711.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2194125
BLAST score
                   307
E value
                   4.0e-28
Match length
                   104
% identity
                   63
NCBI Description
                   (AC002062) ESTs gb R30459, gb N38441 come from this gene.
                   [Arabidopsis thaliana]
                   31173
Seq. No.
                   233992 1.R1040
Contig ID
5'-most EST
                  pxt700943718.hl
Method
                  BLASTX
NCBI GI
                  g3885344
                  157
BLAST score
                   9.0e-11
E value
Match length
                  77
                   42
% identity
                   (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4557057 gb AAD22497.1 AC007154 1 (AC007154) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  31174
```

234013 2.R1040

```
5'-most EST
                   pxt700943740.h1
Seq. No.
                   31175
                   234033 1.R1040
Contig ID
5'-most EST
                   pxt700943766.h1
Method
                   BLASTN
NCBI GI
                   g1816649
BLAST score
                   322
E value
                   0.0e + 00
Match length
                   437
                   94
% identity
                   Lupinus luteus NADH plastiquinone oxidoreductase subunit {\tt J}
NCBI Description
                   (ndhJ) gene, chloroplast gene encoding chloroplast protein,
                   complete cds
                   31176
Seq. No.
Contig ID
                   234054 1.R1040
5'-most EST
                   qsv701\overline{0}53970.h1
Seq. No.
                   31177
                   234083 1.R1040
Contig ID
                   fua701\overline{0}38173.h1
5'-most EST
                   31178
Seq. No.
                   234101 1.R1040
Contig ID
                   fC-gms\u00e4700652534d5
5'-most EST
                   BLASTN
Method
NCBI GI
                   g294667
BLAST score
                   47
                   3.0e-17
E value
Match length
                   59
% identity
                   95
                   Castor bean chloroplast beta-ketoacyl-ACP synthase (50 kDa
NCBI Description
                   synthase) mRNA, complete cds
Seq. No.
                   31179
                   234102 1.R1040
Contig ID
5'-most EST
                   g4285233
                   BLASTX
Method
NCBI GI
                   g2130073
BLAST score
                   269
E value
                   8.0e-24
Match length
                   60
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi_786178 dbj_BAA08845 (D50307) aldolase
                   C-1 [Oryza sativa] > \overline{gi} 790970 dbj_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
Seq. No.
                   31180
                   234107 1.R1040
Contig ID
                   pxt700943860.hl
5'-most EST
                   31181
Seq. No.
Contig ID
                   234181 1.R1040
                   jC-gmro02910056b03a1
5'-most EST
```

Seq. No.

```
Seq. No.
                   31182
Contig ID
                 - 234235 1.R1040
5'-most EST
                   pxt700944032.h1
Method
                   BLASTX
NCBI GI
                   g3540207
BLAST score
                   617
E value
                   3.0e-64
Match length
                   157
                   75
% identity
                   (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   31183
Seq. No.
                   234236 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy100h09b1
Seq. No.
                   31184
                   234264 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}98034.h1
Method
                   BLASTX
NCBI GI
                   g2344889
BLAST score
                   208
E value
                   5.0e-17
                   92
Match length
                   48
% identity
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31185
                   234286 1.R1040
Contig ID
5'-most EST
                   pxt700944094.h1
Seq. No.
                   31186
                   234329 1.R1040
Contig ID
5'-most EST
                   fua701037891.hl
                   BLASTX
Method
NCBI GI
                   g4522009
BLAST score
                   293
E value
                   8.0e-27
Match length
                   87
% identity
NCBI Description
                   (AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31187
                   234346 1.R1040
Contig ID
5'-most EST
                   uC-gmropic020d05b1
Seq. No.
                   31188
                   234356 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400036b09a1
Method
                   BLASTX
NCBI GI
                   q2281090
BLAST score
                   183
                   8.0e-16
E value
Match length
                   82
                   52
% identity
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
```

Contig ID

5'-most EST

```
234451 1.R1040
Contig ID
5'-most EST
                   q42604\overline{3}7
Method
                   BLASTX
NCBI GI
                   g1698548
BLAST score
                   752
E value
                   4.0e-80
Match length
                   170
% identity
                   82
                   (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                   31190
                   234520 1.R1040
Contig ID
                   jC-gmf\overline{1}02220144g09d1
5'-most EST
                   31191
Seq. No.
Contig ID
                   234550 1.R1040
5'-most EST
                   pxt700944454.hl
                   31192
Seq. No.
                   234605 1.R1040
Contig ID
5'-most EST
                   pxt700944523.h1
                   31193
Seq. No.
                   234645 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400031g10d1
                   31194
Seq. No.
                   234648 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400067g01d1
                   31195
Seq. No.
                   234712 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy041d08b1
                   BLASTX
Method
NCBI GI
                   g2462931
BLAST score
                   527
E value
                   7.0e-54
Match length
                   141
                   76
% identity
                   (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31196
Contig ID
                   234735 1.R1040
5'-most EST
                   pxt700944676.h1
Method
                   BLASTX
                   g3758859
NCBI GI
BLAST score
                   199
                   3.0e-15
E value
                   104
Match length
                   35
% identity
                   (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w),
NCBI Description
                   Hypothetical protein, len: 222 aa [Plasmodium falciparum]
Seq. No.
                   31197
```

234778 1.R1040

uC-gmronoir005h03b1

```
BLASTX
Method
NCBI GI
                   g3176686
BLAST score
                   459
E value
                   4.0e-46
Match length
                   106
% identity
                   81
NCBI Description
                   (AC003671) Similar to high affinity potassium transporter,
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   31198
Seq. No.
                   234805 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy098b01b1
                   31199
Seq. No.
Contig ID
                   234825 1.R1040
5'-most EST
                   gsv701\overline{0}46932.h1
Method
                   BLASTX
NCBI GI
                   g3395428
BLAST score
                   217
                   3.0e-17
E value
                   88
Match length
% identity
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31200
                   234834 1.R1040
Contig ID
5'-most EST
                   pxt700944808.hl
                   31201
Seq. No.
                   234852 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy100c03b1
Method
                   BLASTX
NCBI GI
                   g4580395
                   547
BLAST score
E value
                   3.0e-56
Match length
                   124
                   87
% identity
                   (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                   thaliana]
                   31202
Seq. No.
                   234895 1.R1040
Contig ID
5'-most EST
                   uC-gmropic112b01b1
Method
                   BLASTX
NCBI GI
                   g3420052
BLAST score
                   686
E value
                   2.0e-72
Match length
                   166
                   80
% identity
NCBI Description
                   (AC004680) putative ubiqinone reductase [Arabidopsis
                   thaliana]
                   31203
Seq. No.
                   234907 1.R1040
Contig ID
```

4773

1.58

 $k11701\overline{2}08476.h1$

BLASTX

5'-most EST Method

5'-most EST

```
NCBI GI
                  g2914710
BLAST score
                   421
                   1.0e-41
E value
                   108
Match length
% identity
NCBI Description
                   (AC003974) putative beta-D-galactosidase [Arabidopsis
                  thaliana]
                   31204
Seq. No.
                   234960 1.R1040
Contig ID
5'-most EST
                  g5342711
Seq. No.
                  31205
                  234975 1.R1040
Contig ID
                  pxt700944980.h1
5'-most EST
Seq. No.
                  31206
Contig ID
                  234998_1.R1040
5'-most EST
                  jC-gmle01810042c03a1
                  31207
Seq. No.
Contig ID
                  235000 1.R1040
                  k11701206129.h1
5'-most EST
                  31208
Seq. No.
Contig ID
                  235028 1.R1040
5'-most EST
                  asn701137793.h1
                  BLASTX
Method
NCBI GI
                  g3080427
BLAST score
                   425
E value
                   3.0e-42
Match length
                  96
% identity
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
                  31209
Seq. No.
                  235048 1.R1040
Contig ID
5'-most EST
                  pxt700945073.hl
                  31210
Seq. No.
                  235121 1.R1040
Contig ID
5'-most EST
                  pxt700945164.hl
Seq. No.
                  31211
                  235134 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy057h02b1
Method
                  BLASTN
NCBI GI
                  q4193319
BLAST score
                  131
E value
                  2.0e-67
Match length
                  325
% identity
                  88
NCBI Description Zea mays histone deacetylase (hdlb) mRNA, complete cds
Seq. No.
                  31212
                  235173 1.R1040
Contig ID
```

 $jC-gmf\overline{1}02220130c12d1$

```
Seq. No.
                    31213
 Contig ID
                    235182 1.R1040
 5'-most EST
                    uC-gmrominsoy201a03b1
 Method
                    BLASTX
 NCBI GI
                    q4567311
 BLAST score
                    176
 E value
                    1.0e-12
 Match length
                    52
 % identity
                    (AC005956) putative protein kinase [Arabidopsis thaliana]
 NCBI Description
                    31214
 Seq. No.
 Contig ID
                    235238 1.R1040
 5'-most EST
                    jC-gmf\overline{1}02220073e02a1
 Method
                    BLASTX
 NCBI GI
                    g2827621
 BLAST score
                    411
                    5.0e-40
 E value
 Match length
                    207
                    49
 % identity
 NCBI Description
                    (AL021636) putative protein [Arabidopsis thaliana]
 Seq. No.
                    31215
                    235281 1.R1040
 Contig ID
 5'-most EST
                    pxt700945368.hl
 Method
                    BLASTN
 NCBI GI
                    g1946219
 BLAST score
                    120
                    1.0e-60
 E value
                    284
 Match length
 % identity
                    86
 NCBI Description M.domestica mRNA for kn1-like protein (1791 bp)
                    31216
 Seq. No.
 Contig ID
                    235318 1.R1040
 5'-most EST
                    pxt700945415.hl
                    31217
 Seq. No.
 Contig ID
                    235357 1.R1040
 5'-most EST
                    uC-gmflminsoy025e06b1
 Seq. No.
                    31218
 Contig ID
                    235369 1.R1040
 5'-most EST
                    jC-gmle01810025a10a1
                    31219
 Seq. No.
 Contig ID
                    235441 1.R1040
 5'-most EST
                    jC-gmle01810005h06a1
                    31220
 Seq. No.
 Contig ID
                    235573 1.R1040
 5'-most EST
                    uC-gmropic103d04b1
 Method
                    BLASTX
 NCBI GI
                    q3608154
 BLAST score
                    334
```

```
173
Match length
% identity
                  42
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31221
                  235586 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910046d04d1
Method
                  BLASTX
NCBI GI
                  q1698582
BLAST score
                  459
E value
                  1.0e-45
Match length
                  133
% identity
NCBI Description
                  (U60767) integral membrane protein OsNramp3 [Oryza sativa]
Seq. No.
Contig ID
                  235648 1.R1040
5'-most EST
                  jC-gmle01810071e05a1
                  BLASTX
Method
NCBI GI
                  q3549665
BLAST score
                  174
E value
                  2.0e-12
                  54
Match length
% identity
                  (AL031394) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31223
                  235667 1.R1040
Contig ID
5'-most EST
                  pxt700945888.hl
Method
                  BLASTX
NCBI GI
                  g3176965
BLAST score
                  513
                  3.0e-52
E value
                  149
Match length
% identity
                  66
                  (AF067967) pyrroline-5-carboxylate synthetase
NCBI Description
                  [Mesembryanthemum crystallinum]
                  31224
Seq. No.
                  235750 1.R1040
Contig ID
5'-most EST
                  pxt700946018.h1
Seq. No.
                  31225
                  235765 1.R1040
Contig ID
5'-most EST
                  pxt700946037.hl
Seq. No.
                  31226
                  235818 1.R1040
Contig ID
5'-most EST
                  pxt700946108.hl
                  31227
Seq. No.
                  235819 1.R1040
Contig ID
5'-most EST
                  pxt700946110.h1
Method
                  BLASTX
NCBI GI
                  g2160190
BLAST score
                  239
```

```
85
Match length
% identity
                   66
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31228
                  235845 1.R1040
Contig ID
                  zsg701125748.h1
5'-most EST
Seq. No.
                  31229
Contig ID
                  235851 1.R1040
5'-most EST
                  pxt700946153.h1
Seq. No.
                  31230
Contig ID
                  235908 1.R1040
5'-most EST
                  jC-qmro02800025a03a1
Seq. No.
                  31231
Contig ID
                  235917 1.R1040
5'-most EST
                  q4405652
Method
                  BLASTX
NCBI GI
                  q2244989
BLAST score
                   480
E value
                   4.0e-48
Match length
                  143
% identity
                   66
NCBI Description
                   (Z97340) strong similarity to naringenin 3-dioxygenase
                   [Arabidopsis thaliana]
                  31232
Seq. No.
Contig ID
                  235958 1.R1040
5'-most EST
                  pxt700946285.hl
Method
                  BLASTX
NCBI GI
                  g2102679
BLAST score
                  371
E value
                  2.0e-35
Match length
                  91
% identity
NCBI Description
                   (U07424) putative tRNA synthetase-like protein [Homo
                  sapiens] >gi_4104935_gb_AAD02221_ (AF042347) putative
                  phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo
                  sapiens]
Seq. No.
                  31233
Contig ID
                  235998 1.R1040
5'-most EST
                  uC-gmrominsoy048f03b1
Seq. No.
                  31234
Contig ID
                  236021 1.R1040
5'-most EST
                  pxt700946367.hl
                  31235
Seq. No.
Contig ID
                  236047 1.R1040
5'-most EST
                  pxt700946396.h1
Method
                  BLASTX
NCBI GI
                  q4538929
BLAST score
                  223
```

```
65
Match length
% identity
                   60
NCBI Description
                   (AL049483) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   31236
Contig ID
                   236062 1.R1040
5'-most EST
                   pxt700946416.h1
Method
                   BLASTX
NCBI GI
                   g4510421
BLAST score
                   169
E value
                   1.0e-11
Match length
                   52
% identity
                  (AC006929) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31237
Contig ID
                   236072 1.R1040
5'-most EST
                   pxt700946428.h1
Method
                   BLASTX
                   q4455260
NCBI GI
BLAST score
                   515
                   1.0e-52
E value
Match length
                   102
% identity
                   (AL035353) protein kinase-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31238
Contig ID
                   236084 1.R1040
5'-most EST
                   pxt700946462.h1
Seq. No.
                   31239
                   236133 1.R1040
Contig ID
                   jC-gmr<sub>0</sub>02910039c11d1
5'-most EST
                   31240
Seq. No.
Contig ID
                   236168 1.R1040
                   cf1700\overline{8}63553.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2213592
BLAST score
                   386
E value
                   4.0e-38
Match length
                   139 🕝
% identity
                  (AC000348) T7N9.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   236208 1.R1040
5'-most EST
                   uC-gmrominsoy216g12b1
Method
                   BLASTX
NCBI GI
                   g4191789
BLAST score
                   270
E value
                   1.0e-42
Match length
                   119
% identity
                   76
NCBI Description (AC005917) putative transmembrane transport protein
```

5'-most EST

.



[Arabidopsis thaliana]

```
Seq. No.
                   31242
                   236251 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir006c12b1
                   BLASTX
Method
NCBI GI
                   q4454039
BLAST score
                   247
                   5.0e-21
E value
Match length
                   151
% identity
                   (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31243
Contig ID
                   236262 1.R1040
5'-most EST
                   uC-gmrominsoy207a08b1
Seq. No.
                   31244
Contig ID
                   236269 1.R1040
5'-most EST
                   fC-qmf1700863687y1
Method
                  BLASTX
NCBI GI
                   g2494742
BLAST score
                   775
E value
                   1.0e-158
Match length
                   334
% identity
                   78
NCBI Description
                  GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)
                   >gi_2104791_emb CAA73235 (Y12704) glutamine synthetase
                   [Agaricus bisporus]
                   31245
Seq. No.
Contig ID
                   236290 1.R1040
5'-most EST
                  epx701\overline{1}04704.h1
                   31246
Seq. No.
Contig ID
                   236341 1.R1040
5'-most EST
                  jC-gmro02910069g10d1
                   31247
Seq. No.
Contig ID
                   236348 1.R1040
5'-most EST
                  asn701135735.hl
Seq. No.
                   31248
Contig ID
                  236406 1.R1040
5'-most EST
                  q5057320
Method
                  BLASTX
NCBI GI
                  q4559340
BLAST score
                  174
                   2.0e-12
E value
                  51
Match length
% identity
NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31249
Contig ID
                  236412 1.R1040
```

uC-gmrominsoy268h10b1

Seq. No.

```
31250
Seq. No.
Contig ID
                  236477 1.R1040
5'-most EST
                  rlr700895772.h1
Seq. No.
                  31251
Contig ID
                  236492 1.R1040
5'-most EST
                  rlr700895654.h1
Method
                  BLASTX
NCBI GI
                  g1255448
BLAST score
                  316
E value
                   6.0e-29
Match length
                  90
% identity
                  71
NCBI Description
                   (D50468) mitogen-activated protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  31252
                  236524 1.R1040
Contig ID
5'-most EST
                  asn701139977.hl
                  BLASTX
Method
NCBI GI
                  g2252840
BLAST score
                  308
                  8.0e-36
E value
                  158
Match length
% identity
                   47
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                  31253
                  236544 1.R1040
Contig ID
5'-most EST
                  rlr700895727.hl
Method
                  BLASTX
                  q2462822
NCBI GI
BLAST score
                  333
                  5.0e-31
E value
                  110
Match length
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31254
                  236620 1.R1040
Contig ID
5'-most EST
                  rlr700895846.h1
                  31255
Seq. No.
                  236631 1.R1040
Contiq ID
5'-most EST
                  rlr700895865.h1
                  BLASTX
Method
NCBI GI
                  g4467359
BLAST score
                  182
                  8.0e-14
E value
Match length
                  82
% identity
NCBI Description
                   (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
                  thaliana]
```

Seq. No.

```
Contig ID
                   236651 1.R1040
5'-most EST
                   gsv701045260.hl
Seq. No.
                   31257
Contig ID
                   236721 1.R1040
5'-most EST
                   q4291902
Method
                   BLASTX
NCBI GI
                   q2262176
BLAST score
                   266
E value
                   2.0e-23
Match length
                   80
% identity
                   (AC002329) putative RING zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana] >gi 3790573 (AF078824) RING-H2 finger protein
                   RHA3a [Arabidopsis thaliana]
Seq. No.
                   31258
Contig ID
                   236809 1.R1040
5'-most EST
                   uC-qmrominsoy248d01b1
Method
                   BLASTX
NCBI GI
                   g4049410
BLAST score
                   619
E value
                   2.0e-64
Match length
                   168
                   67
% identity
                   (Y10225) L-ascorbate oxidase [Cucumis melo]
NCBI Description
Seq. No.
                   31259
                   236916 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir007c08b1
Method
                   BLASTX
NCBI GI
                   g3935183
BLAST score
                   405
E value
                   3.0e-39
Match length
                   158
                   56
% identity
                   (AC004557) F17L21.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31260
                   236942 1.R1040
Contig ID
                   r1r700\overline{8}96352.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g542812
BLAST score
                   148
                   2.0e-09
E value
Match length
                   95
% identity
                   36
                   estrogen-responsive finger protein, efp (RING finger,
NCBI Description
                   coiled-coil domains) - human >gi 458726 dbj BAA04747
                   (D21205) estrogen responsive finger protein (efp) [Homo
                   sapiens]
Seq. No.
                   31261
Contig ID
                   236964 1.R1040
5'-most EST
                   rlr700896382.h1
```

```
237012 1.R1040
Contig ID
5'-most EST
                  rlr700900992.h1
Seq. No.
                   31263
                  237075 1.R1040
Contig ID
5'-most EST
                   zsg701130250.hl
                  BLASTX
Method
                  g3859659
NCBI GI
BLAST score
                   330
                   6.0e-31
E value
                  111
Match length
                   63
% identity
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31264
                  237098 1.R1040
Contig ID
5'-most EST
                  asn701133396.h1
Seq. No.
                  31265
Contig ID
                  237105 1.R1040
5'-most EST
                  rlr700896607.h1
Method
                  BLASTX
NCBI GI
                  q3434971
BLAST score
                  208
E value
                  3.0e-16
Match length
                  120
% identity
                   (AB008105) ethylene responsive element binding factor 3
NCBI Description
                   [Arabidopsis thaliana]
                   31266
Seq. No.
Contig ID
                  237186 1.R1040
5'-most EST
                  rlr700896731.h1
                  31267
Seq. No.
Contig ID
                  237191 1.R1040
5'-most EST
                  jC-gmst02400039a10a1
Method
                  BLASTX
NCBI GI
                  g2950476
BLAST score
                  166
E value
                  2.0e-11
Match length
                  102
% identity
NCBI Description
                   (AL022070) vesicle transport v-snare protein
                   [Schizosaccharomyces pombe]
Seq. No.
                  31268
Contig ID
                  237259 1.R1040
5'-most EST
                  943971\overline{5}4
               31269
Seq. No.
                  237270 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy294h03b1
Seq. No.
                  31270
                  237352 1.R1040
Contig ID
```

NCBI GI

```
5'-most EST
                   zsg701119837.hl
Seq. No.
                   31271
Contig ID
                   237372 1.R1040
5'-most EST
                   uC-gmropic046b04b1
Method
                   BLASTX
NCBI GI
                   g3641863
BLAST score
                   229
E value
                   4.0e-19
Match length
                   99
% identity
NCBI Description
                   (AJ005042) beta-galactosidase [Cicer arietinum]
Seq. No.
                   31272
                   237426 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}02488.h1
Method
                   BLASTX
NCBI GI
                   q1814424
BLAST score
                   405
                   1.0e-39
E value
                   97
Match length
% identity
                   76
NCBI Description
                   (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
Seq. No.
                   31273
Contig ID
                   237455 1.R1040
5'-most EST
                  r1r700897282.h1
Seq. No.
                   31274
Contig ID
                   237506 1.R1040
                   gsv701\overline{0}51920.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3461836
BLAST score
                   379
E value
                   3.0e-36
Match length
                   189
                   42
% identity
NCBI Description
                   (ACO05315) putative protein kinase [Arabidopsis thaliana]
                   >gi 3927841 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
                   31275
Seq. No.
                   237520 1.R1040
Contig ID
5'-most EST
                   r1r700\overline{8}97244.h1
Method
                   BLASTX
NCBI GI
                   g2781359
BLAST score
                   162
E value
                   5.0e-16
Match length
                   105
% identity
NCBI Description (AC003113) F2501.15 [Arabidopsis thaliana]
Seq. No.
                   31276
Contig ID
                   237524 1.R1040
5'-most EST
                   fC-gmf1700897731a1
Method
                   BLASTX
```

g4415914

BLAST score 387 E value 2.0e-37 Match length 134 48 % identity NCBI Description (AC006282) unknown protein [Arabidopsis thaliana] 31277 Seq. No. Contig ID 237531 1.R1040 5'-most EST rlr700898266.h1 Seq. No. 31278 237555 1.R1040 Contig ID 5'-most EST uC-gmflminsoy074c06b1 Seq. No. 31279 Contig ID 237581 1.R1040 5'-most EST gsv701043841.h1 Seq. No. 31280 Contig ID 237637 1.R1040 5'-most EST g4289894 Seq. No. 31281 237687 1.R1040 Contig ID 5'-most EST $jC-gmf\overline{1}02220065g10a1$ BLASTX Method NCBI GI g3402693 BLAST score 385 E value 2.0e-37 Match length 101 % identity 83 NCBI Description (AC004697) unknown protein [Arabidopsis thaliana] Seq. No. 31282 Contig ID 237706 1.R1040 5'-most EST uC-gmrominsoy081g10b1 Method BLASTX NCBI GI g3776029 628 BLAST score 1.0e-65 E value Match length 141 % identity 84 (AJ010476) RNA helicase [Arabidopsis thaliana] NCBI Description Seq. No. 31283 Contig ID 237738 1.R1040 5'-most EST rlr700897565.h1

BLASTX Method NCBI GI g1619321

BLAST score 188 E value 2.0e-14 Match length 83 % identity 42

NCBI Description (Y07563) hin1 [Nicotiana tabacum]

Seq. No. 31284

Contig ID 237767_1.R1040

Contig ID

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   q4138581
BLAST score
                   499
E value
                   3.0e-91
Match length
                   239
% identity
NCBI Description
                   (X98474) mitochondrial energy transfer protein [Solanum
                   tuberosuml
Seq. No.
                   31285
Contig ID
                   237845 1.R1040
5'-most EST
                   dpv701\overline{1}01422.h1
                   31286
Seq. No.
Contig ID
                   237846 1.R1040
5'-most EST
                   rlr700897740.h1
Method
                   BLASTX
                   g4220537
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   67
% identity
                   39
NCBI Description (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
                   31287
Seq. No.
Contig ID
                   237931 1.R1040
5'-most EST
                   uC-gmronoir041e06b1
Method
                   BLASTX
NCBI GI
                   q4309698
BLAST score
                   1085
E value
                   1.0e-119
Match length
                   243
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   31288
Seq. No.
                   237942 1.R1040
Contig ID
                   fC-gmf1700901262a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3687224
BLAST score
                   496
E value
                   3.0e-50
Match length
                   138
% identity
                   (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
Seq. No.
                   31289
Contig ID
                   237961 1.R1040
                   r1r700\overline{8}97919.h1
5'-most EST
                   31290
Seq. No.
```

238024 1.R1040

uC-gmflminsoy032g07b1

```
Seq. No.
                   238093 1.R1040
Contig ID
5'-most EST
                   dpv701102606.h1
Seq. No.
                   31292
Contig ID
                   238126 1.R1040
5'-most EST
                   uC-gmrominsoy176e11b1
Method
                   BLASTX
NCBI GI
                   q3522931
BLAST score
                   203
E value
                   7.0e-16
Match length
                   67
% identity
NCBI Description
                   (AC002535) putative Na+/Ca2+ exchanger [Arabidopsis
                   thaliana]
Seq. No.
                   31293
Contig ID
                   238166 1.R1040
5'-most EST
                   rlr700898308.h1
                  BLASTX
Method
NCBI GI
                   q2146739
BLAST score
                   335
                   1.0e-31
E value
Match length
                  100
% identity
                   64
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                   31294
Contig ID
                   238167 1.R1040
5'-most EST
                   jC-gmst02400074b11d1
Seq. No.
                   31295
Contig ID
                   238172 1.R1040
5'-most EST
                   r1r700898315.h1
                  BLASTX
Method
NCBI GI
                   g3882239
BLAST score
                   287
                   1.0e-25
E value
Match length
                  154
% identity
                   42
NCBI Description
                   (AB018302) KIAA0759 protein [Homo sapiens]
Seq. No.
                   31296
                   238239 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy107b04b1
Method
                  BLASTX
NCBI GI
                  q2970034
BLAST score
                   436
                   4.0e-43
E value
Match length
                  144
% identity
                  (D88536) delta 9 desaturase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31297
Contig ID
```

238260 1.R1040

rlr700898478.h1

5'-most EST

Method

BLASTX

```
g404688
NCBI GI
BLAST score
                   605
E value
                   1.0e-62
Match length
                   188
% identity
                   56
NCBI Description
                   (L19074) cytochrome P450 [Catharanthus roseus]
                   31298
Seq. No.
Contig ID
                   238322 1.R1040
5'-most EST
                   rlr700898576.hl
Method
                   BLASTX
NCBI GI
                   q3269289
BLAST score
                   239
                   4.0e-20
E value
Match length
                   71
% identity
NCBI Description
                   (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                   31299
                   238434 1.R1040
Contig ID
5'-most EST
                   rlr700898745.hl
                   BLASTX
Method
NCBI GI
                   g3219271
BLAST score
                   192
                   5.0e-15
E value
Match length
                   64
% identity
                   (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
                   31300
Seq. No.
                   238469 1.R1040
Contig ID
5'-most EST
                   rlr700898803.h1
                   31301
Seq. No.
                   238534 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073a12d1
                   31302
Seq. No.
                   238568 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}18545.h1
Seq. No.
                   31303
Contig ID
                   238638 1.R1040
5'-most EST
                   rlr700899094.hl
Method
                   BLASTX
NCBI GI
                   a4490730
BLAST score
                   253
E value
                   4.0e-22
Match length
                   73
% identity
NCBI Description
                   (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   238650 1.R1040
5'-most EST
                   uC-gmrominsoy212d09b1
```

BLAST score

36

```
NCBI GI g3114573
 BLAST score
                    334
 E value
                    4.0e-31
 Match length
                    146
 % identity
                    47
 NCBI Description
                    (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
                    piperita]
                    31305
 Seq. No.
 Contig ID
                    238652 1.R1040
 5'-most EST
                    rlr700899120.hl
 Method
                    BLASTX
 NCBI GI
                    g2443876
 BLAST score
                    183
                    1.0e-13
 E value
 Match length
                    60
 % identity
 NCBI Description
                    (AC002294) Hypothetical protein [Arabidopsis thaliana]
                    31306
 Seq. No.
                    238670 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy265b09b1
                    31307
 Seq. No.
                    238682 1.R1040
. Contig ID
                    r1r700\overline{8}99168.h1
 5'-most EST
 Method
                    BLASTX
                    g3150416
 NCBI GI
 BLAST score
                    257
 E value
                    1.0e-22
                    90
 Match length
 % identity
 NCBI Description
                    (AC004165) putative protein kinase, 5' partial [Arabidopsis
                    thaliana]
                    31308
 Seq. No.
                    238771 1.R1040
 Contig ID
 5'-most EST
                    jC-qmro02910034c02a1
 Seq. No.
                    31309
                    238847 1.R1040
 Contig ID
 5'-most EST
                    rlr700899452.h1
 Seq. No.
                    31310
                    238854 1.R1040
 Contig ID
 5'-most EST
                    jC-gmro02910051d12d1
 Seq. No.
                    31311
 Contig ID
                    238866 1.R1040
 5'-most EST
                    rlr700899483.hl
 Seq. No.
                    31312
                    238902 1.R1040
 Contig ID
 5'-most EST
                    uC-gmflminsoy014c03b1
                    BLASTN
 Method
                    g3821780
 NCBI GI
```

```
1.0e-10
E value
Match length
                   50
% identity
                   51
NCBI Description
                   Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   31313
                   238987 1.R1040
Contig ID
5'-most EST
                   rlr700899662.hl
Seq. No.
                   31314
                   239004 1.R1040
Contig ID
                   r1r700\overline{8}99684.h1
5'-most EST
Seq. No.
                   31315
Contig ID
                   239066 1.R1040
5'-most EST
                   rlr700899820.hl
Seq. No.
                   31316
Contig ID
                   239073 1.R1040
5'-most EST
                   rlr700899832.h1
Method
                   BLASTX
NCBI GI
                   q4006829
BLAST score
                   188
E value
                   2.0e-14
Match length
                   74
% identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   31317
Contig ID
                   239116 1.R1040
5'-most EST
                   rlr700899964.h1
Method
                   BLASTX
                   g3355473
NCBI GI
BLAST score
                   152
                   2.0e-13
E value
Match length
                   89
% identity
NCBI Description
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31318
                   239175 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}21593.h1
Seq. No.
                   31319
                   239185 1.R1040
Contig ID
                   r1r700\overline{9}00113.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   288
                   4.0e-26
E value
Match length
                   82
% identity
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31320
                   239247 1.R1040
Contig ID
```

rlr700900254.h1 ..

5'-most EST

```
Seq. No.
                   31321
Contig ID
                   239299 1.R1040
5'-most EST
                   q4297487
Seq. No.
                   31322
                   239371 1.R1040
Contig ID
5'-most EST
                   rlr700900511.hl
Method
                   BLASTX
NCBI GI
                   g3355467
BLAST score
                   203
E value
                   7.0e-16
                   99
Match length
% identity
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31323
Contig ID
                   239388 1.R1040
                   r1r700\overline{9}00537.h1
5'-most EST
                   BLASTX
Method
                   q3096947
NCBI GI
BLAST score
                   481
E value
                   1.0e-48
Match length
                   105
                   86
% identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   31324
Seq. No.
                   239402 1.R1040
Contig ID
                   r1r700\overline{9}00553.h1
5'-most EST
                   31325
Seq. No.
Contig ID
                   239407 1.R1040
                   rlr700900558.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129635
BLAST score
                   443
E value
                   5.0e-44
Match length
                   141
                   62
% identity
                   light repressible receptor protein kinase - Arabidopsis
NCBI Description
                   thaliana >gi_1321686_emb_CAA66376 (X97774) light
                   repressible receptor protein kinase [Arabidopsis thaliana]
                   31326
Seq. No.
                   239451 1.R1040
Contig ID
                   rlr700900625.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1710628
BLAST score
                   185
E value
                   1.0e-13
Match length
                   78
% identity
NCBI Description
                  HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F)
                   >gi 631210 pir __S43484 hnRNP F protein - human >gi_452048
```

(L28010) HnRNP F protein [Homo sapiens]

```
. . .
                  31327
Seq. No.
                  239462 1.R1040
Contig ID
5'-most EST
                  rlr700900644.h1
Method
                  BLASTX
                   g2288994
NCBI GI
BLAST score
                   160
                   5.0e-24
E value
Match length
                   155
% identity
                   43
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31328
Contig ID
                   239564 1.R1040
5'-most EST
                   rlr700900813.hl
Seq. No.
                   31329
Contig ID
                   239565 1.R1040
5'-most EST
                  rlr700900850.h1
                   31330
Seq. No.
Contig ID
                   239566 1.R1040
5'-most EST
                   jC-qmf102220069b11d1
Method
                  BLASTX
NCBI GI
                  q464900
BLAST score
                   291
E value
                   3.0e-26
Match length
                   68
                   81
% identity
NCBI Description
                  PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR
                   >gi_539008_pir__S39476 kinase-like transmembrane protein
                  TMKL1 precursor - Arabidopsis thaliana
                   >gi_313190_emb_CAA51385_ (X72863) TMKL1 [Arabidopsis
                  thaliana]
                   31331
Seq. No.
                   239609 1.R1040
Contig ID
5'-most EST
                  r1r700\overline{9}00878.h1
Seq. No.
                   31332
                   239621 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy079h09b1
Seq. No.
                  31333
                  239761 1.R1040
Contig ID
5'-most EST
                  qsv701047017.h1
Method
                  BLASTX
NCBI GI
                  q2244869
BLAST score
                  156
                  2.0e-10
E value
                  84
Match length
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  31334
Contig ID
                  239812 1.R1040
```

 $epx701\overline{1}07156.h1$

5'-most EST

```
BLASTX
                  q3114573
BLAST score
                  507
E value
                  1.0e-51
Match length
                  105
% identity
                  88
NCBI Description
                   (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
                  piperita]
                  31335
Seq. No.
Contig ID
                  239842 1.R1040
                  jC-gmle01810085b09d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2191127
BLAST score
                  517
E value
                  1.0e-52
Match length
                  111
% identity
                  (AF007269) A IG002N01.1 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31336
Contig ID
                  239857 1.R1040
5'-most EST
                  jC-gmro02910008d04d1
Method.
                  BLASTX
NCBI GI
                  q4468994
BLAST score
                  657
E value
                  1.0e-102
Match length
                  268
% identity
                  67
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  31337
Contig ID
                  239859 1.R1040
5'-most EST
                  uC-gmrominsoy105d02b1
Seq. No.
                  31338
                  239871 1.R1040
Contig ID
5'-most EST
                  hrw701058964.h1
Method
                  BLASTX
NCBI GI
                  g2244993
BLAST score
                  623
E value
                  5.0e-65
Match length
                  146
% identity
NCBI Description
                  (Z97341) similarity to AMP-activated protein kinase beta
                  [Arabidopsis thaliana]
                  31339
Seq. No.
Contig ID
                  239879 1.R1040
                  asn701142909.h2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3319357
BLAST score
                  147
E value
                  1.0e-09
Match length
                  94
% identity
NCBI Description
                  (AF077407) contains similarity to phosphoenolpyruvate
```

Match length

45

```
synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.
Contig ID
                   239880 1.R1040
5'-most EST
                   rlr700901284.h1
                   31341
Seq. No.
Contig ID
                   239912 1.R1040
5'-most EST
                   dpv701\overline{1}01235.h1
Seq. No.
                   31342
Contig ID
                   239922 1.R1040
5'-most EST
                   g5605974
                   BLASTX
Method
                   g1781299
NCBI GI
BLAST score
                   186
E value
                   9.0e-14
Match length
                   56
% identity
                   (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   31343
                   239956 1.R1040
Contig ID
                   jC-gmro02910027c06a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335359
BLAST score
                   188
E value
                   4.0e-14
Match length
                   96
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31344
                   239968 1.R1040
Contig ID
5'-most EST
                   gsv701052113.h1
                   31345
Seq. No.
                   240065 1.R1040
Contig ID
5'-most EST
                   g4305686
Method
                   BLASTX
NCBI GI
                   g2911077
BLAST score
                   284
                   2.0e-25
E value
Match length
                   106
% identity
                   (AL021960) gibberellin 20-oxidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31346
                   240079 1.R1040
Contig ID
                   rlr700901591.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g285741
BLAST score
                   145
                   4.0e-09
E value
```

Contig ID

5'-most EST

```
% identity.
NCBI Description (D14550) EDGP precursor [Daucus carota]
                   31347
Seq. No.
Contig ID
                   240178 1.R1040
5'-most EST
                   gsv701055354.hl
                   BLASTX
Method
                   g2444231
NCBI GI
BLAST score
                   196
                   3.0e-15
E value
Match length
                   62
% identity
                   (AF026267) ethylene receptor homolog [Nicotiana tabacum]
NCBI Description
                   31348
Seq. No.
Contig ID
                   240208 1.R1040
5'-most EST
                  rlr700901829.hl
Seq. No.
                   31349
Contig ID
                   240268 1.R1040
5'-most EST
                  rlr700901923.hl
Seq. No.
                   31350
                   240298 1.R1040
Contig ID
5'-most EST
                  rlr700902304.hl
                   31351
Seq. No.
                   240373 1.R1040
Contig ID
5'-most EST
                   k11701210880.hl
                   BLASTX
Method
                  g3688284
NCBI GI
BLAST score
                   233
                   8.0e-20
E value
Match length
                   61
% identity
                   (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                   lanata]
Seq. No.
                   31352
                   240385 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy258b01b1
Method
                   BLASTX
NCBI GI
                   g3036871
BLAST score
                   319
E value
                   1.0e-35
Match length
                   127
% identity
                   61
                   (AJ005340) IAA amidohydrolase [Linum usitatissimum]
NCBI Description
                   31353
Seq. No.
                   240412 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir070c10b1
Seq. No.
                   31354
```

240412 2.R1040

uC-gmrominsoy127h01b1

```
31355
Seq. No.
Contig ID
                   240434 1.R1040
5'-most EST
                   rlr700902244.h1
Seq. No.
                   31356
Contig ID
                   240481 1.R1040
5'-most EST
                   zsq701121831.hl
Method
                  BLASTX
NCBI GI
                   q2194117
BLAST score
                   379
E value
                   2.0e-36
Match length
                   127
% identity
NCBI Description
                   (AC002062) Strong similarity to Arabidopsis receptor
                  protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]
Seq. No.
                   31357
Contig ID
                   240488 1.R1040
5'-most EST
                  jC-gmst02400014a03a1
                   31358
Seq. No.
Contig ID
                   240525 1.R1040
5'-most EST
                  rlr700902392.h1
                   31359
Seq. No.
                   240533 1.R1040
Contig ID
5'-most EST
                  rlr700902407.h1
                   31360
Seq. No.
Contig ID
                   240534 1.R1040
5'-most EST
                  jC-gmro02910044b02a1
Seq. No.
                   31361
                   240727 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy300g02b1
                  31362
Seq. No.
Contig ID
                  240789 1.R1040
5'-most EST
                  uC-gmropic014f12b1
Method
                  BLASTX
NCBI GI
                   g4204295
BLAST score
                   286
E value
                   2.0e-25
Match length
                  173
% identity
                   38
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  31363
                   240819 1.R1040
Contig ID
5'-most EST
                  epx701104050.hl
                  31364
Seq. No.
Contig ID
                  240823 1.R1040
5'-most EST
                  uC-gmrominsoy111g05b1
```

31365

Seq. No.

32.5

```
240830 1.R1040
Contig ID
                   jC-gmf102220132ag07d1
5'-most EST
Seq. No.
                   31366
Contig ID
                   240839 1.R1040
5'-most EST
                   uC-qmronoir011c08b1
Seq. No.
                   31367
Contig ID
                   240935 1.R1040
5'-most EST
                   uC-gmrominsoy262g09b1
Method
                   BLASTX
NCBI GI
                   g1657615
BLAST score
                   379
E value
                   2.0e-36
Match length
                   99
% identity
                   72
NCBI Description
                   (U72502) Glp [Arabidopsis thaliana] >gi 3068706 (AF049236)
                   putative transmembrane protein Glp [Arabidopsis thaliana]
Seq. No.
                   240944 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}98646.h1
                   BLASTN
Method
                   g3128137
NCBI GI
BLAST score
                   50
                   3.0e-19
E value
Match length
                   126
% identity
                   85
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31369
Contig ID
                   240950 1.R1040
5'-most EST
                   dpv701\overline{0}97313.h1
Seq. No.
                   31370
                   240989 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy043h10b1
Method
                   BLASTX
NCBI GI
                   g4335751
BLAST score
                   183
E value
                   1.0e-21
Match length
                   125
% identity
                   (AC006284) putative methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   31371
Seq. No.
                   240993 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97361.h1
Method
                   BLASTX
                   g4006915
NCBI GI
BLAST score
                   143
E value
                   6.0e-09
Match length
                   75
% identity
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
```

5'-most EST

q4297977

```
Seq. No.
                   31372
                   241096 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy045a06b1
Method
                   BLASTX
NCBI GI
                   g2129550
BLAST score
                   146
                   2.0e-09
E value
Match length
                   33
% identity
                   82
NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
                   Arabidopsis thaliana >gi 2129554 pir S71901
                   calcium-dependent protein kinase 6 - Arabidopsis thaliana
                   >gi 836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi 836944 (U20625)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                   >qi 4454034 emb CAA23031.1 (AL035394) calcium-dependent
                   protein kinase (CDPK6) [Arabidopsis thaliana]
                   31373
Seq. No.
Contig ID
                   241097 1.R1040
5'-most EST
                   uC-qmrominsoy062e01b1
Method
                   BLASTX
NCBI GI
                   q1666096
BLAST score
                   249
                   3.0e-21
E value
Match length
                   89
% identity
                   (Y09113) dioxygenase [Marah macrocarpus]
NCBI Description
Seq. No.
                   31374
                   241150 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}98766.h2
                   31375
Seq. No.
                   241169 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97591.h1
Seq. No.
                   31376
                   241230 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy247a11b1
Method
                   BLASTX
NCBI GI
                   g2191151
BLAST score
                   246
E value
                   1.0e-20
Match length
                   164
% identity
                   35
NCBI Description
                   (AF007269) contains similarity to membrane associated
                   salt-inducible protein [Arabidopsis thaliana]
                   31377
Seq. No.
                   241242 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}97695.h1
Seq. No.
                   31378
                   241259 1.R1040
Contig ID
```

```
31379
Seq. No.
                   241275 1.R1040
Contig ID
5'-most EST
                   leu701157858.h1
                   31380
Seq. No.
                   241276 1.R1040
Contig ID
5'-most EST
                   dpv701097780.hl
Seq. No.
                   31381
Contig ID
                   241355 1.R1040
                   dpv701\overline{0}97986.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4454019
BLAST score
                   234
E value
                   2.0e-19
Match length
                   95
% identity
NCBI Description
                   (AL035396) SRG1-like protein [Arabidopsis thaliana]
                   31382
Seq. No.
Contig ID
                   241369 1.R1040
5'-most EST
                   dpv701098007.h1
                   31383
Seq. No.
Contig ID
                   241392 1.R1040
5'-most EST
                   uC-gmrominsoy241e11b1
Method
                   BLASTX
NCBI GI
                   g4218011
BLAST score
                   481
E value
                   3.0e-48
Match length
                   187
% identity
                   53
                   (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_4309721_gb_AAD15491_ (AC006439) putative
                   serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                   31384
Contig ID
                   241475 1.R1040
5'-most EST
                   dpv701\overline{0}98205.h1
Method
                   BLASTX
NCBI GI
                   q3522939
BLAST score
                   260
E value
                   2.0e-22
Match length
                   87
% identity
                   (AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   31385
Seq. No.
Contig ID
                   241475 2.R1040
5'-most EST
                   jC-gmro02910037h09a1
Seq. No.
                   31386
Contig ID
                   241495 1.R1040
5'-most EST
                   jC-qmle01810042q06a1
Method
                   BLASTN
```

5'-most EST

```
g349158
BLAST score
                   278
E value
                   1.0e-155
Match length
                   436
% identity
                   92
NCBI Description
                   Vigna aconitifolia AIR carboxylase (purE) mRNA, partial cds
Seq. No.
                   31387
                   241512 1.R1040
Contig ID,
5'-most EST
                   epx701107812.hl
Method
                   BLASTX
NCBI GI
                   g4432814
BLAST score
                   399
E value
                   1.0e-38
Match length
                   134
% identity
                   57
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
                   31388
Seq. No.
Contig ID
                   241513 1.R1040
5'-most EST
                   zsg701123289.hl
                   31389
Seq. No.
Contig ID
                   241531-1.R1040 --
5'-most EST
                   k11701\overline{2}11402.h1
                   BLASTX
Method
NCBI GI
                   g1809127
BLAST score
                   239
E value
                   2.0e-20
Match length
                   76
% identity
                   54
                   (U77674) terminal flower 1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2208929 dbj BAA20483 (D86932) terminal flower1
                   [Arabidopsis thaliana] >qi 2208931 dbj BAA20484 (D87130)
                   terminal flower1 [Arabidopsis thaliana]
                   >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1
                   [Arabidopsis thaliana]
                   31390
Seq. No.
Contig ID
                   241534 1.R1040
5'-most EST
                   dpv701\overline{0}98921.h1
Seq. No.
                   31391
Contig ID
                   241540 1.R1040
5'-most EST
                   dpv701102459.h1
Method
                   BLASTX
NCBI GI
                   a1491776
BLAST score
                   201
E value
                   7.0e-16
Match length
                   56
% identity
NCBI Description
                   (M37636) cationic peroxidase [Arachis hypogaea]
Seq. No.
Contig ID
                   241551 1.R1040
```

dpv701098365.hl

Method

BLASTX

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Seq. No.
                   31393
                   241562 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}98389.h1
Method
                   BLASTX
NCBI GI
                   q1086252
BLAST score
                   380
                   1.0e-36
E value
Match length
                   130
% identity
                   sucrose cleavage protein - Potato >gi 707001 bbs 157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                   tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
                   31394
Seq. No.
Contig ID
                   241628 1.R1040
5'-most EST
                   dpv701\overline{0}98513.h1
Method
                   BLASTX
                   q3367519
NCBI GI
BLAST score
                   184
                   6.0e-26
E value
Match length
                   142
% identity
                   51
                   (AC004392) Contains similarity to gb U51898
NCBI Description-
                   Ca2+-independent phospholipase A2 from Rattus norvegicus.
                   [Arabidopsis thaliana]
Seq. No.
                   31395
                   241715 1.R1040
Contig ID
5'-most EST
                   dpv701103463.hl
                   BLASTX
Method
NCBI GI
                   g2765093
BLAST score
                   227
E value
                   6.0e-19
Match length
                   95
% identity
                   (Y10983) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
                   31396
                   241720 1.R1040
Contig ID
5'-most EST
                   zsg701123531.h1
                   31397
Seq. No.
Contig ID
                   241774 1.R1040
                   dpv701098794.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4454482
BLAST score
                   283
E value
                   1.0e-25
Match length
                   78
% identity .
NCBI Description
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
                   31398
Seq. No.
Contig ID
                   241778 1.R1040
                   xzy700\overline{9}66851.h1
5'-most EST
```

Seq. No.

31407

```
g1575556
 NCBI GI
                     224
 BLAST score
                     2.0e-54
  E value
 Match length
                     131
  % identity
  NCBI Description
                     (U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True
                     Lady']
                     31399
  Seq. No.
  Contig ID
                     241794 1.R1040
  5'-most EST
                     uC-gmrominsoy045h04b1
  Seq. No.
                     31400
                     241850 1.R1040
  Contig ID -
  5'-most EST
                     dpv701\overline{0}98934.h1
 Method
                     BLASTX
 NCBI GI
                     q2262116
 BLAST score
                     143
 E value
                     6.0e-09
 Match length
                     116
  % identity
 NCBI Description
                     (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
-- Seq. No. -
                  --- · 31401--- - --· · · · · · - --
  Contig ID
                     241891 1.R1040
  5'-most EST
                     dpv701\overline{0}99004.h1
 Seq. No.
                     31402
 Contig ID
                     241898 1.R1040
  5'-most EST
                     gsv701051813.h1
 Seq. No.
                     31403
 Contig ID
                     241909 1.R1040
  5'-most EST
                     dpv701\overline{0}99026.h1
 Seq. No.
                     31404
 Contig ID
                     241912 1.R1040
  5'-most EST
                     jC-gmst02400062b05d1
 Method
                     BLASTX
 NCBI GI
                     q1346261
 BLAST score
                     240
 E value
                     4.0e-20
 Match length
                     63
  % identity
 NCBI Description
                     GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
                     >gi 1015319 dbj BAA11091 (D67088) glutamyl-tRNA reductase
                     [Cucumis sativus]
 Seq. No.
                     31405
 Contig ID
                     241950 1.R1040
 5'-most EST
                     dpv701\overline{0}99090.h1
 Seq. No.
                     31406
 Contig ID
                     241992 1.R1040
 5'-most EST
                     asn701141457.h1
```

```
Contig ID 242029_1.R1040
5'-most EST
                   dpv701099213.h1
Seq. No.
                   31408
Contig ID
                   242047 1.R1040
5'-most EST
                   uC-gmrominsoy041c04b1
Method
                   BLASTX
NCBI GI
                   q3252866
BLAST score
                   285
E value
                   2.0e-25
Match length
                   88
% identity
NCBI Description
                   (AF033535) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
Contig ID
                   242047 2.R1040
5'-most EST
                   uC-gmronoir024d04b1
Method
                   BLASTX
NCBI GI
                   q2388566
BLAST score
                   222
E value
                   4.0e-18
Match length
                   93
% identity
NCBI Description (AC000098) Similar to Arabidopsis Fe(II) transport protein
                   (gb U27590). [Arabidopsis thaliana]
Seq. No.
                   31410
Contig ID
                   242075 1.R1040
5'-most EST
                   q42903\overline{4}4
Method
                   BLASTX
NCBI GI
                   g1781326
BLAST score
                   372
E value
                   2.0e-35
Match length
                   139
% identity
                   (Y10464) peroxidase [Spinacia oleracea]
NCBI Description
Seq. No.
                   31411
                   242091 1.R1040
Contig ID
5'-most EST
                   dpv701099303.hl
Method
                   BLASTN
NCBI GI
                   g166929
BLAST score
                   70
E value
                   3.0e - 31
Match length
                   156
% identity
                   91
                  A.thaliana ubiquitin extension protein (UBQ1) gene,
NCBI Description
                   complete cds
                   31412
Seq. No.
                   242156 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}99383.h1
Method
                   BLASTX
NCBI GI
                   g2642445
BLAST score
                   205
                   8.0e-16
E value
```

122

Match length

```
43
% identity
NCBI Description (AC002391) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  31413
Contig ID
                  242217 1.R1040
5'-most EST
                  fua701043047.h1
Method
                  BLASTX
NCBI GI
                  g1781279
BLAST score
                  151
                  4.0e-10
E value
Match length
                  62
% identity
                  45
NCBI Description
                  (Y10455) MtN13 [Medicago truncatula]
Seq. No.
                  31414
                  242300 1.R1040
Contig ID
5'-most EST
                  dpv701099685.hl
Seq. No.
                  31415
Contig ID
                  242328 1.R1040
5'-most EST
                  dpv701099656.h1
Seq. No.
                  31416
Contig ID
                  242354 1.R1040
                  dpv701099701.h1
5'-most EST
Seq. No.
                  31417
Contig ID
                  242369 1.R1040
5'-most EST
                  fua701036913.hl
Method
                  BLASTN
NCBI GI
                  q18590
BLAST score
                  433
E value
                  0.0e + 00
Match length
                  507
% identity
                  100
NCBI Description G.max GH3 gene for auxin-regulated protein
Seq. No.
                  31418
Contig ID
                  242378 1.R1040
5'-most EST
                  uC-gmrominsoy126e03b1
Seq. No.
                  31419
Contig ID
                  242378 2.R1040
5'-most EST
                  dpv701099729.hl
Seq. No.
                  31420
Contig ID
                  242480 1.R1040
5'-most EST
                  jC-qmst02400049a09a1
Method
                  BLASTX
NCBI GI
                  g2292907
BLAST score
                  527
E value
                  8.0e-54
Match length
                  151
% identity
```

NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]

NCBI Description

```
Seq. No.
                    31421
*Contig ID
                   242546 1.R1040
5'-most EST
                   uC-gmrominsoy256g01b1
Method
                   BLASTX
NCBI GI
                   g2920839
BLAST score
                    341
                    6.0e-32
E value
Match length
                   142
% identity
                    (U95136) Os-FIERG2 gene product [Oryza sativa]
NCBI Description
Seq. No.
                    242555 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{0}99968.h1
                   31423
Seq. No.
Contig ID
                   242592 1.R1040
5'-most EST
                   uC-gmrominsoy109b10b1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   48
                    65
% identity -
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                    31424
Contig ID
                   242603 1.R1040
5'-most EST
                   dpv701100033.h2
                   31425
Seq. No.
Contig ID
                   242608 1.R1040
5'-most EST
                   dpv701100043.h2
Seq. No.
                   31426
Contig ID
                   242634 1.R1040
5'-most EST
                   g5508996
Method
                   BLASTX
NCBI GI
                   g2088647
BLAST score
                    473
E value
                    3.0e-47
Match length
                   163
% identity
NCBI Description
                    (AF002109) hypothetical protein [Arabidopsis thaliana]
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                    [Arabidopsis thaliana]
Seq. No.
                   31427
                   242758 1.R1040
Contig ID
5'-most EST
                   dpv701100380.hl
Method
                   BLASTX
NCBI GI
                   g3868940
BLAST score
                   145
E value
                   1.0e-10
Match length
                   63
% identity
```

(AB015054) Alg2 [Rhizomucor pusillus]

Seq. No.

31433

```
>gi_3868942_dbj_BAA34297_ (AB015055) Alg2 [Rhizomucor
                  pusīllus]
Seq. No.
                  31428
Contig ID
                  242767 1.R1040
5'-most EST
                  dpv701100283.hl
Method
                  BLASTX
NCBI GI
                  q2961380
BLAST score
                  183
E value
                  1.0e-13
Match length
                  45
% identity
                  67
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
                  31429
Seq. No.
Contig ID
                  242808 1.R1040
                  dpv701100346.h1
5'-most EST
                  31430
Seq. No.
Contig ID
                  242861 1.R1040 -
5'-most EST
                  uC-gmrominsov180a09b1
Method
                  BLASTX
NCBI GI
                  q2465923
BLAST score
                  270 ---
E value
                  2.0e-23
Match length
                  91
% identity
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana]
                  31431
Seq. No.
Contig ID
                  242862 1.R1040
5'-most EST
                  jC-qmf102220085g05a1
Method ·
                  BLASTX
NCBI GI
                  a3643603
BLAST score
                  240 ..
E value
                  3.0e-20
Match length
                  118
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31432
Contig ID
                  242864 1.R1040
5'-most EST
                  jC-qmst02400008q12d1
Method
                  BLASTX
NCBI GI
                  q1170409
BLAST score
                  190
E value
                  2.0e-14
Match length
                  53
% identity
                  72
NCBI Description
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
                  >qi 549887 (U09336) homeobox protein [Arabidopsis thaliana]
                  >qi 549888 (U09337) homeobox protein [Arabidopsis thaliana]
                  >gi 4490724 emb CAB38927.1 (AL035709) homeobox protein
                  HAT22 [Arabidopsis thaliana]
```

```
242869 1.R1040
Contig ID
                                                              .
                   fua701038752.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1279640
BLAST score
                   185
E value
                   6.0e-14
Match length
                   52
% identity
                   69
NCBI Description
                   (X92204) NAM [Petunia x hybrida]
Seq. No.
                   31434
Contig ID
                   242884 1.R1040
5'-most EST
                   dpv701100446.h1
                   31435
Seq. No.
Contig ID
                   242928 1.R1040
                   jC-gmro02800039d01a1
5'-most EST
                   31436
Seq. No.
Contig ID
                   242932 1.R1040
5'-most EST
                   dpv701\overline{1}00514.h1
Method
                   BLASTX
                   q1752734
NCBI GI
BLAST score -
                 - 517
                   2.0e-52
E value
Match length
                   166
% identity
                   (D78510) beta-glucan-elicitor receptor [Glycine max]
NCBI Description
Seq. No.
Contig ID
                   242940 1.R1040
5'-most EST
                   uC-gmropic111e08b1
Seq. No.
                   31438
                   242961 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}00548.h1
Method
                   BLASTX
NCBI GI
                   g1255951
BLAST score
                   612
E value
                   8.0e-64
Match length
                   152
% identity
NCBI Description (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                   31439
                   242963 1.R1040
Contig ID
                   dpv701\overline{1}00551.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1546704
BLAST score
                   245
E value
                   4.0e-21
Match length
                   95
% identity
NCBI Description
                   (X98854) peroxidase ATP7a [Arabidopsis thaliana]
Seq. No.
                   31440
```

242981 1.R1040

Contig ID

Seq. No.

Contig ID

31445

243049 1.R1040

```
dpv701100579.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1169892
BLAST score
                  177
E value
                  3.0e-13
Match length
                  65
% identity
NCBI Description
                  PUTATIVE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
                   (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE)
                   (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT)
                  >gi 1006748 emb CAA90824 (Z54140)
                  glucosamine-fructose-6-phosphate aminotransferase
                  [Schizosaccharomyces pombe] >gi 3560205 emb CAA20758
                   (AL031536) glucosamine--fructose-6-phosphate
                  aminotransferase (isomerizing) [Schizosaccharomyces pombe]
Seq. No.
                  31441
Contig ID
                  243021 1.R1040
5'-most EST
                  dpv701100648.h1
                  31442
Seq. No.
Contig ID
                  243022 1.R1040
5'-most EST
                  jC-qmro02800034f04a1
Method -
                  BLASTX
NCBI GI
                  g2346974
BLAST score
                  177
E value
                  7.0e-13
Match length
                  69
% identity
NCBI Description
                  (AB006599) ZPT2-12 [Petunia x hybrida]
Seq. No.
                  31443
Contig ID
                  243023 1.R1040
5'-most EST
                  jC-gmro02910031d02a1
Method
                  BLASTX
NCBI GI
                  q1732513
BLAST score
                  431
E value
                  1.0e-51
Match length
                  125
% identity
NCBI Description
                  (U62743) snapdragon myb protein 305 homolog [Arabidopsis
                  thalianal
Seq. No.
                  31444
Contig ID
                  243044 1.R1040
5'-most EST
                  hrw701062605.hl
Method
                  BLASTX
NCBI GI
                  q2342682
BLAST score
                  296
E value
                  8.0e-27
Match length
                  77
% identity
NCBI Description
                  (AC000106) Contains similarity to Rattus AMP-activated
                  protein kinase (gb X95577). [Arabidopsis thaliana]
```

5'-most EST

```
5'-most EST
                  dpv701100682.h1
Seq. No.
                   31446
Contig ID
                   243054 1.R1040
5'-most EST
                   dpv701100688.hl
                   31447
Seq. No.
Contig ID
                   243138 1.R1040
5'-most EST
                   uC-gmronoir029b10b1
Method
                   BLASTX
                   g3135253
NCBI GI
BLAST score
                   363
E value
                   2.0e-34
Match length
                   151
% identity
NCBI Description
                   (AC003058) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   31448
Seq. No.
                   243184 1.R1040
Contig ID
5'-most EST
                   fC-qmse7000756053r1
Method
                   BLASTX
                   g4006914
NCBI GI
BLAST score
                   206
                   4.0e-16
E value
Match length
                   56
                   73
% identity
                   (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31449
                   243237 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810018a01a2
Method
                   BLASTX
                   g4455334
NCBI GI
BLAST score
                   189
E value
                   3.0e-14
Match length
                   119
% identity
NCBI Description
                   (AL035525) myosin-like protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   243261 1.R1040
5'-most EST
                   dpv701\overline{1}00953.h1
Seq. No.
                   31451
                   243330 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800034h07a1
Seq. No.
                   31452
                   243360 1.R1040
Contig ID
5'-most EST
                   jC-gmr002800040f02a1
                   31453
Seq. No.
Contig ID
                   243368_1.R1040
```

jC-gmro02910008g11a1

5'-most EST

```
31454
Seq. No.
Contig ID
                  243373 1.R1040
5'-most EST
                  uC-gmrominsoy087a03b1
Method
                  BLASTN
NCBI GI
                  q169980
BLAST score
                  438
E value
                  0.0e + 00
Match length
                  446
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  243460 1.R1040
Contig ID
5'-most EST
                  zsg701127693.h1
                  31456
Seq. No.
Contig ID
                  243463 1.R1040
5'-most EST
                  uC-gmropic105h10b1
Method
                  BLASTX
NCBI GI
                  g4263784
BLAST score
                  265
E value
                  3.0e-23
Match length
                  67
% identity
                  (AC006068) putative glycogenin-2 protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  31457
                  243464 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy182b03b1
Seq. No.
                  31458
                  243542_1.R1040
Contig ID
                  dpv701\overline{1}01402.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4469009
BLAST score
                  181
E value
                  2.0e-13
Match length
                  81
% identity
                 (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31459
                  243599 1.R1040
Contig ID
5'-most EST
                  dpv701103581.h1
Method
                  BLASTX
                  g2879799
NCBI GI
BLAST score
                  138
E value
                  1.0e-08
Match length
                  34
% identity
NCBI Description (ALO21813) 60s ribosomal protein [Schizosaccharomyces
                  pombe]
Seq. No.
                  31460
                  243662 1.R1040
Contig ID
```

uC-gmrominsoy110h12b1

Method

BLASTX

415

```
Method
                   BLASTX
               g629561
BLAST score
                   218
E value
                   1.0e-17
Match length
                   108
% identity
                   39
NCBI Description
                   SRG1 protein - Arabidopsis thaliana
                   >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thalianal
Seq. No.
                   31461
Contig ID
                   243690 1.R1040
5'-most EST
                   dpv701101586.h1
Method
                   BLASTX
NCBI GI
                   g1935918
BLAST score
                   156
E value
                   1.0e-10
Match length
                   84
% identity
NCBI Description
                   (U93559) putative serine/threonine protein kinase [Brassica
                   rapa]
                   31462
Seq. No.
Contig ID -
                   243723 1:R1040 ---
5'-most EST
                   dpv701\overline{1}01644.h1
Seq. No.
                   31463
                   243760 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir049e05b1
Method
                   BLASTX
                   g629669
NCBI GI
BLAST score
                   174
E value
                   1.0e-12
Match length
                   87
% identity
                   hypothetical protein - tomato.
NCBI Description
Seq. No.
                   31464
                   243766 1.R1040
Contig ID
5'-most EST
                   dpv701101709.h1
Seq. No.
                   31465
Contig ID
                   243771 1.R1040
5'-most EST
                   dpv701101750.h1
Seq. No.
                   31466
                   243821 1.R1040
Contig ID
5'-most EST
                   g42912\overline{8}2
Seq. No.
                   31467
                   243874 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910048e02a1
Seq. No.
                   31468
Contig ID
                   243912 1.R1040
5'-most EST
                   dpv701\overline{1}01924.h1
```

Seq. No.

31474

```
NCBI GI
                  q3850582
BLAST score
                   335
                   4.0e-31
E value
                   111
Match length
% identity
NCBI Description
                   (AC005278) F15K9.14 [Arabidopsis thaliana]
                   31469
Seq. No.
                  243919 1.R1040
Contig ID
5'-most EST
                  uC-qmropic110f08b1
Method
                  BLASTX
                  g3550661
NCBI GI
BLAST score
                   441
                  7.0e-44
E value
Match length
                  121
                   46
% identity
NCBI Description
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
                  tuberosum]
                  31470
Seq. No.
             3 300
                  243922_1.R1040
Contig ID
5'-most EST
                  zsq701117757.h2
Method
                  BLASTX
NCBI-GI-
                  g3451078-
BLAST score
                  234
                  1.0e-19
E value
Match length
                  118
% identity
                   41
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  31471
Contig ID
                  243958_1.R1040
5'-most EST
                  dpv701\overline{1}02015.h1
Method
                  BLASTX
NCBI GI
                  q3258568
BLAST score
                  218
E value
                  1.0e-17
Match length
                  114
% identity
                   46
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  31472
Seq. No.
                  243969_1.R1040
Contig ID
                  jC-gmro02910069b03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3510249
BLAST score
                  452
E value
                  5.0e-45
Match length
                  143
% identity
                  57
NCBI Description
                  (AC005310) unknown protein [Arabidopsis thaliana]
                  31473
Seq. No.
                  244031 1.R1040
Contig ID
5'-most EST
                  dpv701102116.h1
```

Method

BLASTN

F. 1

```
244083 1.R1040
Contig ID
                  epx701104596.h1
5'-most EST
                   31475
Seq. No.
Contig ID
                   244118 1.R1040
5'-most EST
                   dpv701102217.h1
Method
                   BLASTX
NCBI GI
                   g3127045
BLAST score
                   200
E value
                   5.0e-32
Match length
                   172
% identity
                   48
                   (AF020545) bHLH transcription factor JAF13 [Petunia x
NCBI Description
                   hybrida]
                   31476
Seq. No.
Contig ID
                   244177 1.R1040
5'-most EST
                   jC-gmro02910046g04d1
Seq. No.
                   31477
                   244251 1.R1040
Contig ID
5'-most EST
                   dpv701102403.hl
                   31478 ----
Seq. No.
                   244254 1.R1040
Contig ID
5'-most EST
                   k11701204911.h1
Method
                   BLASTX
NCBI GI
                   g2136107
BLAST score
                   231
E value
                   6.0e-19
Match length
                   150
                   36
% identity
NCBI Description
                   retinoblastoma protein binding protein RBQ-3 - human
                   >gi 755750 emb_CAA59446 (X85134) RB protein binding
                   protein [Homo sapiens]
                   31479
Seq. No.
                   244262 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810056d07a1
Seq. No.
                   31480
                   244302 1.R1040
Contig ID
5'-most EST
                   fua701042796.h1
Method
                   BLASTX
NCBI GI
                   g4206210
BLAST score
                   402
E value
                   3.0e-39
Match length
                   137
                   56
% identity
NCBI Description
                   (AF071527) putative calcium channel [Arabidopsis thaliana]
                   >qi 4263043 qb AAD15312 (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
                   31481
Seq. No.
Contig ID
                   244466 1.R1040
5'-most EST
                   dpv701\overline{1}02676.h1
```

NCBI Description

```
g2264318
NCBI GI
BLAST score
                   34
E value
                   9.0e-10
Match length
                   116
% identity
                   87
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31482
Contig ID
                   244467 1.R1040
5'-most EST
                   qsv701044845.h1
Method
                   BLASTX
NCBI GI
                   g1002796
BLAST score
                   186
E value
                   3.0e-14
Match length
                   57
% identity
NCBI Description
                   (U33915) Cpm10 [Craterostigma plantagineum]
                   31483
Seq. No.
                   244522 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}02747.h1
Method
                   BLASTX
NCBI GI - --
                   g3779024 - -- -
BLAST score
                   554
E value
                   4.0e-57
Match length
                   122
% identity
                   87
                   (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
                   31484
Seq. No.
                   244543 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400054g08a1
Seq. No.
                   31485
                   244603 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810003g02d1
Seq. No.
                   31486
                   244682 1.R1040
Contig ID
5'-most EST
                   dpv701102942.h1
Seq. No.
                   31487
                   244709 1.R1040
Contig ID
5'-most EST
                   dpv701102973.hl
Seq. No.
                   31488
                   244711 1.R1040
Contig ID
5'-most EST
                   dpv701\overline{1}02975.h1
Method
                   BLASTX
NCBI GI
                   g4006829
BLAST score
                   265
E value
                   3.0e-23
Match length
                   70
% identity
```

(AC005970) putative protein kinase [Arabidopsis thaliana]

BLAST score

355

```
31489
Seq. No.
Contig ID
                   244721 1.R1040
5'-most EST
                   asn701\overline{1}42469.h1
Method
                   BLASTX
NCBI GI
                   g2388580
BLAST score
                   451
E value
                   3.0e-45
Match length
                   94
% identity
NCBI Description
                   (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb 1253956). [Arabidopsis thaliana]
                   31490
Seq. No.
Contig ID
                   244727 1.R1040
5'-most EST
                   uC-gmrominsoy233e04b1
Seq. No.
                   31491
Contig ID
                   244791 1.R1040
5'-most EST
                   uC-gmropic078c12b1
Method
                   BLASTX
NCBI GI
                   g2569940
BLAST score
                   342
E value
                   3.0e - 32
Match length "
                   134
% identity
                   51
NCBI Description
                   (Y15194) GRS protein [Arabidopsis thaliana]
Seq. No.
                   31492
                   244834 1.R1040
Contig ID
5'-most EST
                   dpv701103152.h1
Method
                   BLASTX
                   g4572669
NCBI GI
BLAST score
                   666
E value
                   4.0e-70
Match length
                   154
                   82
% identity
                   (AC006954) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   31493
Seq. No.
                   244954 1.R1040
Contig ID
5'-most EST
                   gsv701053674.hl
Seq. No.
                   31494
                   244974 1.R1040
Contig ID
5'-most EST
                   uC-gmropic110a11b1
Seq. No.
                   31495
Contig ID
                   245045 1.R1040
5'-most EST
                   jC-gmro02910059a03d1
                   31496
Seq. No.
                   245144 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}50419.h1
Method
                   BLASTX
NCBI GI
                   q4371280
```

4.

```
E value
                   9.0e-34
Match length
                   113
% identity
                   59
NCBI Description
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31497
Contig ID
                   245173 1.R1040
5'-most EST
                   uC-gmrominsoy248f11b1
Seq. No.
                   31498
Contig ID
                   245240 1.R1040
5'-most EST
                   fua701037513.h1
Seq. No.
                   31499
Contig ID
                   245253 1.R1040
5'-most EST
                   xzy700\overline{9}66706.h1
Seq. No.
                   31500
                                                     42 ...
Contig ID
                   245347 1.R1040
5'-most EST
                   xzy700966827.h1
Method
                   BLASTX
NCBI GI
                   q3116212
BLAST score
                   365
E value
                   5.0e-35
                   79
Match length
% identity
NCBI Description
                   (AB004797) homeobox gene [Nicotiana tabacum]
Seq. No.
                   31501
Contig ID
                   245395 1.R1040
5'-most EST
                   xzy700966883.h1
Seq. No.
                   31502
                   245399 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910037g11a1
                   31503
Seq. No.
Contig ID
                   245413 1.R1040
5'-most EST
                   fua701036906.hl
Seq. No.
                   31504
Contig ID
                   245429 1.R1040
5'-most EST
                   fua701036924.hl
                   BLASTX
Method
NCBI GI
                   q1946355
BLAST score
                   299
                   2.0e-27
E value
                   93
Match length
% identity
                   65
NCBI Description
                   (U93215) maize transposon MuDR mudrA protein isolog
                   [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                   31505
Contig ID
                   245434 1.R1040
```

 $jsh701\overline{0}63843.h1$

5'-most EST

5'-most EST

```
Seq. No.
                   31506
                   245437 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220071e12a1
Seq. No.
                   31507
Contig ID
                   245441 1.R1040
                   fua701036936.hl
5'-most EST
Seq. No.
                   31508
Contig ID
                   245445 1.R1040
5'-most EST
                   jC-gmro02910036a04d1
Method
                   BLASTX
NCBI GI
                   g1654140
BLAST score
                   169
E value
                   8.0e-12
Match length
                   56
% identity
NCBI Description
                   (U37840) lipoxygenase [Lycopersicon esculentum]
Seq. No.
Contig ID
                   245447 1.R1040
5'-most EST
                   fua701036942.h1
                   BLASTX
Method
NCBI GI ....
                   q1172874
BLAST score
                   179
                   3.0e-13
E value
Match length
                   51
% identity
                   59
                   DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                   >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                   [Arabidopsis thaliana]
Seq. No.
                   31510
                   245455 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy045d09b1
Seq. No.
                   31511
                   245456 1.R1040
Contig ID
                   fC-gms\(\overline{t}\)700893453d3
5'-most EST
Seq. No.
                   31512
Contig ID
                   245483 1.R1040
5'-most EST
                   fua701036984.h1
Method
                   BLASTX
                   q3941448
NCBI GI
BLAST score
                   424
                   4.0e-48
E value
Match length
                   110
% identity
NCBI Description
                   (AF062878) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   31513
                   245490 1.R1040
Contig ID
```

200

fua701036991.hl

NCBI Description

```
4
                   31514
 Seq. No.
 Contig ID
                   245609 1.R1040
 5'-most EST
                   jC-gmro02910022e08a1
 Method
                   BLASTX
 NCBI GI
                   q3269301
 BLAST score
                   288
 E value
                   3.0e-47
 Match length
                   148
                   63
 % identity
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
 Seq. No.
                   31515
                   245614 1.R1040
 Contig ID
 5'-most EST
                   uC-gmrominsoy194d08b1
 Method
                   BLASTX
 NCBI GI
                   g3860266
 BLAST score
                   147
                   2.0e-09
 E value
 Match length
                   85
 % identity
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
            31516 ---
 Seq. No.
                   245623 1.R1040
 Contig ID
                   fua701037159.hl
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g3941524
 BLAST score
                   400
 E value
                   3.0e-39
 Match length
                   83
 % identity
                   83
 NCBI Description
                   (AF062916) putative transcription factor [Arabidopsis
                   thaliana]
                   31517
: Seq. No.
                   245645 1.R1040
 Contig ID
 5'-most EST
                   fua701037181.hl
 Method
                   BLASTX
 NCBI GI
                   g3395440
 BLAST score
                   295
 E value
                   9.0e-27
Match length
                   95
 % identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   31518
                   245688 1.R1040
 Contig ID
 5'-most EST
                   jC-gmst02400027f08d1
Method
                   BLASTX
                   g2606077
 NCBI GI
 BLAST score
                   261
                   1.0e-22
 E'value
Match length
                   74
 % identity
                   (AF030301) auxin-induced protein [Helianthus annuus]
```

NCBI Description

```
31519
Seq. No.
Contig ID
                   245703 1.R1040
                                                                  · 1888
5'-most EST
                   fua701037254.h1
                   BLASTX
Method
NCBI GI
                  g3341678
BLAST score
                   161
                   5.0e-11
E value
Match length
                   71
% identity
                   (AC003672) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                   31520
Seq. No.
                  245705 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir034h07b1
                  BLASTX
Method
NCBI GI
                  g2292907
BLAST score
                  579
E value
                   2.0e-62
Match length
                  217
                  32
% identity
                  (Y10099) P-glycoprotein homologue [Hordeum vulgare]
NCBI Description
                  31521 - ----
Seq. No.
                  245719 1.R1040
Contig ID
5'-most EST
                  uC-gmropic033a03b1
Method
                  BLASTX
NCBI GI
                  g4097522
BLAST score
                  381
                  8.0e-37
E value
Match length
                  88
                  81
% identity
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                  ananassa]
                  31522
Seq. No.
                  245810 1.R1040
Contig ID
5'-most EST
                  fua701037375.hl
                  BLASTX
Method
NCBI GI
                  g2465008
BLAST score
                  618
                   4.0e-64
E value
                  162
Match length
                  73
% identity
NCBI Description
                  (AJ001445) ripening-induced protein [Fragaria vesca]
                  31523
Seq. No.
                  245841 1.R1040
Contig ID
5'-most EST
                  fua701\overline{0}37419.h1
Method
                  BLASTX
NCBI GI
                  g3068705
BLAST score
                  156
                                              2.0e-10
E value
Match length
                  84
% identity
                  45
```

(AF049236) unknown [Arabidopsis thaliana]

```
Seq. No.
                   31524
                  245853 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220142c01a1
Seq. No.
                   31525
Contig ID
                   245889 1.R1040
5'-most EST
                   fua701037472.hl
Seq. No.
                   31526
Contig ID -
                  245912 1.R1040
5'-most EST
                  g4276943
Method
                  BLASTX
NCBI GI
                  q3080393
BLAST score
                   393
E value
                   4.0e-38
Match length
                  77
% identity
NCBI Description
                  (AL022603) NADH dehydrogenase like protein [Arabidopsis
                  thaliana]
Seq. No.
                   31527
Contig ID
                  245927 1.R1040
5'-most EST
                  fua701037534.h1
                  31528
Seq. No.
Contig ID
                  246084 1.R1040
5'-most EST
                  fua701037815.h1
Method
                  BLASTX
NCBI GI
                  g3785989
BLAST score
                  135
E value
                   6.0e-18
Match length
                  63
% identity
NCBI Description
                  (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  246117 1.R1040
5'-most EST
                   jC-gmst02400058f12a1
Method
                  BLASTX
NCBI GI
                  q4056421
BLAST score
                  165
E value
                   3.0e-11
Match length
                  36
% identity
NCBI Description
                  (AC005322) Similar to gb Z30094 basic transcripion factor
                  2, 44 kD subunit from Homo sapiens. EST gb W43325 comes
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  31530
Contig ID
                  246153 1.R1040
5'-most EST
                  1eu701\overline{1}52312.h1
Seq. No.
                  31531
Contig ID
                  246155 1.R1040
5'-most EST
                  uC-gmropic039b08b1
Method
                  BLASTX
```

g2982434

NCBI GI

NCBI Description

```
448
BLAST score
                   3.0e-44
E value
Match length
                  144
% identity
                   60
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                  31532
                  246160 1.R1040
Contig ID
                  leu701151955.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4056506
BLAST score
                  272
E value
                  5.0e-24
Match length
                  91
% identity
NCBI Description
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
                  31533
Seq. No.
                  246199 1.R1040
Contig ID
                  hrw701062931.hl
5'-most EST
                  31534
Seq. No.
Contig ID
                  246225 1.R1040
5'-most EST
                  jC-gmf102220085b12d1
Seq. No.
                  31535
                  246311_1.R1040
Contig ID
5'-most EST
                  uC-gmropic112a07b1
Method
                  BLASTX
NCBI GI
                  g1117793
BLAST score
                  399
E value
                  5.0e-39
                  104
Match length
                  73
% identity
NCBI Description (U24232) lipoxygenase [Solanum tuberosum]
Seq. No.
                  31536
                  246340 1.R1040
Contig ID
5'-most EST
                  fua701041137.hl
                  BLASTX
Method
NCBI GI
                  g1402920
BLAST score
                  193
                  6.0e-15
E value
Match length
                  58
% identity
NCBI Description
                  (X98321) peroxidase [Arabidopsis thaliana]
                  31537
Seq. No.
                  246341 1.R1040
Contig ID
5'-most EST
                  fua701038152.hl
                  BLASTX
Method
NCBI GI
                  g2088651
BLAST score
                  169
                  7.0e-12
E value
Match length
                  148
% identity
                  39
```

(AF002109) hypersensitivity-related gene 201 isolog

5'-most EST

```
[Arabidopsis thaliana]
Seq. No.
                   31538
                   246393 1.R1040
Contig ID
5'-most EST
                   fua701040387.hl
Method
                   BLASTX
                   q2739008
NCBI GI
BLAST score
                   402
                   6.0e-39
E value
Match length
                   154
% identity
                   53
NCBI Description
                   (AF022463) CYP78A3p [Glycine max]
                   31539
Seq. No.
Contig ID
                   246404 1.R1040
5'-most EST
                   asn701\overline{1}38624.h1
                   31540
Seq. No.
Contig ID
                   246414 1.R1040
5'-most EST
                   jC-gmst02400046d08a1
                   31541
Seq. No.
Contig ID
                   246436 1.R1040
5'-most EST
                   jC-gmf102220093a06a1
Method
                   BLASTX
NCBI GI
                   g119640
BLAST score
                   253
E value
                   1.0e-21
Match length
                   109
% identity
                   44
NCBI Description
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
                   E8) >gi_82109_pir__S01642 ripening protein E8 - tomato
                   >gi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon
                   esculentum]
                   31542
Seq. No.
                   246438 1.R1040
Contig ID
5'-most EST
                   fua701038275.h1
                   31543
Seq. No.
                   246482 1.R1040
Contig ID
5'-most EST
                   fua701038350.h1
Seq. No.
                   31544
Contig ID
                   246509 1.R1040
5'-most EST
                   jC-gmst02400041e03a1
Method
                   BLASTX
NCBI GI
                   g2213602
BLAST score
                   152
E value
                   7.0e-10
Match length
                   52
% identity
NCBI Description
                  (AC000348) T7N9.22 [Arabidopsis thaliana]
Seq. No.
                   31545
Contig ID
                   246512 1.R1040
```

jC-gmst02400055d01a1

Match length

```
Method
                  BLASTX
NCBI GI
                  g3426039
BLAST score
                  271
                  6.0e-24
E value
Match length
                  76
% identity
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31546
Contig ID
                  246575 1.R1040
5'-most EST
                  jC-gmle01810060e09d1
                  31547
Seq. No.
Contig ID
                  246589 1.R1040
5'-most EST
                  fua701038535.hl
Method
                  BLASTX
NCBI GI
                  g3892050
BLAST score
                  200
                  2.0e-15
E value
                  96
Match length
% identity
NCBI Description
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
                  31548-
Seq. No.
                  246621 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy133h11b1
Method
                  BLASTX
NCBI GI
                  g3786007
BLAST score
                  159
E value
                  1.0e-10
Match length
                  114
% identity
                  33
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
                  31549
Seq. No.
                  246642 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy044d11b1
Method
                  BLASTX
NCBI GI
                  g3953470
BLAST score
                  146
E value
                  5.0è-09
Match length
                  89
% identity
NCBI Description
                  (AC002328) F20N2.15 [Arabidopsis thaliana]
Seq. No.
                  31550
                  246704 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy236e08b1
Seq. No.
                  31551
                  246800 1.R1040
Contig ID
5'-most EST
                  jC-gmr002910061b06a1
Method
                  BLASTX
NCBI GI
                  g1403134
BLAST score
                  278
E value
                  1.0e-24
```

```
% identity
NCBI Description (X98453) peroxidase [Arabidopsis thaliana]
                   31552
Seq. No.
Contig ID
                   246807 1.R1040
5'-most EST
                   fua701038813.hl
Seq. No. 🙀
                   31553
                   246840 1.R1040
Contig ID
                   uC-gmronoir0001g01b1
.5'-most EST
                                                                               N. 19
Method
                   BLASTX
NCBI GI
                   g2262178
BLAST score
                   388
E value
                   3.0e-37
Match length
                   141
                   58
% identity
                   (AC002329) putative Mlo-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31554
                   246841 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400060c06a1
Seq. No.
                   31555
                   246860 1.R1040
Contig ID
                   k11701\overline{2}11237.h1
5'-most EST
                   31556
Seq. No.
                   246957 1.R1040
Contig ID
                   fua701039013.hl
5'-most EST
Seq. No.
                   31557
                   246971 1.R1040
Contig ID
5'-most EST
                   fua701039063.hl
                   31558
Seq. No.
                   247066 1.R1040
Contig ID
5'-most EST
                   g5753703
Method
                   BLASTX
NCBI GI
                   g3695019
BLAST score
                   599
E value
                   3.0e-62
Match length
                   173
% identity
NCBI Description
                   (AF055848) subtilisin-like protease [Arabidopsis thaliana]
                   31559
Seq. No.
Contig ID
                   247068 1.R1040
5'-most EST
                   uC-qmflminsoy053d03b1
Method
                   BLASTX
NCBI GI
                   q2052510
BLAST score
                   603
E value
                   9.0e-63
Match length
                   138
% identity
NCBI Description
                   (U95758) lysine-ketoglutarate reductase/saccharopine
```

dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

% identity -

```
31560
Seq. No.
                   247090 1.R1040
Contig ID 💬
5'-most EST
                   uC-gmrominsoy229e05b1
Seq. No.
                   31561
Contig ID
                   247093 1.R1040
5'-most EST
                   jC-qmro02910066b03a1
Method
                   BLASTX
                   g4063751
NCBI GI
BLAST score
                   152
E value
                   9.0e-10
Match length
                   60
% identity
                   52
NCBI Description
                   (AC005851) putative white protein [Arabidopsis thaliana]
                   >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   31562
Seq. No.
                   247152 1.R1040
Contig ID
                   fua701039274.hl
5'-most EST
                   31563
Seq. No.
                   247256 1.R1040
Contig ID
5'-most EST
                   g42967\overline{1}2
Seq. No.
                   31564
Contig ID
                   247259 1.R1040
5'-most EST
                   fua701039432.hl
Seq. No.
                   31565
                   247372 1.R1040
Contig ID
                   leu701156929.h1
5'-most EST
                   31566
Seq. No.
                   247444 1.R1040
Contig ID
                   jC-gmst02400054f04a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1293835
BLAST score
                   288
                   2.0e-27
E value
Match length
                   130
                   45
% identity
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]
Seq. No.
                   31567
Contig ID
                   247476 1.R1040
5'-most EST
                   fua701039812.hl
                   31568
Seq. No.
Contig ID
                   247488 1.R1040
                   fua701039833.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                  ~g1149556
BLAST score
                   152
E value
                   5.0e-23
Match length
                   92
```

Method

BLASTX

```
NCBI Description
                   (X94443) pectinmethylesterase [Vigna radiata]
                   31569
Seq. No.
Contig ID
                   247490 1.R1040
5'-most EST
                  gsv701046837.h1
                   31570
Seq. No.
Contig ID
                   247523 1.R1040
5'-most EST
                   fua701039911.h1
Seq. No.
                   31571
Contig ID
                   247533 1.R1040
5'-most EST
                   fua701039923.h1
                  BLASTX
Method
                  g4151319
NCBI GI
BLAST score
                  240
E value
                   2.0e-20
Match length
                   52
% identity
                   (AF089084) putative auxin efflux carrier protein; AtPIN1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  31572
                  247548 1.R1040
Contig ID
5'-most EST
                  jC-gmf\overline{1}02220080a04d1
Seq. No.
                  31573
                  247553 1.R1040
Contig ID
5'-most EST
                  fua701039971.h1
                  BLASTX
Method
NCBI GI
                  g2829910
BLAST score
                  147
                  1.0e-09
E value
Match length
                  84
% identity
                   45
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                  31574
                  247667 1.R1040
Contig ID
                  fua701040157.hl
5'-most EST
                  31575
Seq. No.
Contig ID
                  247674 1.R1040
                  fua701040166.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1002800
BLAST score
                  629
E value
                  2.0e-65
Match length
                  139
                  82
% identity
NCBI Description
                  (U33917) Cpm7 [Craterostigma plantagineum]
                  31576
Seq. No.
Contig ID
                  247708 1.R1040
                  epx701108580.h1
5'-most EST
```

% identity

```
g3746059
NCBI GI
BLAST score
                   603
E value
                   9.0e-63
Match length
                   148
% identity
                   72
NCBI Description
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
                   thaliana] >gi 4432812 gb AAD20662_ (AC006593) putative
                  cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   31577
Seq. No.
Contig ID
                   247717 1.R1040
5'-most EST
                   jC-gmro02910001g08d1
Method
                  BLASTX
NCBI GI
                   q1708424
BLAST score
                   301
E value
                   2.0e-27
Match length
                  71
% identity
                  76
                  ISOFLAVONE REDUCTASE HOMOLOG >qi 1230614 (U48590)
NCBI Description
                  isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                  247727 1.R1040
Contig ID
                  uC-gmflminsoy076b01b1
5'-most EST
Seq. No.
                  31579
Contig ID
                  247738 1.R1040
5'-most EST
                  fua701040272.h1
Seq. No.
                  31580
Contig ID
                  247759 1.R1040
5'-most EST
                  fua701040314.hl
Seq. No.
                   31581
Contig ID
                   247761 1.R1040
5'-most EST
                  fua701040318.h1
Seq. No.
                  31582
Contig ID
                  247766 1.R1040
5'-most EST
                  fua701040324.h1
Method
                  BLASTN
NCBI GI
                  q166411
BLAST score
                  180
E value
                  1.0e-96
Match length
                  374
% identity
NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds
Seq. No.
                  31583
Contig ID
                  247783 1.R1040
5'-most EST
                  fua701040345.hl
Method
                  BLASTX
NCBI GI
                  q3935168
BLAST score
                  494
E value
                  8.0e-50
Match length
                  187
```

Seq. No.

```
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
                    31584
 Seq. No.
 Contig ID
                    247846 1.R1040
 5'-most EST
                    fua701040528.hl
 Method
                    BLASTX
 NCBI GI
                    q3927836
 BLAST score
                    296
 E value
                    8.0e-27
 Match length
                    76
 % identity
 NCBI Description
                    (AC005727) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    247889 1.R1040
 Contig ID
 5'-most EST
                    fua701040581.hl
                    31586
 Seq. No.
                    247930 1.R1040
 Contig ID
 5'-most EST
                    fua701040629.h1
                    31587
 Seq. No.
                    247936 1.R1040
 Contig ID
                    jC-gms\overline{t}02400058h11a1 -
- 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2781348
 BLAST score
                    559
 E value
                    2.0e-57
 Match length
                    183
                    59
 % identity
 NCBI Description (AC003113) F2401.4 [Arabidopsis thaliana]
                    31588
 Seq. No.
                    247954 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810051h11d1
                    BLASTX
 Method
 NCBI GI
                    q4263695
 BLAST score
                    363
 E value
                    1.0e-34
 Match length
                    152
 % identity
 NCBI Description
                    (AC006223) putative myosin II heavy chain [Arabidopsis
                    thaliana]
 Seq. No.
                    31589
                    247996 1.R1040
 Contig ID
 5'-most EST
                    asn701\overline{1}40715.h1
 Seq. No.
                    31590
                    248013 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy314e11b1
                    31591
 Seq. No.
                    248025 1.R1040
 Contig ID
 5'-most EST
                    leu701\overline{1}54384.h1
```

% identity

```
248028 1.R1040
Contig ID
5'-most EST
                   fC-gmro700835214b1
                   BLASTX
Method
NCBI GI
                   g860676
BLAST score
                   958
                   1.0e-104
E value
                   232
Match length
                   77
% identity
                   (U24188) calcium/calmodulin-dependent protein kinase
NCBI Description
                   [Lilium longiflorum] >gi 1097385 prf 2113422A
                   Ca/calmodulin-dependent protein kinase [Lilium longiflorum]
Seq. No.
                   31593
Contig ID
                   248031 1.R1040
5'-most EST
                   fua701040753.h1
Seq. No.
                   31594
Contig ID
                   248079 1.R1040
5'-most EST
                   fua701040818.hl
Seq. No.
                   31595
Contig ID
                   248089 1.R1040
5'-most EST
                   fua701040834.hl
                   31596
Seq. No.
Contig ID :
                   248102 1.R1040
5'-most EST
                   leu701153459.hl
                   31597
Seq. No.
Contig ID
                   248164 1.R1040
5'-most EST
                   uC-gmflminsoy093e01b1
Seq. No.
                   31598
Contig ID
                   248176 1.R1040
5'-most EST
                   fua701040948.hl
Method
                   BLASTX
NCBI GI
                   g3928543
BLAST score
                   206
E value
                   2.0e-16
Match length
                   85
% identity
NCBI Description
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   31599
Contig ID
                   248413 1.R1040
5'-most EST
                   jC-gmst02400048g08a1
Seq. No.
                   31600
Contig ID
                   248488 1.R1040
5'-most EST
                   fua701042965.hl
Method
                   BLASTN
NCBI GI
                   g3985955
BLAST score
                   33
E value
                   4.0e-09
Match length
                   87
```

E value

6.0e-20

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                  248504 1.R1040
5'-most EST
                  fua701041350.hl
Method
                  BLASTX
NCBI GI
                  q4522004
BLAST score
                  370
E value
                  3.0e-35
Match length
                  168
                  56
% identity
                  (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  31602
Contig ID
                  248506 1.R1040
5'-most EST
                  fua701041354.hl
                  31603
Seq. No.
                  248518 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy116e12b1
Method
                  BLASTN
NCBI GI -
                  q4138138
BLAST score
                  40
E value
                  5.0e-13
Match length
                  52
% identity
                  94
NCBI Description Lycopersicon esculentum mRNA for ss-galactosidase, clone
                  tEG1B
Seq. No.
                  31604
Contig ID
                  248542 1.R1040
                  fua701041435.hl
5'-most EST
Seq. No.
                  31605
                  248614 1.R1040
Contig ID
5'-most EST
                  fua701041504.hl
                  31606
Seq. No.
                  248615 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy169a04b1
Method
                  BLASTX
NCBI GI
                  g4572674
BLAST score
                  524
E value
                  4.0e-53
Match length
                  157
% identity
NCBI Description
                  (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  31607
                  248633 1.R1040
Contig ID
5'-most EST
                  jC-gmr002910068f04a1
Method
                  BLASTX
NCBI GI
                  q2827637
BLAST score
                  238
```

```
Match length
                    133
  % identity
                    38
  NCBI Description
                    (AL021636) putative protein [Arabidopsis thaliana]
  Seq. No.
                    31608
  Contig ID
                    248655 1.R1040
  5'-most EST
                    fua701041554.h1
  Method
                    BLASTX
  NCBI GI
                    q4510348
  BLAST score
                    140
  E value
                    1.0e-08
  Match length
                    84
  % identity
  NCBI Description
                    (AC006921) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    31609
  Contig ID
                    248681 1.R1040
  5'-most EST
                   leu701154148.h1
  Method
                    BLASTX
                    g2497219
  NCBI GI
  BLAST score
                    182
  E value
                    3.0e-13
 Match length
                    89
---% identity-
                    42
                    HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION
  NCBI Description
                   .>gi 626266 pir S47453 probable membrane protein YMR292w -
                    yeast (Saccharomyces cerevisiae) >gi_530349_emb_CAA56801_
                    (X80836) len:138, CAI:0.12, potential spliced gene,
                    hydropho bic composition [Saccharomyces cerevisiae]
  Seq. No.
                    31610
  Contig ID
                    248699 1.R1040
  5'-most EST
                    fua701041608.hl
  Method
                    BLASTX
  NCBI GI
                    q4558673
  BLAST score
                    170
  E value
                    3.0e-12
  Match length
                    67
  % identity
                    (AC007063) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    31611
                    248712 1.R1040
  Contig ID
  5'-most EST
                    fua701041635.hl
  Seq. No.
                    31612
                    248739 1.R1040
  Contig ID
  5'-most EST
                    jC-gmro02910011a05d1
  Seq. No.
                    31613
                    248746 1.R1040
  Contig ID
  5'-most EST
                    jC-gmst02400062e06a1
                    31614
  Seq. No.
                    248750 1.R1040
  Contig ID
```

leu701152047.hl

5'-most EST

Seq. No.

```
Seq. No.
                  31615
                  248756 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400050h11a1
Seq. No.
Contig ID
                  248764 1.R1040
5'-most EST
                  fua701041707.h1
Seq. No.
                  31617
Contig ID
                  248771 1.R1040
5'-most EST
                  fua701041815.hl
Method
                  BLASTX
NCBI GI
                  g2924509
BLAST score
                  403
E value
                  1.0e-39
Match length
                  88
% identity
NCBI Description
                   (AL022023) subtilisin proteinase - like [Arabidopsis
                  thaliana]
Seq. No.
                  31618
Contig ID
                  248780 1.R1040
                  fua701041824.hl
5'-most EST
                  31619
Seq. No.
                  248805 1.R1040
Contig ID
5'-most EST
                  fua701041754.hl
Seq. No.
                  31620
Contig ID
                  248807 1.R1040
5'-most EST
                  fua701041856.hl
Method
                  BLASTX
NCBI GI
                  g100226
BLAST score
                  174
                  8.0e-13
E value
Match length
                  92
% identity
NCBI Description
                  hypothetical protein - tomato >gi 19275 emb CAA78112
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                  [Lycopersicon esculentum]
Seq. No.
                  31621
                  248818 1.R1040
Contig ID
5'-most EST
                  fua701041767.hl
Method
                  BLASTX
NCBI GI
                  g116337
BLAST score
                  262
E value
                  4.0e-23
Match length
                  83
% identity
NCBI Description
                  BASIC ENDOCHITINASE PRECURSOR >gi_100310_pir___$23545
                  chitinase (EC 3.2.1.14) III, basic - common tobacco
                  >gi_19803_emb_CAA77657_ (Z11564) basic chitinase III
                  [Nicotiana tabacum]
```

```
Contig ID
                   248831 1.R1040
5'-most EST
                   fua701041785.hl
                                                     F(
                   31623
Seq. No.
Contig ID
                   248833 1.R1040
5'-most EST
                   fua701041888.hl
                   31624
Seq. No.
Contig ID
                   248929 1.R1040
5'-most EST
                   uC-qmronoir045e11b1
Method
                   BLASTN
NCBI GI
                   g438248
BLAST score
                   80
                   5.0e-37
E value
                   224
Match length
% identity
                   84
NCBI Description
                   S.tuberosum mRNA for precursor of the mitochondrial
                   NAD+-dependent malic enzyme (malate dehydrogenase)
                   31625
Seq. No.
                   248950 1.R1040
Contig ID
5'-most EST
                   fua701041968.h1
                   31626~
-Seq.-No.
                   248951 1.R1040
Contig ID
                   fua701041969.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                   g3941493
BLAST score
                   81
                   8.0e-38
E value
Match length
                   161
% identity
                   88
                  Arabidopsis thaliana putative transcription factor (MYB68)
NCBI Description
                  mRNA, complete cds
                   31627
Seq. No.
                   248983 1.R1040
Contig ID
5'-most EST
                   fua701042011.hl
Method
                  BLASTX
NCBI GI
                   g1396054
BLAST score
                   591
E value
                   4.0e-61
Match length
                   154
% identity
NCBI Description
                   (D86180) phosphoribosylanthranilate transferase [Pisum
                   sativum]
                   31628
Seq. No.
                   249001 1.R1040
Contig ID
                   fua701042031.hl
5'-most EST
Method
                  BLASTX
                  g2498629
NCBI GI
                  171
BLAST score
E value
                   4.0e-12
Match length
                  82
% identity
                   43
NCBI Description TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869
```

j., .

```
factor, X-box binding
Seq. No.
                  31629
Contig ID
                  249006 1.R1040
5'-most EST
                  uC-gmrominsoy192a04b1
Method
                  BLASTX
                  g2335096
NCBI GI
BLAST score
                  355
E value
                  1.0e-33
                  156
Match length
% identity
                  (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  31630
Seq. No.
                  249016 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910051e06a1
Method
                  BLASTX
NCBI GI
                  g119351
BLAST score
                  209
E value
                  1.0e-16
Match length
                  51
                  82
% identity --
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 84950 pir S07586
                  phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly
                  (Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)
                  enolase (AA 1-433) [Drosophila melanogaster]
Seq. No.
                  31631
Contig ID
                  249023 1.R1040
5'-most EST
                  leu701144413.h1
Seq. No.
                  31632
                  249058 2.R1040
Contig ID
5'-most EST
                  fua701042108.h1
Method
                  BLASTX
NCBI GI
                  g3695392
BLAST score
                  160
E value
                  1.0e-10
Match length
                  35
% identity
NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]
Seq. No.
                  31633
                  249119 1.R1040
Contiq ID
5'-most EST
                  uC-gmrominsoy044h11b1
Method
                  BLASTX
NCBI GI
                  g3176686
BLAST score
                  706
E value
                  1.0e-74
Match length
                  169
% identity
NCBI Description
                  (AC003671) Similar to high affinity potassium transporter,
                  HAK1 protein gb U22945 from Schwanniomyces occidentalis.
```

NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens] >gi_4505387_ref_NP_002495.1 pNFX1 nuclear transcription

[Arabidopsis thaliana]

Contig ID

```
31634
Seq. No.
                   249129 1.R1040
Contig ID
                   jsh701\overline{0}67681.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4008372
BLAST score
                   193
E value
                   7.0e-15
Match length
                   113
                   37
% identity
                  (Z27079) cDNA EST CEMSF67FB comes from this gene; cDNA EST
NCBI Description
                   CEMSF67R comes from this gene; cDNA EST yk195e10.3 comes
                   from this gene; cDNA EST yk195e10.5 comes from this gene;
                   cDNA EST yk397a5.3 comes from this gene; cDNA EST yk3
                   31635
Seq. No.
Contig ID
                   249180 1.R1040
5'-most EST
                   g43971\overline{4}3
Method
                   BLASTN
NCBI GI
                   g169348
                  144
BLAST score
E value
                   5.0e-75
Match length
                   276
                 --22
-%-identity-
NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'
                   end
                   31636
Seq. No.
                   249237 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910073h08a1
                   BLASTX
Method
NCBI GI
                   g4063742
                   320
BLAST score
E value
                   2.0e-29
Match length
                   176
                   48
% identity
                   (AC005851) putative phaseolin G-box binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31637
                   249241 1.R1040
Contig ID
5'-most EST
                   uC-gmropic075e12b1
                   31638
Seq. No.
Contig ID
                   249241 2.R1040
5'-most EST
                   gsv701049418.hl
                   31639
Seq. No.
                   249275 1.R1040
Contig ID
5'-most EST
                   fua701042384.h1
                   31640
Seq. No.
                   249313 1.R1040
Contig ID
5'-most EST
                   fua701042540.h1
Seq. No.
                   31641
```

249323 1.R1040

```
5'-most EST
                   asn701143432.h1
Seq. No.
                   31642
                   249329 1.R1040
Contig ID
5'-most EST
                   fua701042561.h1
Seq. No.
                   31643
                   249369 1.R1040
Contig ID
                   fua701042610.hl
5'-most EST
                   31644
Seq. No.
                   249386 1.R1040
Contig ID
5'-most EST
                   fua701042629.hl
                   BLASTX
Method
                   g3924604
NCBI GI
BLAST score
                   346
                   1.0e-32
E value
Match length
                   89
                   74
% identity
                   (AF069442) putative leucine-rich repeat protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   31645
                   249389 1.R1040
Contig ID ---
5'-most EST
                   fua701042632.hl
Seq. No.
                   31646
                   249515 1.R1040
Contig ID
                   fua701043364.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g129813
BLAST score
                   192
E value
                   6.0e-15
Match length
                   77
% identity
                   49
                   PEROXIDASE C1A PRECURSOR >gi_2144377_pir__OPRHC peroxidase (EC 1.11.1.7) C1 precursor - horseradish
NCBI Description
Seq. No.
                   31647
                   249570 1.R1040
Contig ID
5'-most EST
                   leu701151908.h1
Seq. No.
                   31648
                   249592 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024h02d1
Seq. No.
                   31649
                   249609 1.R1040
Contig ID
                   uC-gmflminsoy061h06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2497539
BLAST score
                   322
E value
                   4.0e-30
                   76
Match length
                   79
% identity
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703
NCBI Description
```

(M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

NCBI GI

```
Seq. No.
                      31650
                      249705 1.R1040
   Contig ID
                      jC-gmro02910051a02a1
   5'-most EST
   Method
                      BLASTX
   NCBI GI
                      q2492820
                      253
   BLAST score
                      2.0e-21
   E value
🧦 Match length
                      104
   % identity
                      41
                      HYPOTHETICAL 54.0 KD PROTEIN IN NRGA-USD INTERGENIC REGION
   NCBI Description
                      >gi 1684649 emb CAB05378 (Z82987) unknown, similar to
                      uracil permease from Schizosaccharomyces pombe [Bacillus
                      subtilis] >gi 2636172_emb_CAB15664.1_ (Z99122) similar to
                      permease [Bacillus subtilis]
   Seq. No.
                      31651
   Contig ID
                      249731 1.R1040
                      leu701150624.h1
   5'-most EST
                      31652
   Seq. No.
                      249784 1.R1040
   Contig ID
                      asn701\overline{1}42062.h1
   5'-most EST
                      31653
   Seq. No.
                      249811 1.R1040
   Contig ID
   5'-most EST
                      fua701043283.hl
                      31654
   Seq. No.
                      249817 1.R1040
   Contig ID
                      fua701043290.h1
   5'-most EST
   Method
                      BLASTX
   NCBI GI
                      g3540183
   BLAST score
                      407
                      8.0e-40
   E value
   Match length
                      138
                      59
   % identity
                      (AC004122) Highly Similar to branched-chain amino acid
   NCBI Description
                      aminotransferase [Arabidopsis thaliana]
                      31655
   Seq. No.
   Contig ID
                      249827 1.R1040
   5'-most EST
                      fua701043305.h1
   Method
                      BLASTN
   NCBI GI
                      g3860320
   BLAST score
                      92
   E value
                      2.0e-44
   Match length
                      258
                      85
   % identity
                      Cicer arietinum mRNA for beta-galactosidase, clone
   NCBI Description
                      CanBGal-5
   Seq. No.
                      31656
   Contig ID
                      249832 1.R1040
   5'-most EST
                      leu701145936.hl
   Method
                      BLASTN
```

q2598574

```
BLAST score
                     114
                     4.0e-57
 E value
                                 .
 Match length
                     358
                     83
  % identity
 NCBI Description Medicago truncatula mRNA for MtN21 gene
  Seq. No.
                     31657
                     249838 1.R1040
  Contig ID
                     jC-gmf\overline{1}02220053e06a1
  5'-most EST
                     BLASTX
 Method
 NCBI GI
                     q3152566
 BLAST score
                     309
                     3.0e-28
 E value
                     148
 Match length
                     45
  % identity
 NCBI Description
                     (AC002986) Similar to hypothetical protein YLR002c,
                     gb Z7314 from S. cerevisiae. [Arabidopsis thaliana]
  Seq. No.
                     31658
                     249860 1.R1040
 Contig ID
. 5'-most EST
                     k11701\overline{2}11805.h1
                     31659
 Seq. No.
                     249915 1.R1040---
 Contig ID-
  5'-most EST
                     fua701043414.h1
 Method
                     BLASTX
 NCBI GI
                     q1791307
 BLAST score
                     570
 E value
                     1.0e-58
 Match length
                     198
                     57
  % identity
 NCBI Description (U83501) permease homolog [Arabidopsis thaliana]
 Seq. No.
                     249980 1.R1040
  Contig ID
  5'-most EST
                     lus701015749.h1
  Seq. No.
                     31661
                     249990 1.R1040
  Contig ID
  5'-most EST
                     asn701131156.hl
 Seq. No.
                     31662
                     250041 1.R1040
 Contig ID
  5'-most EST
                     fC-gmro700564066f2
 Seq. No.
                     31663
                     250063 1.R1040
 Contig ID
 5'-most EST
                     fua701043589.hl
 Seq. No.
                     31664
                     250069 1.R1040
 Contig ID
                   hrw701\overline{0}60533.h1
 5'-most EST
                     31665
 Seq. No.
                     250074 1.R1040
 Contig ID
 5'-most EST
                    kl1701202347.h1
```

BLASTX

Method

NCBI GI

```
q557472
NCBI GI
                  234
BLAST score
                  2.0e-19
E value
                  148
Match length
                  39
% identity
                  (U15178) arabinosidase [Bacteroides ovatus]
NCBI Description
Seq. No.
                  31666
                  250082 1.R1040
Contig ID
                  jC-gmst02400071f09a1
5'-most EST
                  BLASTX
Method
                  q3281861
NCBI GI
BLAST score
                  557
                  3.0e-57
E value
                  177
Match length
                  62
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31667
                  250112 1.R1040
Contig ID
                  fua701043660.hl
5'-most EST
Method
                  BLASTX
                  g3859112
NCBI GI
BLAST score
                  231 --
E value
                  3.0e-19
Match length
                  56
% identity
                   (AF031607) male sterility MS5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  31668
                  250116 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810021d02a1
Seq. No.
                   250117 1.R1040
Contig ID
                   fua701043666.hl
5'-most EST
                   31670
Seq. No.
                   250129 1.R1040
Contig ID
                  uC-gmflminsoy031d08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3329368
BLAST score
                   430
                   2.0e-42
E value
Match length
                  175
% identity
                   53
                   (AF031244) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   31671
Seq. No.
                   250134 1.R1040
Contig ID
5'-most EST
                   fua701043686.hl
                   31672
Seq. No.
                  250144 1.R1040
Contig ID
5'-most EST
                  yz1700966904.h1
Method
                  BLASTX
```

g2765821

Seq. No.

Contig ID

31678

250237 1.R1040

```
BLAST score
                   1.0e-21
E value
                   112
Match length
% identity
                   46
NCBI Description
                  (295496) Mlo-hl protein [Hordeum vulgare]
Seq. No.
                   31673
                   250152 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy042f08b1
                   31674
Seq. No.
                   250217 1.R1040
Contig ID
                   leu701\overline{1}50261.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4415918
BLAST score
                  211
E value
                   4.0e-17
Match length
                   91
% identity
NCBI Description
                  (AC006282) hypothetical protein [Arabidopsis thaliana]
                   31675
Seq. No.
                   250219 1.R1040
Contig ID
5'-most EST
                   yz1700966990.h1
Method
                  BLASTX
                  g2809264
NCBI GI
BLAST score
                   398
E value
                   1.0e-38
                  172
Match length
                   48
% identity
NCBI Description
                  (AC002560) F21B7.33 [Arabidopsis thaliana]
Seq. No.
                   31676
                  250226 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220068h03a1
                  BLASTX
Method
                  g3096925
NCBI GI
BLAST score
                  222
E value
                   1.0e-17
Match length
                  153
                   42
% identity
NCBI Description
                  (AL023094) putative protein [Arabidopsis thaliana]
                   31677
Seq. No.
Contig ID
                  250229 1.R1040
5'-most EST
                  gsv701055909.hl
                  BLASTX
Method
NCBI GI
                  g3236241
BLAST score
                  293
E value
                  1.0e-26
                  73
Match length
% identity
                   (AC004684) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
```

Method

BLASTX

```
5'-most EST
                   uC-gmropic050e08b1
                   31679
Seq. No.
Contig ID
                   250340 1.R1040
5'-most EST
                   asj700<del>9</del>67375.h1
Method
                   BLASTX
NCBI GI
                   g4097522
BLAST score
                   381
                   7.0e-37
E value
Match length
                   107
% identity
                   60
NCBI Description
                   (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                   ananassa]
Seq. No.
                   31680
                   250355 1.R1040
Contig ID
5'-most EST
                   leu701152742.h1
Method
                   BLASTX
NCBI GI
                   g3047114
BLAST score
                   149
E value
                   8.0e-10
Match length
                   44
% identity
                   66
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                   31681
                   250381 1.R1040
Contig ID
5'-most EST
                   gsv701056131.h1
                   31682
Seq. No.
                   250388 1.R1040
Contig ID
5'-most EST
                   asj700967463.hl
Seq. No.
                   31683
                   250428 1.R1040
Contig ID
5'-most EST
                   leu701144353.h1
                   31684
Seq. No.
                   250485 1.R1040
Contig ID
5'-most EST
                   leu701156763.h1
                   BLASTX
Method
NCBI GI
                   g3757525
BLAST score
                   413
E value
                   3.0e-40
Match length
                   184
% identity
                   51
                   (AC005167) tetracycline transporter-like protein, 3'
NCBI Description
                   partial [Arabidopsis thaliana]
                   31685
Seq. No.
                   250497 1.R1040
Contig ID
                   leu701\overline{1}56076.h1
5'-most EST
                   31686
Seq. No.
                   250551 1.R1040
Contig ID
5'-most EST
                   uC-gmropic045d10b1
```

```
NCBI GI
                   g4454484
                   370
BLAST score
                   2.0e-35
E value
                   126
Match length
                   61
% identity
                   (AC006234) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31687
                   250569 1.R1040
Contig ID
5'-most EST
                   q5058429
                   BLASTX
Method
NCBI GI
                   q3540182
BLAST score
                   183
                   2.0e-13
E value
                   106
Match length
% identity
                   44
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   250624 1.R1040
Contig ID
                   leu701154368.h1
5'-most EST
Seq. No.
                   31689
                   250662 1.R1040
Contig ID
                   leu701144823.hl
5'-most EST
Seq. No.
                   31690
                   250667 1.R1040
Contig ID
5'-most EST
                   leu701144826.hl
Seq. No.
                   31691
                   250686 1.R1040
Contig ID
5'-most EST
                   leu701150509.hl
Method
                   BLASTX
NCBI GI
                   g3075399
BLAST score
                   230
E value
                   2.0e-19
Match length
                   81
% identity
NCBI Description
                   (AC004484) SF16-like protein [Arabidopsis thaliana]
Seq. No.
                   31692
                   250760 1.R1040
Contig ID
                   leu701145018.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g282964
                   308
BLAST score
                   2.0e-28
E value
                   67
Match length
                   76
% identity
NCBI Description
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
                   petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia
                   x hybrida]
Seq. No.
                   31693
```

250806 1.R1040

Contig ID

Seq. No.

```
5'-most EST
                   gsv701045130.hl
                   BLASTN
Method
                                                               į.,
NCBI GI
                   g3510331
                   38
BLAST score
E value
                   3.0e-12
Match length
                   98
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K13P22, complete sequence [Arabidopsis thaliana]
                   31694
Seq. No.
Contig ID
                   250835 1.R1040
                   leu701145151.h1
5'-most EST
                   31695
Seq. No.
                   250994 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}04441.h2
                   31696
Seq. No.
                   251026 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}07713.h1
Method
                   BLASTX
NCBI GI
                   g129021
                   149--
BLAST score
E value
                   7.0e-10
Match length
                   74
                   43
% identity
                   SPOOB-ASSOCIATED GTP-BINDING PROTEIN >gi 98326 pir B32804
NCBI Description
                   GTP-binding protein, spo0B 3'-region - Bacillus subtilis
                   >gi_508979 (M24537) GTP-binding protein [Bacillus subtilis]
                   >gi_2635257_emb_CAB14752_ (Z99118) GTPase activity
                   [Bacillus subtilis]
                   31697
Seq. No.
                   251036_1.R1040
Contig ID
5'-most EST
                   leu701145455.h1
                   31698
Seq. No.
Contig ID
                   251046 1.R1040
5'-most EST
                   leu701145467.hl
Seq. No.
                   31699
                   251047 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}45468.h1
Seq. No.
                   31700
                   251066 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810012d06d1
Method
                   BLASTX
NCBI GI
                   g1652078
BLAST score
                   279
                   8.0e-25
E value
                   110
Match length
% identity
                   46
                   (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
```

E value

1.0e-16

```
Contig ID
                   251070 1.R1040
5'-most EST
                   uC-gmropic088b04b1
Method
                   BLASTX
NCBI GI
                   g3892055
BLAST score
                   372
E value
                   1.0e-35
Match length
                   90
% identity
                   (AC002330) putative transport protein [Arabidopsis
NCBI Description
                   thaliana
                   31702
Seq. No.
                   251119 1.R1040
Contig ID
                   leu701\overline{1}45607.h1
5'-most EST
Seq. No.
                   31703
                   251159 1.R1040
Contig ID
5'-most EST
                   leu701150940.h1
Seq. No.
                   31704
                   251163 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}45667.h1
Method
                   BLASTN
NCBI-GI
                   g12979-
BLAST score
                   99
                   2.0e-48
E value
Match length
                   113
                   97
% identity
                   Soybean mitDNA for elongator tRNA-Met and tRNA-Glu
NCBI Description
Seq. No.
                   31705
Contig ID
                   251232 1.R1040
5'-most EST
                   uC-gmflminsoy036b03b1
Method
                   BLASTX
NCBI GI
                   g4530126
BLAST score
                   511
E value
                   5.0e-52
Match length
                   134
                   72
% identity
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
Seq. No.
                   31706
                   251238 1.R1040
Contig ID
5'-most EST
                   leu701149221.hl
                   31707
Seq. No.
                   251311 1.R1040
Contig ID
5'-most EST
                   leu701157740.hl
Seq. No.
                   31708
                   251392 1.R1040
Contig ID
                   leu701145987.hl
5'-most EST
                   BLASTX
Method
                   g1352267
NCBI GI
BLAST score
                   180
```

```
Match length
                   75
% identity
                   63
                   DEOXYHYPUSINE SYNTHASE >gi 994715 (L39068) deoxyhypusine
NCBI Description
                   synthase [Homo sapiens] >qi 1710220 (U79262) deoxyhypusine
                   synthase [Homo sapiens] >gi 3021398_emb_CAA04940
                   (AJ001701) deoxyhypusine synthase [Homo sapiens]
                   >gi 4503325 ref NP 001921.1 pDHPS deoxyhypusine synthase
                   31709
Seq. No.
                   251454 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}05335.h1
                   31710
Seq. No.
                   251527 1.R1040
Contig ID
                   k11701\overline{2}09769.h1
5'-most EST
Seq. No.
                   31711
Contig ID
                   251535 1.R1040
                   leu701146226.hl
5'-most EST
                   31712
Seq. No.
                   251596 1.R1040
Contig ID
                   leu701146322.h1
5'-most EST
Seq. No.
                   31713
                   251656 1.R1040
Contig ID
5'-most EST
                   leu701146466.hl
Seq. No.
                   31714
                   251672 1.R1040
Contig ID
                   leu701146441.hl
5'-most EST
                   31715
Seq. No.
                   251710 1.R1040
Contig ID
5'-most EST
                   leu701146504.h1
                   31716
Seq. No.
                   251715 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy022g07b1
Method
                   BLASTX
NCBI GI
                   g2190535
BLAST score
                   165
E value
                   1.0e-13
Match length
                   131
                   37
% identity
                  (U31240) luciferase [Photuris pennsylvanica]
NCBI Description
                   31717
Seq. No.
                   251744 1.R1040
Contig ID
5'-most EST
                   leu701146550.hl
Method
                   BLASTX
NCBI GI
                   g114974
BLAST score
                  133
E value
                   3.0e-12
Match length
                   53
% identity
                   51
```

NCBI Description NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR

Method

BLASTX

```
>gi 21955 emb CAA40058.1 (X56734) beta-glucosidase
                   [Trifolium repens]
Seq. No.
                   31718
Contig ID
                   251809 1.R1040
5'-most EST
                   iC-qmf102220062f12a1
Method
                   BLASTX
NCBI GI
                   q2062167
BLAST score
                   577
E value
                   1.0e-59
Match length
                   137
% identity
                   (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   31719
Seq. No.
                   251958 1.R1040
Contig ID
                   leu701\overline{1}46890.h1
5'-most EST
                   31720
Seq. No.
                   251966 1.R1040
Contig ID
                   asn701143134.hl
5'-most-EST-
                   31721
Seq. No.
                   251971 1.R1040
Contig ID
                   leu701146909.h1
5'-most EST
                   31722
Seq. No.
                   251975 1.R1040
Contig ID
                   leu701149831.h1
5'-most EST
                   31723
Seq. No.
                   252053 1.R1040
Contig ID
                   hrw701061054.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2275202
BLAST score
                   488
                   2.0e-49
E value
Match length
                   132
% identity
                   (ACO02337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31724
                   252069 1.R1040
Contig ID
5'-most EST
                   leu701147048.hl
                   31725
Seq. No.
                   252113 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}47115.h1
                   31726
Seq. No.
                   252136 1.R1040
Contig ID
5'-most EST
                   leu701147236.h1
```

>gi 67491 pir GLJY31 beta-glucosidase (EC 3.2.1.21)

precursor (clone TRE361) - white clover

```
NCBI GI
                  g3912919
BLAST score
                  594
                  1.0e-61
E value
Match length
                  166
% identity
                  73
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  31727
Contig ID
                  252139 1.R1040
5'-most EST
                  gsv701045770.hl
Method
                  BLASTX
NCBI GI
                  q3183617
BLAST score
                  413
E value
                  2.0e-40
Match length
                  126
% identity
NCBI Description
                  (AJ005586) MYB-related transcription factor [Antirrhinum
                  majus]
                  31728
Seq. No.
                  252141 1.R1040
Contig ID
5'-most EST
                  epx701109413.hl
Seq. No.
               252177 1.R1040
Contig ID
5'-most EST
                  leu701147211.h1
Seq. No.
                  31730
                  252196 1.R1040
Contig ID
5'-most EST
                  leu701\overline{1}47232.h1
Method
                  BLASTN
NCBI GI
                  g3510539
BLAST score
                  66
E value
                  8.0e-29
Match length
                  126
% identity
                  88
NCBI Description Prunus armeniaca expansin (Exp2) mRNA, complete cds
Seq. No.
                  31731
                  252424 1.R1040
Contig ID
                  leu701147568.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g629693
BLAST score
                  171
E value
                  1.0e-12
Match length
                  51
% identity
NCBI Description
                  probable integrase - common tobacco (fragment)
                  >gi 530742 emb CAA56791 (X80830) integrase [Nicotiana
                  tabacum]
                  31732
Seq. No.
                  252436 1.R1040
Contig ID
5'-most EST
                  leu701147851.hl
Seq. No.
                  31733
```

252449 1.R1040

Contig ID

BLAST score

```
gsv701056660.hl
5'-most EST
Seq. No.
                   31734
Contig ID
                   252454 1.R1040
5'-most EST
                   leu701147662.h1
Method
                   BLASTX
NCBI GI
                   g2760328
BLAST score
                   151
E value
                   4.0e-10
Match length
                   86
% identity
NCBI Description
                   (AC002130) F1N21.13 [Arabidopsis thaliana]
                   31735
Seq. No.
                   252475 1.R1040
Contig ID
5'-most EST
                   leu701150839.hl
Method
                   BLASTX
NCBI GI
                   q3292829
BLAST score
                   160
E value
                   4.0e-11
Match length
                   75
                   48
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   31736
                 252492 1.R1040
Contig ID
                   zsg701127494.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462825
BLAST score
                   265
                   9.0e-25
E value
Match length
                   79
                   73
% identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   31737
Seq. No.
Contig ID
                   252606 1.R1040
                   leu701147908.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244784
BLAST score
                   388
E value
                   1.0e-37
Match length
                   133
% identity
                   63
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   31738
Contig ID
                   252691 1.R1040
                   leu701148059.h1
5'-most EST
                   31739
Seq. No.
                   252811_1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}48184.h1
Method
                   BLASTX
                   g1653395
NCBI GI
```

% identity

```
E value
                   2.0e-21
Match length
                   92
% identity
NCBI Description
                   (D90913) PET112 [Synechocystis sp.]
Seq. No.
                   31740
Contig ID
                   252818 1.R1040
5'-most EST
                   leu701148193.hl
                   31741
Seq. No.
Contig ID
                   252826 1.R1040
5'-most EST
                   leu701\overline{1}48207.h1
                   BLASTX
Method
NCBI GI
                   g3241943
BLAST score
                   678
E value
                   2.0e-71
Match length
                   148
                   82
% identity
                   (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31742
Seq. No.
Contig ID
                   253029 1.R1040
5'-most EST
                   uC-gmropic039d03b1
                   31743
Seq. No.
                   253029 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy067a08b1
                   31744
Seq. No.
                   253037 1.R1040
Contig ID
                   leu701148509.hl
5'-most EST
                   31745
Seq. No.
                   253113 1.R1040
Contig ID
5'-most EST
                   leu701148606.hl
                   31746
Seq. No.
                   253123 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910041085a1
                   31747
Seq. No.
                   253126 1.R1040
Contig ID
5'-most EST
                   epx701104995.hl
Seq. No.
                   31748
                   253162 1.R1040
Contig ID
5'-most EST
                   leu701155120.h1
                   31749
Seq. No.
Contig ID
                   253167 1.R1040
5'-most EST
                   jC-gmro02800032f04a1
Method
                   BLASTX
NCBI GI
                   g3831451
BLAST score
                   563
                   4.0e-58
E value
Match length
                   114
```

Method

BLASTX

```
NCBI Description
                    (AC005700) putative O-GlcNAc transferase [Arabidopsis
                    thaliana]
                    31750
 Seq. No.
                    253173 1.R1040
 Contig ID
 5'-most EST
                    leu701148706.hl
                    BLASTX
 Method
 NCBI GI
                    g2190187
                                   7
 BLAST score
                    313
 E value
                    4.0e-29
                    102
 Match length
 % identity
                    33
 NCBI Description
                    (D64087) nuclear matrix constituent protein 1 (NMCP1)
                    [Daucus carota]
 Seq. No.
                    31751
                    253181 1.R1040
 Contig ID
 5'-most EST
                    leu701\overline{1}48717.h1
 Seq. No.
                    31752
                    253222 1.R1040
 Contig ID
 5'-most EST
                    kl1701214281.hl
 Method
                    BLASTX
NCBI GI
                    q1706371
 BLAST score
                    194
 E value
                    4.0e-15
                    62
 Match length
 % identity
                    66
                    DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                    4-REDUCTASE) >gi_486744_pir__S35189
dihydroflavonol-4-reductase (EC 1.-.-.) - gerbera hybrid
                    >gi_312777_emb_CAA78930_ (Z17221)
                    dihydroflavonol-4-reductase [Gerbera hybrida]
 Seq. No.
                    31753
                    253228 1.R1040
 Contig ID
                    leu701156342.h1
 5'-most EST
                    31754
 Seq. No.
                    253304 1.R1040
 Contig ID
 5'-most EST
                    leu701\overline{1}48887.h1
 Method
                    BLASTX
 NCBI GI
                    g3426039
 BLAST score
                    239
 E value
                    4.0e-20
 Match length
                    99
 % identity
                    49
 NCBI Description
                    (AC005168) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    31755
                    253324 1.R1040
 Contig ID
 5'-most EST
                    leu701148919.h1
 Seq. No.
                    31756
                    253355 1.R1040
 Contig ID
                    g5126801
 5'-most EST
```

Match length

```
NCBI GI
                   q4376592
BLAST score
                   156
                   4.0e-10
E value
                   144
Match length
                   9
% identity
                    (AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae]
NCBI Description
Seq. No.
                   253359 1.R1040
Contig ID
                   leu701156353.h1
5'-most EST
                   31758
Seq. No.
                   253515 1.R1040
Contig ID
                   leu701149235.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g114974
BLAST score
                   458
                   1.0e-45
E value
Match length
                   138
                   63
% identity
                   NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21)
                   precursor (clone TRE361) - white clover >gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
                    [Trifolium repens]
                   31759
Seq. No.
                   253588 1.R1040
Contig ID
                   leu701\overline{1}49335.h1
5'-most EST
                   31760
Seq. No.
                   253599 1.R1040
Contig ID
                   leu701150064.h1
5'-most EST
Seq. No.
                    31761
                   253603 1.R1040
Contig ID
5'-most EST
                   q4395889
Method
                   BLASTX
                   q1703052
NCBI GI
BLAST score
                   145
E value
                    5.0e-18
                   137
Match length
% identity
                    40
                   ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD
NCBI Description
                   SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37)
                   >qi 1498256 (M87339) replication factor C, 37-kDa subunit
                   [Homo sapiens] >gi_4506491_ref_NP_002907.1_pRFC4_
                   replication factor C (activator 1) 4 (37kD)
Seq. No.
                   31762
                   253610 1.R1040
Contig ID
                   qsv701\overline{0}45948.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2132184
BLAST score
                   201
                   8.0e-16
E value
```

```
% identity
                   hypothetical protein YPL093w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_1151233 (U43281) Lpg15p [Saccharomyces
                   cerevisiae]
Seq. No.
                   31763
Contig ID
                   253628 1.R1040
5'-most EST
                   leu701150093.hl
                                                                          ...
                   31764
Seq. No.
Contig ID
                   253645 1.R1040
                   asn701134216.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2335100
BLAST score
                   474
E value
                   8.0e-48
Match length
                   112
                   79
% identity
NCBI Description
                   (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31765
                   253699 1.R1040
Contig ID
5'-most EST
                   leu701151830.h1
Seq. No.
                   31766
                   253700 1.R1040
Contig ID
                   leu701149508.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3128136
BLAST score
                   39
E value
                   2.0e-12
Match length
                   51
% identity
                   94
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K1F13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   31767
                   253791 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}13583.h1
Method
                   BLASTX
NCBI GI
                   g2213629
BLAST score
                   258
E value
                   1.0e-22
Match length
                   52
% identity
NCBI Description
                  (AC000103) F21J9.21 [Arabidopsis thaliana]
Seq. No.
                   31768
                   253867 1.R1040
Contig ID
                   leu701\overline{1}49741.h1
5'-most EST
                   31769
Seq. No.
                   253887 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}49768.h1
Seq. No.
                   31770
                   253934_1.R1040
Contig ID
```

NCBI Description

thaliana]

```
5'-most EST
                   uC-gmflminsoy001e12b1
Method
                   BLASTX
                   g3080389
NCBI GI
BLAST score
                   253
                   1.0e-21
E value
Match length
                   58
% identity
                   86
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   31771
Seq. No.
                   254085 1.R1040
Contig ID
5'-most EST
                   leu701150058.h1
                   31772
Seq. No.
                   254086 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810023g06d1
                   31773
Seq. No.
                   254112 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400067d03d1
Seq. No.
                   31774
                   254116 1.R1040
Contig ID ~
                   leu701\overline{1}50107.h1
5'-most EST
Seq. No.
                   31775
                   254119 1.R1040
Contig ID
5'-most EST
                   leu701150110.h1
Seq. No.
                   31776
                   254192 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400053b09d1
Seq. No.
                   31777
                   254262 1.R1040
Contig ID
                   leu701150330.h1
5'-most EST
Seq. No.
                   31778
                   254283 1.R1040
Contig ID
                   leu701\overline{1}50359.h1
5'-most EST
                   31779
Seq. No.
                   254298 1.R1040
Contig ID
5'-most EST
                   leu701151987.h1
                   31780
Seq. No.
                   254339 1.R1040
Contig ID
                   asn701140117.hl
5'-most EST
Method
                   BLASTX
                   g4559342
NCBI GI
BLAST score
                   626
E value
                   2.0e-65
Match length
                   121
                   92
% identity
                   (AC007087) putative copper methylamine oxidase [Arabidopsis
```

5'-most EST

```
31781 254385 1.R1040
Seq. No.
Contig ID
5'-most EST
                   leu701151904.h1
                   31782
Seq. No.
Contig ID
                   254471_1.R1040
5'-most EST
                   uC-gmrominsoy034c12b1
                   31783
Seq. No.
                   254488 1.R1040
Contig ID
5'-most EST
                   qsv701047738.hl
Seq. No.
                   31784
                   254530 1.R1040
Contig ID
                   jC-gmf\overline{1}02220051g07a1
5'-most EST
                   31785
Seq. No.
                   254541 1.R1040
Contig ID `
5'-most EST
                   leu701150790.h1
                   BLASTX
Method
NCBI GI
                   g3402692
BLAST score
                   338
                   8.0e-32
E value
Match length
                   82
% identity
                   (AC004697) putative
NCBI Description
                   CDP-diacylglycerol--glycerol-3-phosphate
                   3-phosphatidyltransferase [Arabidopsis thaliana]
Seq. No.
                   31786
                   254630 1.R1040
Contig ID
                   leu701155825.hl
5'-most EST
Seq. No.
                   31787
                   254654 1.R1040
Contig ID
5'-most EST
                   g56061<del>2</del>3
Method
                   BLASTX
NCBI GI
                   q4455202
BLAST score
                   671
E value
                   6.0e-73
Match length
                   210
% identity
                   (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   254798 1.R1040
Contig ID
                   leu701151278.hl
5'-most EST
                   31789
Seq. No.
                   254815 1.R1040
Contig ID
                   asn701\overline{1}39715.h1
5'-most EST
Seq. No.
                   31790
                   254959 1.R1040
Contig ID
```

gsv701056139.hl

E value

```
Seq. No.
                   31791
                   254975 1.R1040
Contig ID
5'-most EST
                   leu701151630.hl
                   31792
Seq. No.
Contig ID
                   254986 1.R1040
5'-most EST
                   gsv701048289.hl
Method
                   BLASTX
NCBI GI
                   g953179
BLAST score
                   168
E value
                   7.0e-12
Match length
                   45
% identity
                   69
NCBI Description
                  (Z37980) ORF14 [Escherichia coli]
                  31793
Seq. No.
                   254990 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}51649.h1
                   31794
Seq. No.
                   255104 1.R1040
Contig ID
5'-most EST
                   leu701151824.h1
                   31795--
Seq. No. -
                   255105_1.R1040
Contig ID
                   leu701151825.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2190549
BLAST score
                   325
E value
                   4.0e-30
                   105
Match length
% identity
                   58
NCBI Description (AC001229) No definition line found [Arabidopsis thaliana]
Seq. No.
                   31796
                   255116 1.R1040
Contig ID
5'-most EST
                   leu701151844.h1
Seq. No.
                   31797
                   255127 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400001a02a1
Method
                   BLASTX
NCBI GI
                   g2950472
BLAST score
                   200 -
E value
                   2.0e-15
Match length
                   86
% identity
                   49
                   (AL022070) putative autophagocytosis protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   31798
Seq. No.
                   255147 1.R1040
Contig ID
5'-most EST
                   leu701151905.h1
Method
                   BLASTX
NCBI GI
                   g2335106
BLAST score
                   267
```

9.0e-24

5'-most EST

```
Match length
                   85
% identity
                   31
NCBI Description
                   (AC002339) salt inducible protein-like [Arabidopsis
                   thaliana]
Seq. No.
                   31799
                   255151 1.R1040
Contig ID
                   leu701151909.hl
5'-most EST
                   31800
Seq. No.
                   255202 1.R1040
Contig ID
                   leu701\overline{1}52071.h1
5'-most EST
                   31801
Seq. No.
                   255206 1.R1040
Contig ID
5'-most EST
                   leu701151982.h1
Method
                   BLASTN
NCBI GI
                   g3860320
BLAST score
                   161
E value
                   1.0e-85
Match length
                   249
% identity
                   91
NCBI Description
                   Cicer arietinum mRNA for beta-galactosidase, clone
                   CanBGal-5-
Seq. No.
                   31802
                   255219 1.R1040
Contig ID
5'-most EST
                   leu701152005.h1
Seq. No.
                   31803
                   255234 1.R1040
Contig ID
5'-most EST
                   leu701152032.h1
Seq. No.
                   31804
                   255287 1.R1040
Contig ID
                   epx701\overline{1}08938.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3021354
BLAST score
                   131
E value
                   1.0e-67
Match length
                   299
                   86
% identity
                   Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,
NCBI Description
                   clone GEPI42
Seq. No.
                   31805
                   255301 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}52137.h1
                   31806
Seq. No.
                   255307 1.R1040
Contig ID
5'-most EST
                   leu701152188.hl
Seq. No.
                   31807
                   255346 1.R1040
Contig ID
```

leu701152226.h1

```
31808
Seq. No.
                   255355 1.R1040
Contig ID
                   epx701105781.hl
5'-most EST
                   31809
Seq. No.
                   255364 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}42396.h1
Seq. No.
                   31810
                   255388 1.R1040
Contig ID
                   asn701140536.h1
5'-most EST
                   31811
Seq. No.
                   255441 1.R1040
Contig ID
                   leu701152366.h1
5'-most EST
                   31812
Seq. No.
                   255447 1.R1040
Contig ID
                   leu701152364.hl
5'-most EST
                   31813
Seq. No.
                   255550 1.R1040
Contig ID
                   1eu701\overline{1}52549.h1
5'-most EST
Seq. No.
                   31814
                   255604 1.R1040
Contig ID
                   leu701\overline{1}52607.h1
5'-most EST
Method
                   BLASTX
                   g3641834
NCBI GI
BLAST score
                   274
                   1.0e-24
E value
Match length
                   65
% identity
                   78
NCBI Description
                   (AJ007312) pyruvate dehydrogenase kinase [Arabidopsis
                   thaliana]
                   31815
Seq. No.
                   255670 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810004c05d1
Seq. No.
                   31816
                   255705 1.R1040
Contig ID
                   leu701152767.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2135070
BLAST score
                   157
                   2.0e-10
E value
                   90
Match length
                   36
% identity
NCBI Description
                   enoyl-CoA hydratase (EC 4.2.1.17) / AU-specific RNA-binding
                   protein - human >gi_780241_emb_CAA56260_ (X79888)
                   AU-binding protein/Enoyl-CoA hydratase [Homo sapiens]
                   >qi 4502327 ref NP 001689.1 pAUH AU RNA-binding
                   protein/enoyl-Coenzyme A hydratase
Seq. No.
                   31817
```

255760 1.R1040

Contig ID

Seq. No.

```
5'-most EST
                   leu701152950.h1
                   31818
Seq. No.
                   255786 1.R1040
Contig ID
5'-most EST
                   leu701152986.h1
                   BLASTX
Method
NCBI GI
                   g1946366
BLAST score
                   410
                   2.0e-40
E value
Match length
                   106
% identity
                   77
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   255791 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}52993.h1
Seq. No.
                   31820
Contig ID
                   255798 1.R1040
5'-most EST
                   leu701\overline{1}53008.h1
Seq. No.
                   31821
                   255861 1.R1040
Contig ID
5'-most-EST-
                   gsv701<del>0</del>52033.h1
Seq. No.
                   31822
                   255870 1.R1040
Contig ID
5'-most EST
                   leu701153136.h1
Seq. No.
                   31823
                   255877 1.R1040
Contig ID
                  leu701153464.hl
5'-most EST
Seq. No.
                   31824
                   255909 1.R1040
Contig ID
5'-most EST
                   g5126284
                                       秦信 双门
                   31825
Seq. No.
                   255958 1.R1040
Contig ID
5'-most EST
                   q4277036
Method
                   BLASTX
NCBI GI
                   g3482919
BLAST score
                   246
                   6.0e-21
E value
Match length
                   77
% identity
NCBI Description
                  (AC003970) Putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   31826
                   255964 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810048b11a1
Seq. No.
                   31827
                   255981 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}55318.hl
```

```
Contig ID
                   255989 1.R1040
5'-most EST
                   leu701153444.h1
                   31829
Seq. No.
                   255995 1.R1040
Contig ID
5'-most EST
                   leu701157044.hl
Seq. No.
                   31830
                   256053 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}53536.h1
Method
                   BLASTX
NCBI GI
                   q82056
BLAST score
                   346
E value
                   4.0e-33
Match length
                   81
% identity
                   84
                   protein kinase, calcium-dependent (EC 2.7.1.-) - carrot
NCBI Description
                   (fragment)
Seq. No.
                   31831
                   256065 1.R1040
Contig ID
5'-most EST
                   leu701154631.h1
                   31832--- - - --
Seq. No.
                   256067 1.R1040
Contig ID
5'-most EST
                   leu701157703.h1
Method
                   BLASTX
NCBI GI
                   q4455202
BLAST score
                   198
E value
                   1.0e-15
                   49
Match length
                   73
% identity
NCBI Description
                   (AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.
                   31833
                                                                            e de la cons
                   256103 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400048h05a1
Method
                   BLASTX
                   g4406778
NCBI GI
BLAST score
                   424
E value
                   4.0e-42
Match length
                   90
                   87
% identity
NCBI Description
                   (AC006532) putative brassinosteroid insensitive protein
                   [Arabidopsis thaliana]
Seq. No.
                   31834
                   256105 1.R1040
Contig ID
5'-most EST
                   leu701153775.h1
Method
                   BLASTN
NCBI GI
                   q3599418
BLAST score
                   33
E value
                   3.0e-09
                   58
Match length
% identity
                   90
                   Glycine max alternative oxidase precursor (Aox1) gene,
NCBI Description
```

nuclear gene encoding mitochondrial protein, complete cds

```
Seq. No.
                   31835
                   256232 1.R1040
Contig ID
                   k11701\overline{2}15249.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244818
BLAST score
                   227
E value
                   5.0e-19
Match length
                   85
% identity
                   59
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31836
Seq. No.
                   256247 1.R1040
Contig ID
5'-most EST
                   leu701156002.hl
                   31837
Seq. No.
                   256284 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy250d07b1
Method
                   BLASTX
NCBI GI
                   g4454470
BLAST score
                   396
E value
                   9.0e-39
                   96
Match length --
% identity
                   77
NCBI Description (AC006234) putative sugar transporter [Arabidopsis
                   thaliana]
Seq. No.
                   31838
                   256490 1.R1040
Contig ID
                   leu701154354.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3036795
BLAST score
                   188
E value
                   7.0e-14
Match length
                   100
% identity
                   34
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3805857_emb_CAA21477_ (AL031986) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   31839
                   256526 1.R1040
Contig ID
5'-most EST
                   leu701154409.hl
Method
                   BLASTX
NCBI GI
                   g1170619
BLAST score
                   494
                   6.0e-50
E value
                   156
Match length
% identity
                   66
                   KINESIN-LIKE PROTEIN A >qi 479594 pir S34830
NCBI Description
                   kinesin-related protein katA - Arabidopsis thaliana
                   >qi 303502 dbj BAA01972 (D11371) kinesin-like motor
                   protein heavy chain [Arabidopsis thaliana]
                   >gi_2911084_emb_CAA17546_ (AL021960) kinesin-related
protein katA [Arabidopsis thaliana]
```

Seq. No.

```
31840
Seq. No.
                    256562 1.R1040
Contig ID
                    leu701154463.hl
5'-most EST
                    31841
Seq. No.
                    256640 1.R1040
Contig ID
5'-most EST
                    leu701154583.h1
Seq. No.
                    31842
                    256660 1.R1040
Contig ID
                    leu701154616.h1
5'-most EST
                    31843
Seq. No.
                    256677 1.R1040
Contig ID
                    qsv701\overline{0}51142.h1
5'-most EST
                    31844
Seq. No.
                    256686 1.R1040
Contig ID
5'-most EST
                    leu701\overline{1}54688.h1
Method
                    BLASTX
                    g3892052
NCBI GI
BLAST score
                    143
E value
                    3.0e-09
Match length
                    72 -
% identity
                    43
                    (AC002330) predicted protein of unknown function
NCBI Description
                    [Arabidopsis thaliana]
                    31845
Seq. No.
                    256696 1.R1040
Contig ID
                    k11701\overline{2}12105.h1
5'-most EST
Seq. No.
                    31846
                    256717 1.R1040
Contig ID
5'-most EST
                    leu701\overline{1}54812.h1
Method
                    BLASTX
                    q1076715
NCBI GI
BLAST score
                    159
E value
                    4.0e-11
Match length
                    51
% identity
                    57
                    abscisic acid-induced protein HVA22 - barley >gi 404589
NCBI Description
                    (L19119) A22 [Hordeum vulgare]
                    31847
Seq. No.
Contig ID
                    256718 1.R1040
5'-most EST
                    leu701154813.h1
                    31848
Seq. No.
                    256780 1.R1040
Contig ID
                    leu701157246.h1
5'-most EST
                    31849
Seq. No.
                    256866 1.R1040
Contig ID
                    leu701\overline{1}55254.h1
5'-most EST
```

BLAST score

```
256908 1.R1040
 Contig ID
 5'-most EST
                    leu701155323.h1
                    31851
 Seq. No.
 Contig ID
                    256936 1.R1040
 5'-most EST
                    leu701156683.h1
                    31852
 Seq. No.
                    256991 1.R1040
 Contig ID
 5'-most EST
                    leu701155434.h1
 Seq. No.
                    31853
                    257028 1.R1040
 Contig ID
                    leu701155488.hl
 5'-most EST
                    31854
 Seq. No.
 Contig ID
                    257062 1.R1040
 5'-most EST
                    leu701\overline{1}55537.h1
 Seq. No.
                    31855
                    257081 1.R1040
 Contig ID
                    jC-qmf102220070c02d1
 5'-most EST
                    31856 - -
-Seq.-No.-
                    257084 1.R1040
 Contig ID
 5'-most EST
                    leu701155563.h1
 Seq. No.
                    31857
                    257106 1.R1040
 Contig ID
 5'-most EST
                    leu701155594.h1
 Seq. No.
                    31858
                    257125 1.R1040
 Contig ID
 5'-most EST
                    gsv701\overline{0}51789.h1
 Seq. No.
                    31859
                    257271 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810089b10a1
 Method
                    BLASTX
 NCBI GI
                    q3004564
 BLAST score
                    532
 E value
                    1.0e-70
 Match length
                    164
                    79
 % identity
 NCBI Description
                    (AC003673) putative receptor Ser/Thr protein kinase
                    [Arabidopsis thaliana]
 Seq. No.
                    31860
                    257340 1.R1040
 Contig ID
 5'-most EST
                    leu701155940.h1
 Seq. No.
                    31861
                    257371 1.R1040
 Contig ID
 5'-most EST
                    g4289134
 Method
                    BLASTX
 NCBI GI
                    g3695019
```

5'-most EST

```
2.0e-62
E value
                   166
Match length
                   69
% identity
                   (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   257379 1.R1040
                   jC-gmr002800030a11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3004551
BLAST score
                   134
                   2.0e-12
E value
Match length
                   83
% identity
                   48
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   31863
Seq. No.
                   257382 1.R1040
Contig ID
                   leu701155988.h1
5'-most EST
                   31864
Seq. No.
                   257383 1.R1040
Contig ID
                   leu701156155.hl
5'-most EST
Seq. No.
                   31865
                   257415 1.R1040
Contig ID
5'-most EST
                   leu701157027.hl
                   31866
Seq. No.
                   257420 1.R1040
Contig ID
                   leu701157020.h1
5'-most EST
Seq. No.
                   31867
                   257427 1.R1040
Contig ID
5'-most EST
                   leu701156709.hl
Method -
                   BLASTX
NCBI GI
                   g2129675
BLAST score
                   102
E value
                   1.0e-08
Match length
                   38
% identity
                   92
                   probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                   >gi_972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi 3068709 (AF049236) putative
                   chlorophyll synthetase [Arabidopsis thaliana]
Seq. No.
                   31868
                   257432 1.R1040
Contig ID
5'-most EST
                   leu701156068.h1
                   31869
Seq. No.
                   257457 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}56109.h1
                   31870
Seq. No.
                   257521 1.R1040
Contig ID
                   jsh701\overline{0}69515.h1
```

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g2213538
BLAST score
                  169
                  4.0e-12
E value
Match length
                  45
                  80
% identity
NCBI Description (X98740) DNA-binding protein PD2 [Pisum sativum]
                  31871
Seq. No.
                  257560 1.R1040
Contig ID
                  leu701156284.hl
5'-most EST
Seq. No.
                  31872
                  257607 2.R1040
Contig ID
                  leu701156572.h1
5'-most EST
                  31873
Seq. No.
                  257673_1.R1040
Contig ID
5'-most EST
                  jC-gmro02800039b09d1
                  31874
Seq. No.
                  257682 1.R1040
Contig ID
                  leu701156601.h1
5'-most EST
Seq. No.
                  31875
                  257720 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400057h11a1
                  BLASTX
Method
NCBI GI
                  g3236261
BLAST score
                  304
E value
                  1.0e-27
Match length
                  86
% identity
                  67
NCBI Description
                   (AC004684) putative zinc finger protein [Arabidopsis
                  thaliana]
                  31876
Seq. No.
                  257767 1.R1040
Contiq ID
5'-most EST
                  leu701156585.h1
Seq. No.
                  31877
                  257804 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910061h05a1
                  BLASTX
Method
NCBI GI
                  g3033377
BLAST score
                  273
E value
                  5.0e-24
                  137
Match length
% identity
                  43
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  31878
                  257824 1.R1040
Contig ID
                  leu701156664.h1
5'-most EST
```

```
257831 1.R1040
Contig ID
                   leu701\overline{1}56671.h1
5'-most EST
                   31880
Seq. No.
                   257832 1.R1040
Contig ID
                   leu701156672.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1101770
BLAST score
                   475
E value
                   1.0e-47
Match length
                   149
                   58
% identity
                   (U39448) MYB-like transcriptional factor MBF1 [Picea
NCBI Description
                   marianal
                   31881
Seq. No.
                   257834 1.R1040
Contig ID
                   k11701\overline{2}09132.h1
5'-most EST
Method
                   BLASTX :
NCBI GI
                   g2959781
BLAST score
                   316
E value
                   4.0e-29
Match length
                   145
% identity --
                   35-
NCBI Description
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
Seq. No.
                   31882
                   257853 1.R1040
Contig ID
5'-most EST
                   epx701107054.hl
Seq. No.
                   31883
                   257856 1.R1040
Contig ID
5'-most EST
                   leu701156706.hl
Method
                   BLASTX
NCBI GI
                   q3646324
BLAST score
                   206
E value
                   1.0e-16
Match length
                   78
% identity
NCBI Description
                   (AJ000761) MADS-box protein [Malus domestica]
Seq. No.
                   257863 1.R1040
Contig ID
5'-most EST
                   leu701156715.hl
Seq. No.
                   31885
Contig ID
                   257894 1.R1040
5'-most EST
                   leu701156756.hl
Method
                   BLASTX
NCBI GI
                   q2921336
BLAST score
                   581
E value
                   5.0e-60
Match length
                   119
% identity
                   87
NCBI Description
                   (AF034132) MYB-like DNA-binding domain protein [Gossypium
```

hirsutum]

```
31886
Seq. No.
                  257926 1.R1040
Contig ID
                  leu701157083.hl
5'-most EST
Seq. No.
                  31887
                  257973 1.R1040
Contig ID
5'-most EST
                  leu701156974.hl
Seq. No.
                  31888
                  257976 1.R1040
Contig ID
                  leu701156988.h1
5'-most EST
                  31889
Seq. No.
                  257986 1.R1040
Contig ID
                  leu701156994.h1
5'-most EST
                  31890
Seq. No.
                  257992 1.R1040
Contig ID
                  leu701157008.h1
5'-most EST
Method
                  BLASTX
                  g3776559
NCBI GI
BLAST score
                  436
E value
                  2.0e-43
Match length -
                  106-
% identity
NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  31891
Seq. No.
                  258018 1.R1040
Contig ID
                  leu701157043.h1
5'-most EST
Seq. No.
                  31892
                  258054 1.R1040
Contig ID
                  leu701157092.h1
5'-most EST
Method
                  BLASTX
                  q2623304
NCBI GI
BLAST score
                  181
E value
                   3.0e-13
Match length
                  119
% identity
                  32
                   (AC002409) similar to Medicago nodulin N21 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  31893
                  258080 1.R1040
Contig ID
5'-most EST
                  leu701157163.hl
                  31894
Seq. No.
                  258095 1.R1040
Contig ID
                  leu701157186.hl
5'-most EST
Seq. No.
                  31895
                  258096 1.R1040
Contig ID
```

leu701157204.h1

5'-most EST

Contig ID .

```
Seq. No.
                   31896
                   258117 1.R1040
Contig ID
                   leu701157227.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2689720
BLAST score
                   255
E value
                   3.0e-22
                   78
Match length
                   71
% identity
                   (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
                   31897
Seq. No.
                   258219 1.R1040
Contig ID
5'-most EST
                   zsq701123070.hl
                   31898
Seq. No.
                   258261 1.R1040
Contig ID
                   hrw701061515.hl
5'-most EST
Seq. No.
                   31899
                   258266 1.R1040
Contig ID
5'-most EST
                   leu701157545.hl
Method -- -
                  BLASTX
NCBI GI
                   q4530126
BLAST score
                   205
E value
                   4.0e-16
Match length
                   113
% identity
                   42
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
Seq. No.
                   31900
                   258282 1.R1040
Contig ID
5'-most EST
                   leu701\overline{1}57704.h1
Seq. No.
                   31901
                   258328 1.R1040
Contig ID
5'-most EST
                   leu701157879.h1
Seq. No.
                   31902
                   258334 1.R1040
Contig ID
5'-most EST
                   leu701157733.h1
Seq. No.
                   31903
Contig ID
                   258547 1.R1040
5'-most EST
                   jC-gmst02400055e10a1
Method
                   BLASTX
NCBI GI
                   q2737926
BLAST score
                   641
E value
                   4.0e-67
Match length
                   155
% identity
                   77
                   (U77673) fimbrin-like protein AtFim2 [Arabidopsis thaliana]
NCBI Description
                   31904
Seq. No.
```

258614 1.R1040

Contig ID

```
uC-gmflminsoy065a10b1
5'-most EST
                   31905
Seq. No.
                   258642 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy089c09b1
Method
                   BLASTX
NCBI GI
                   g3201627
BLAST score
                   181
E value
                   2.0e-13
Match length
                   36
                   83
% identity
NCBI Description
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.
                   31906
                   258668 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy018b04b1
Method
                   BLASTX
                   g2529707
NCBI GI
BLAST score
                   400
E value
                   5.0e-39
Match length
                   127
% identity
                   57
NCBI Description
                   (AF001434) Hpast [Homo sapiens]
Seq. No.
                   31907
                   258676 1.R1040
Contig ID
5'-most EST
                   qsv701043806.hl
Method
                   BLASTX
NCBI GI
                   g4309698
BLAST score
                   420
E value
                   1.0e-41
Match length
                   99
% identity
NCBI Description
                   (AC006266) putative glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   31908
                   258684 1.R1040
Contig ID
5'-most EST
                   gsv701046676.hl
Seq. No.
                   31909
                   258714 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400078g05d1
Method
                   BLASTX
NCBI GI
                   q4056482
BLAST score
                   353
E value
                   2.0e-33
Match length
                   99
% identity
                   41
NCBI Description
                   (AC005896) putative ABC transporter [Arabidopsis thaliana]
                   31910
Seq. No.
                   258740 1.R1040
Contig ID
5'-most EST
                   gsv701043922.hl
                   31911
Seq. No.
```

258760_1.R1040

NCBI GI

```
5'-most EST
                   gsv701051971.hl
Method
                   BLASTX
NCBI GI
                   g1362091
BLAST score
                   369
                   9.0e-36
E value
Match length
                   83
% identity
                   81
                   cellulase (EC 3.2.1.4) precursor - tomato >gi 924622
NCBI Description
                   (U20590) endo-1,4-beta-glucanase precursor [Solanum
                  lycopersicum]
                   31912
Seq. No.
                   258866 1.R1040
Contig ID
                   qsv701\overline{0}50088.h1
5'-most EST
Method
                   BLASTX
                   g2288988
NCBI GI
BLAST score
                   370
                   8.0e-36
E value
Match length
                   88
                   77
% identity
                   (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31913
                   258870 1.R1040 -----
Contig ID-
5'-most EST
                   uC-qmflminsoy082g05b1
                   31914
Seq. No.
                   258890 1.R1040
Contig ID
                   jC-gmf102220108h02a1
5'-most EST
Method
                   BLASTX
                   g4432814
NCBI GI
BLAST score
                   703
E value
                   3.0e-74
Match length
                   158
% identity
                   84
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
Seq. No.
                   31915
                   258910 1.R1040
Contiq ID
                   g50584\overline{17}
5'-most EST
Method
                   BLASTX
                   g4220480
NCBI GI
BLAST score
                   229
                   3.0e-23
E value
                   133
Match length
% identity
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
                   31916
Seq. No.
                   258928 1.R1040
Contig ID
5'-most EST
                   asn701142720.h1
                   31917
Seq. No.
                   258930 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}67648.h1
                   BLASTN
Method
```

g1669590

Match length

```
BLAST score
                    76
. E value
                    1.0e-34
Match length
                    249
                    82
 % identity
                    Glycyrrhiza echinata mRNA for O-methyltransferase, complete
 NCBI Description
                    31918
 Seq. No.
                    258936 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy193a01b1
Method
                    BLASTX
NCBI GI
                    q2258469
 BLAST score
                    348
 E value
                    3.0e-33
Match length
                    98
 % identity
                    69
                    (AF009179) replication protein A1 [Oryza sativa]
NCBI Description
 Seq. No.
                    31919
                    258990 1.R1040
Contig ID
 5'-most EST
                    g4313401
Method
                    BLASTX
NCBI GI
                    g2781359
BLAST-score
                    -326--
 E value
                    3.0e-30
Match length
                    137
 % identity
                    53
                    (AC003113) F2501.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    31920
                    259028 1.R1040
 Contig ID
 5'-most EST
                    gsv701\overline{0}44331.h1
Seq. No.
                    31921
Contig ID
                    259298 1.R1040
 5'-most EST
                    gsv701044745.hl
Method
                    BLASTX
NCBI GI
                    q3687654
BLAST score
                    148
E value
                    1.0e-18
Match length
                    78
 % identity
                    (AF047975) putative ethylene receptor; ETR2 [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    31922
                    259331 1.R1040
Contig ID
5'-most EST
                    gsv701044741.hl
Seq. No.
                    31923
                    259484 1.R1040
Contig ID
5'-most EST
                    qsv701\overline{0}44930.h1
Method
                    BLASTX
NCBI GI
                    g1237250 .
BLAST score
                    387
                    2.0e-37
E value
```

```
% identity
NCBI Description
                   (X96784) cytochrome P450 [Nicotiana tabacum]
                   31924
Seq. No.
                   259525_1.R1040
Contig ID
5'-most EST
                   gsv701044982.h1
Method
                   BLASTN
NCBI GI
                   g3832511
BLAST score
                   114
                   2.0e-57
E value
                   246
Match length
                   87
% identity
NCBI Description
                   Astragalus membranaceus granule-bound glycogen (starch)
                   synthase mRNA, complete cds
Seq. No.
                   31925
                   259544 1.R1040
Contig ID
                   gsv701\overline{0}45212.h1
5'-most EST
                   31926
Seq. No.
                   259549 1.R1040
Contig ID
5'-most EST
                   zsg701118809.h1
                   BLASTX
Method
NCBI GI
                   g2623298-
BLAST score
                   485
                   3.0e-49
E value
Match length
                   87
                   97
% identity
                    (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   31927
                   259627 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}45149.h1
Seq. No.
                   31928
                   259727 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}45381.h1
Seq. No.
                   31929
                   259798 1.R1040
Contig ID
                   gsv701\overline{0}45392.h1
5'-most EST
Seq. No.
                   31930
Contig ID
                   259853 1.R1040
5'-most EST
                   jC-gmst02400045g10a1
Seq. No.
                   31931
                   259914 1.R1040
Contig ID
5'-most EST
                   gsv701045560.hl
Seq. No.
                   31932
                   260018_1.R1040
Contig ID
                   ek1700968110.hl
5'-most EST
Seq. No.
                   31933
                   260105 1.R1040
Contig ID
```

Seq. No.

```
5'-most EST
                      gsv701045809.h1
  Method
                      BLASTX
  NCBI GI
                      g2258469
  BLAST score
                      288
                      7.0e-26
  E value
  Match length
                      115
  % identity
                      54
  NCBI Description
                      (AF009179) replication protein Al [Oryza sativa]
  Seq. No.
                      31934
                      260369 1.R1040
  Contig ID
  5'-most EST
                      qsv701\overline{0}53741.h1
  Seq. No.
                      31935
                      260459 1.R1040
  Contig ID
                      gsv701\overline{0}51136.h1
  5'-most EST
                      31936
  Seq. No.
                      260476 1.R1040
  Contig ID
                      gsv701\overline{0}46270.h1
  5'-most EST
                      BLASTX
  Method
  NCBI GI
                      g2832408
                      404
  BLAST score
-- E value ---
                     1.0e-39 ---
  Match length
                      75
  % identity
                      (Y14209) R2R3-MYB transcription factor [Arabidopsis
  NCBI Description
                      thaliana]
  Seq. No.
                      31937
                      260526 1.R1040
  Contig ID
  5'-most EST
                      uC-gmropic107e05b1
  Seq. No.
                      31938
  Contig ID
                      260533 1.R1040
  5'-most EST
                      gsv701046344.hl
                      31939
  Seq. No.
                      260661 1.R1040
  Contig ID
                      k11701215484.hl
  5'-most EST
                      31940
  Seq. No.
                      260664 1.R1040
  Contig ID
  5'-most EST
                      gsv701048389.h1
  Seq. No.
                      31941
                      260713 1.R1040
  Contig ID
  5'-most EST
                      jC-gmle01810014d09d1
  Method
                      BLASTX
  NCBI GI
                      g2911058
  BLAST score
                      266
                      3.0e-23
  E value
                      72
  Match length
                      58
  % identity
                      (AL021961) putative protein [Arabidopsis thaliana]
  NCBI Description
```

```
260849 1.R1040
Contig ID
5'-most EST
                    gsv701046733.hl
Seq. No.
                    31943
                    260881 1.R1040
Contig ID
5'-most EST
                    jC-gmst02400005d09d1
Seq. No.
                    31944
                    261125 1.R1040
Contig ID
5'-most EST
                    gsv701047135.h1
Method
                    BLASTX
NCBI GI
                    q1619300
BLAST score
                    254
E value
                    8.0e-22
                    108
Match length
% identity
                    47
NCBI Description
                    (X95269) LRR protein [Lycopersicon esculentum]
                    31945
Seq. No.
                    261385 1.R1040
Contig ID
5'-most EST
                    qsv701\overline{0}47665.h1
                    BLASTX
Method
                    g3080452
NCBI GI
BLAST score
                    624
E value
                    5.0e-65
Match length
                    166
                    66
% identity
                    (AL022605) putative L-ascorbate oxidase [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    31946
                    261488 1.R1040
Contig ID
5'-most EST
                    qsv701\overline{0}47785.h1
                    31947
Seq. No.
Contig ID
                    261495 1.R1040
5'-most EST
                    qsv701\overline{0}47792.h1
Method
                    BLASTX
                    q4559355
NCBI GI
BLAST score
                    268
E value
                    9.0e-24
Match length
                    73
                    64
% identity
NCBI Description
                    (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    31948
Contig ID
                    261508 1.R1040
5'-most EST
                    qsv701\overline{0}47811.h1
Seq. No.
                    31949
                    261596 1.R1040
Contig ID
5'-most EST
                    qsv701\overline{0}47921.h1
Method
                    BLASTX
NCBI GI
                    q2119719
BLAST score
                    418
                    2.0e-41
E value
```

94

Match length

```
% identity
                   84
                   heat-shock cognate protein 70-3 - tomato >gi 762844
NCBI Description
                   (L41253) Hsc70 [Lycopersicon esculentum]
                   31950
Seq. No.
Contig ID
                   261665 1.R1040
5'-most EST
                   g57531\overline{4}5
                   31951
Seq. No.
                   261707 1.R1040
Contig ID
                   jC-gmro02910062a07d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2435522
                   198
BLAST score
E value
                   2.0e-15
                   62
Match length
                   61
% identity
NCBI Description
                   (AF024504) contains similarity to other AMP-binding enzymes
                   [Arabidopsis thaliana]
Seq. No.
                   31952
                   261714 1.R1040
Contig ID
                   gsv701048715.h1
5'-most EST
Seq. No.
                   31953
                   261746 1.R1040
Contig ID
5'-most EST
                   gsv701048116.h1
                   31954
Seq. No.
                   261752 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy169b08b1
Method
                   BLASTX
                   g2443329
NCBI GI
BLAST score
                   193
E value
                   3.0e-14
Match length
                   135
                   39
% identity
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.
                   261790 1.R1040
Contig ID
5'-most EST
                   uC-gmropic040b10b1
                   31956
Seq. No.
                   261819 1.R1040
Contig ID
5'-most EST
                   gsv701048211.hl
                   31957
Seq. No.
                   261868 1.R1040
Contig ID
5'-most EST
                   gsv701048270.h1
Seq. No.
                   31958
                   261886 1.R1040
Contig ID
                   hrw701\overline{0}61252.h1
5'-most EST
                   31959
Seq. No.
                   261965 1.R1040
Contig ID
```

Contig ID

```
5'-most EST
                      jC-gmst02400063c04a1
Method
                      BLASTX
 NCBI GI
                      g2827709
 BLAST score
                      459
 E value
                      1.0e-45
Match length
                      246
 % identity
                      21
 NCBI Description
                      (AL021684) predicted protein [Arabidopsis thaliana]
 Seq. No.
                      31960
                      261982 1.R1040
 Contig ID
                      qsv701\overline{0}48432.h1
 5'-most EST
 Seq. No.
                      31961
                      261984 1.R1040
 Contig ID
 5'-most EST
                      gsv701048434.hl
 Seq. No.
                      31962
 Contig ID
                      262103 1.R1040
 5'-most EST
                      qsv701\overline{0}48573.h1
Method
                      BLASTX
NCBI GI
                      q2497542
 BLAST score
                      467
E value
                      5.0e-47
Match length
                      110
 % identity
                      85
                      PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir_S44287 pyruvate kinase, plastid - common tobacco >gi_482938 emb_CAA82223_(Z28374) Pyruvate kinase;
NCBI Description
                      plastid isozyme [Nicotiana tabacum]
                      31963
 Seq. No.
                      262173 1.R1040
 Contig ID
 5'-most EST
                      gsv701\overline{0}48667.h1
 Seq. No.
                      31964
                      262199 1.R1040
 Contig ID
 5'-most EST
                      q5752535
                      31965
 Seq. No.
 Contig ID
                      262223 1.R1040
 5'-most EST
                      qsv701\overline{0}48741.h1
                      31966
Seq. No.
                      262260 1.R1040
 Contig ID
 5'-most EST
                      jC-gmf\overline{1}02220138b03a1
Method
                      BLASTX
NCBI GI
                      q4376203
BLAST score
                      204
E value
                      6.0e-16
Match length
                      114
 % identity
NCBI Description
                      (U35226) putative cytochrome P-450 [Nicotiana
                      plumbaginifolia]
                      31967
 Seq. No.
```

262304 1.R1040

```
5'-most EST
                   qsv701048838.h1
Method
                   BLASTX
NCBI GI
                   q3834307
BLAST score
                   260
E value
                   2.0e-22
Match length
                   113
% identity
                   61
NCBI Description
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs gb N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   31968
                   262337 1.R1040
Contig ID
5'-most EST
                   zsq701\overline{1}27365.h1
Method
                   BLASTX
NCBI GI
                   g2462835
BLAST score
                   476
E value
                   7.0e-48
Match length
                   124
% identity
                   72
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
                 - 31969------
Seq. No:
                   262392 1.R1040
Contig ID
5'-most EST
                   asn701140958.hl
Sea. No.
                   31970
                   262400 1.R1040
Contig ID
5'-most EST
                   uC-gmropic110f02b1
Seq. No.
                   262402 1.R1040
Contig ID
5'-most EST
                   uC-gmropic016f02b1
Seq. No.
                   31972
                   262444 1.R1040
Contig ID .
5'-most EST
                   uC-gmrominsoy319b10b1
Seq. No.
                   31973
Contig ID
                   262463 1.R1040
5'-most EST
                   qsv701\overline{0}49036.h1
Seq. No.
                   31974
Contig ID
                   262480 1.R1040
5'-most EST
                   asn701\overline{1}38395.h1
Method
                   BLASTX
NCBI GI
                   q1168609
BLAST score
                   353
E value
                   8.0e-34
Match length
                   90
% identity
NCBI Description
                  AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir $35071
                   auxin-resistance protein AXR1 - Arabidopsis thaliana
                   >gi 304104 (L13922) ubiquitin-activating enzyme E1
                   [Arabidopsis thaliana] >gi 2388579 (AC000098) Match to
```

Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]

```
[Arabidopsis thaliana]
Seq. No.
                    31975
                    262521 1.R1040
Contig ID
                    gsv701\overline{0}49112.h1
5'-most EST
Seq. No.
                    31976
                    262529 1.R1040
Contig ID
                    gsv701\overline{0}49122.h1
5'-most EST
                    31977
Seq. No.
                    262551 1.R1040
Contiq ID
                    qsv701\overline{0}49144.h1
5'-most EST
Seq. No.
                    31978
                    262639 1.R1040
Contig ID
                    k11701\overline{2}13755.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3059122
BLAST score
                    499
E value
                    1.0e-50
Match length
                    121
%-identity -
                    80
                    (AJ003783) glyeraldehyde-3-phosphate dehydrogenase
NCBI Description
                    [Marsilea quadrifolia]
Seq. No.
                    31979
                    262640 1.R1040
Contig ID
5'-most EST
                    jC-gmro02910004c12a1
                    31980
Seq. No.
                    262673 1.R1040
Contig ID
5'-most EST
                    q56059\overline{3}8
Method
                    BLASTX
NCBI GI
                    q2739279
BLAST score
                    447
E value
                    2.0e-44
Match length
                    165
% identity
NCBI Description
                    (AJ223177) short chain alcohol dehydrogenase [Nicotiana
                    tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain
                    alcohol dehydrogenase [Nicotiana tabacum]
Seq. No.
                    31981
                    262742 1.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy096e06b1
Method
                    BLASTX
NCBI GI
                    q2832304
BLAST score
                    466
E value
                    1.0e-46
Match length
                    149
% identity
NCBI Description
                    (AF044489) receptor-like protein kinase [Oryza sativa]
Seq. No.
                    31982
```

>qi 448755 prf 1917337A ubiquitin-activating enzyme E1

262772_1.R1040

Contig ID

```
5'-most EST
                   q5175517
Method
                   BLASTX
NCBI GI
                   q2529677
BLAST score
                   148
E value
                   1.0e-09
Match length
                   37
% identity
                   73
NCBI Description
                   (ACO02535) kinesin-like protein, heavy chain [Arabidopsis
                   thaliana]
Seq. No.
                   31983
                   262777 1.R1040
Contig ID
                   jC-gmro02800027d11d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2739378
BLAST score
                   141
                   8.0e-09
E value
                   63
Match length
% identity
                   48
NCBI Description
                   (AC002505) AR781 [Arabidopsis thaliana]
                   31984
Seq. No.
Contig ID
                   262855_1.R1040
5 -most EST
                   -jC-gmr002910007b01a1
                   31985
Seq. No.
                   262865 1.R1040
Contig ID
                   gsv701\overline{0}49586.h1
5'-most EST
                   31986
Seq. No.
Contig ID
                   262925 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220103e08a1
                   31987
Seq. No.
                   262932_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy178c11b1
                   31988
Seq. No.
                   262946 1.R1040
Contig ID
                   qsv701\overline{0}49693.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1946368
BLAST score
                   258
E value
                   2.0e-22
                   119
Match length
% identity
                   48
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   31989
                   263020 1.R1040
Contig ID
5'-most EST
                   q5753325
Method
                   BLASTX
NCBI GI
                   q3367531
BLAST score
                   131
                   7.0e-12
E value
Match length
                   148
                   36
% identity
```

```
NCBI Description (AC004392) Strong similarity to gi_2160138 F19K23.6 gene
                   product from A. thaliana BAC gb AC000375. [Arabidopsis
                . thaliana]
                   31990
Seq. No.
                   263102 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}49942.h1
                   BLASTN
Method
NCBI GI
                   q169980
BLAST score
                   188
E value.
                   1.0e-101
Match length
                   282
                   92
% identity
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
NCBI Description
Seq. No.
                   31991
                   263175 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}51306.h1
                   31992
Seq. No.
                   263203 1.R1040
Contig ID
                   gsv701\overline{0}50068.h1
5'-most EST
Method
                   BLASTX
NCBI- GI ---- ---
                  -q2827621
BLAST score
                   194
E value
                   4.0e-15
Match length
                   38
                   82
% identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                   31993
Seq. No.
                   263309 1.R1040
Contig ID
5'-most EST
                   q5753498
Method
                   BLASTX
NCBI GI
                   g2191168
BLAST score
                   147
E value
                   7.0e-21
Match length
                   91
                   60
% identity
                    (AF007270) contains similarity to myosin heavy chain
NCBI Description
                    [Arabidopsis thaliana]
                   31994
Seq. No.
                   263364 1.R1040
Contig ID
5'-most EST
                   zsg701124991.hl
                   31995
Seq. No.
Contig ID
                   263422 1.R1040
5'-most EST
                   gsv701\overline{0}50367.h1
                   31996
Seq. No.
                   263439_1.R1040
Contig ID
5'-most EST
                   q50582\overline{0}4
Method
                   BLASTX
                   g4038044
NCBI GI
BLAST score
                   235
```

2.0e-19

E value

Seq. No.

```
83
Match length
                   66
% identity
NCBI Description
                   (AC005936) unknown protein [Arabidopsis thaliana]
                   >gi_4406788_gb_AAD20098_ (AC006532) unknown protein
                   [Arabidopsis thaliana]
                   31997
Seq. No.
Contig ID
                   263481 1.R1040
5'-most EST
                   uC-gmflminsoy071c11b2
                   31998
Seq. No.
                   263483 1.R1040
Contig ID
5'-most EST
                   qsv701055252.h1
Seq. No.
                   31999
                   263544 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}50526.h1
Seq. No.
                   32000
                   263548 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400055e04a1
Seq. No.
                   32001
Contig ID
                   263611 1.R1040
5'-most EST
                   g53427\overline{2}1
Method
                   BLASTX
NCBI GI
                   g1234900
BLAST score
                   313
E value
                   6.0e-59
Match length
                   168
% identity
                   73
NCBI Description
                   (X92489) homeobox-leucine zipper protein [Glycine max]
Seq. No.
                   32002
                   263694_1.R1040
Contig ID
5'-most EST
                   uC-gmropic034f11b1
Seq. No.
                   32003
Contig ID
                   263724_1.R1040
5'-most EST
                   uC-gmropic047c06b1
Method
                   BLASTX
NCBI GI
                   q1871187
BLAST score
                   357
E value
                   1.0e-33
Match length
                   149
% identity
NCBI Description
                   (U90439) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32004
                   263731 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400004c05d1
Seq. No.
                   32005
                   263731 2.R1040
Contiq ID
5'-most EST
                   g5688425
```

```
Contig ID
                   263747 1.R1040
5'-most EST
                   k11701\overline{2}13958.h1
Method
                   BLASTX
NCBI GI
                   g2335100
BLAST score
                   470
E value
                   2.0e-47
                   108
Match length
% identity
                   81
NCBI Description
                   (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32007
                   263777 1.R1040
Contig ID
                   qsv701\overline{0}50836.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3482920
BLAST score
                   251
E value
                   2.0e-21
Match length
                   63
                   73
% identity
NCBI Description
                   (AC003970) Hypothetical protein [Arabidopsis thaliana]
                   32008
Seq. No.
                   263822 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220080c07a1 --
                   32009
Seq. No.
                   263837 1.R1040
Contig ID
5'-most EST
                   qsv701050960.hl
                   BLASTX
Method
NCBI GI
                   g1800223
BLAST score
                   150
                   7.0e-10
E value
Match length
                   57
% identity
                   53
                   (U65018) mannosyltransferase [Dictyostelium discoideum]
NCBI Description
Seq. No.
                   32010
                   263995 1.R1040
Contig ID
5'-most EST
                   gsv701051161.hl
Method
                   BLASTX
NCBI GI
                   q3668171
BLAST score
                   422
                   3.0e-41
E value
Match length
                   190
% identity
                   44
                   (AB006052) RNA polymerase I second-largest subunit
NCBI Description
                   [Neurospora crassa]
Seq. No.
                   32011
                   264077 1.R1040
Contig ID
                   uC-qmflminsoy018b08b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455171
BLAST score
                   262
                   1.0e-42
E value
Match length
                   185
                   51
% identity
```

Method

BLASTX

```
NCBI Description
                   (AL035521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32012
                   264119 1.R1040
Contig ID
5'-most EST
                   gsv701054444.hl
                   32013
Seq. No.
                   264223 1.R1040
Contig ID
5'-most EST
                   fC-gmle700554943d3
                   BLASTX
Method
                   g2982301
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
Match length
                   44
% identity
NCBI Description
                   (AF051235) YGL010w-like protein [Picea mariana]
Seq. No.
                   264286 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}51519.h1
Seq. No.
                   32015
                   264324 1.R1040
Contig ID
5'-most EST
                   gsv701051566.hl
Seq. No.
                   32016
                   264429 1.R1040
Contig ID
5'-most EST
                   gsv701051722.hl
Method
                   BLASTX
NCBI GI
                   q2961346
BLAST score
                   167
E value
                   5.0e-12
Match length
                   37
% identity
NCBI Description
                   (AL022140) pectinesterase like protein [Arabidopsis
                   thalianal
Seq. No.
                   32017
                   264454 1.R1040
Contig ID
5'-most EST
                   gsv701056174.hl
Seq. No.
                   32018
                   264536 1.R1040
Contig ID
5'-most EST
                   gsv701054288.h1
                   32019
Seq. No.
Contig ID
                   264565 1.R1040
5'-most EST
                   gsv701054339.h1
                   32020
Seq. No.
                   264566 1.R1040
Contig ID
5'-most EST
                   qsv701\overline{0}51941.h1
                   32021
Seq. No.
                   264617 1.R1040
Contig ID
5'-most EST
                   zsq701125604.h1
```

1.50

NCBI Description

```
q4220519
NCBI GI
BLAST score
                   161
E value
                   5.0e-11
Match length
                   61
% identity
                   (AL035356) putative protein binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   32022
                   264667 1.R1040
Contig ID
5'-most EST
                   gsv701052072.h1
                   32023
Seq. No.
                   264775 1.R1040
Contig ID
5'-most EST
                   gsv701052304.hl
                   32024
Seq. No.
                   264818 1.R1040
Contig ID
                   qsv701\overline{0}52381.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2262115
BLAST score
                   449
E value
                   2.0e-44
Match length
                   261
% identity
                   36
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                   32025
Seq. No.
                   264961 1.R1040
Contig ID
                   qsv701\overline{0}52605.h1
5'-most EST
                   32026
Seq. No.
                   264986_1.R1040
Contig ID
5'-most EST
                   uC-gmronoir000g05b1
                   32027
Seq. No.
Contig ID
                   264998 1.R1040
5'-most EST
                   gsv701052745.hl
                   32028
Seq. No.
                   265158 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}52877.h1
                   32029
Seq. No.
                   265180 1.R1040
Contig ID
5'-most EST
                   uC-gmropic109h08b1
                   32030
Seq. No.
                   265232_1.R1040
Contig ID
                   jC-gmf102220063c04d1
5'-most EST
                   BLASTX
Method
                   g2281085
NCBI GI
BLAST score
                   315
E value
                   7.0e-29
Match length
                   70
% identity
                   74
```

(ACO02333) CTR1 protein kinase isolog [Arabidopsis

Seq. No. 32031 265232 2.R1040 Contig ID fC-gmse700658724d3 5'-most EST Method BLASTX NCBI GI g2281085 BLAST score 203 E value 7.0e-16 Match length 42 % identity 76 (AC002333) CTR1 protein kinase isolog [Arabidopsis NCBI Description thaliana] 32032 Seq. No. 265252 1.R1040 Contig ID gsv701053004.hl 5'-most EST BLASTX Method NCBI GI q1172633 BLAST score 179 2.0e-13 E value Match length 91 % identity 53 NCBI Description PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana] 32033 Seq. No. 265256 1.R1040 Contig ID 5'-most EST uC-gmropic102g10b1 BLASTX Method q1083160 NCBI GI BLAST score 468 8.0e-47 E value Match length 176 % identity 51 mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC NCBI Description 3.2.1.113) - rabbit (fragment) 32034 Seq. No. 265317 1.R1040 Contig ID 5'-most EST g5677973 32035 Seq. No. 265389 1.R1040 Contig ID 5'-most EST uC-gmrominsoy258f09b1 Method BLASTX g3600039 NCBI GI BLAST score 374 E value 5.0e-46 Match length 201 % identity 53 (AF080119) similar to Schizosaccharomyces pombe isp4 NCBI Description protein (GB:D14061) [Arabidopsis thaliana]

thaliana]

32036

Seq. Nò.

```
265550 1.R1040
Contiq ID
                    k11701\overline{2}04243.h2
5'-most EST
Method
                    BLASTN
NCBI GI
                    g3449326
BLAST score
                    33
E value
                    4.0e-09
Match length
                    77
% identity
                    86
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K19M22, complete sequence [Arabidopsis thaliana]
                    32037
Seq. No.
                    265600 1.R1040
Contig ID
5'-most EST
                    uC-gmronoir026h07b1
                    32038
Seq. No.
                    265673 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}53601.h1
Seq. No.
                    32039
                    265696_1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}56138.h1
Method
                    BLASTX
NCBI GI ----
                   g2245020 -
                    299
BLAST score
E value
                    3.0e-27
Match length
                    67
                    75
% identity
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.
                    32040
                    265724 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}53686.h1
                    32041
Seq. No.
                    265776 1.R1040
Contig ID
5'-most EST
                    jsh701063921.hl
                    32042
Seq. No.
                    265779_1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}53759.h1
Seq. No.
                    32043
                    265788 1.R1040
Contig ID
                    gsv701\overline{0}53763.h1
5'-most EST
                    32044
Seq. No.
Contig ID
                    265802 1.R1040
5'-most EST
                    gsv701\overline{0}53880.h1
Method
                    BLASTX
NCBI GI
                    g2191136
BLAST score
                    234
E value
                    7.0e-20
Match length
                    91
                    55
% identity
NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;
```

coded for by A. thaliana cDNA T46230; coded for by A.

5'-most EST

Method

NCBI GI

q4307829

q3116019

BLASTN

```
32045
Seq. No.
                    265881 1.R1040
Contig ID
5'-most EST
                    jC-gmro02910024a09d1
Seq. No.
                    32046
                    265900 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}53916.h1
                    32047
Seq. No.
                    265938 1.R1040
Contig ID
5'-most EST
                    gsv701053964.hl
Seq. No.
                    32048
                    265959 1.R1040
Contig ID
5'-most EST
                    jC-gmf\overline{1}02220090g07a1
Seq. No.
                    32049
                    265975 1.R1040
Contig ID
5'-most EST
                    asn701\overline{1}39792.h1
Seq. No.
                    32050---
                    265983 1.R1040
Contig ID
5'-most EST
                    qsv701054023.hl
Seq. No.
                    32051
                    265995 1.R1040
Contig ID
5'-most EST
                    uC-gmropic113c02b1
Seq. No.
                    266077 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}54136.h1
Seq. No.
                    32053
                    266080 1.R1040
Contig ID
5'-most EST
                    jsh701\overline{0}64056.h1
Seq. No.
                    32054
                    266090 1.R1040
Contig ID
5'-most EST
                    asn701\overline{1}31030.h1
Method
                    BLASTX
NCBI GI
                    q2833378
BLAST score
                    319
E value
                    3.0e-29
Match length
                    172
% identity
NCBI Description
                    HEXOKINASE >qi 619928 (U18754) hexokinase [Arabidopsis
                    thaliana] >gi 1582383 prf_2118367A hexokinase [Arabidopsis
                    thaliana]
Seq. No.
                    32055
                    266111 1.R1040
Contig ID
```

[Arabidopsis thaliana]

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

```
BLAST score
E value
                   6.0e-12
                                                          Sec.
Match length
                  90
% identity
                  86
NCBI Description Pisum sativum mRNA for ftsZ gene
                  32056
Seq. No.
                  266143 1.R1040
Contig ID
5'-most EST
                  gsv701054229.h1
Seq. No.
                  32057
                  266229 1.R1040
Contig ID
                  uC-gmropic056g11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q629561
BLAST score
                  248
                   4.0e-21
E value
Match length
                  121
                   44
% identity
                  SRG1 protein - Arabidopsis thaliana
NCBI Description
                  >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  32058 --- --- - ----
Contig ID
                  266238 1.R1040
5'-most EST
                  zsg701119112.h1
                  32059
Seq. No.
                  266276 1.R1040
Contig ID
5'-most EST
                  gsv701054413.h1
                  32060
Seq. No.
                  266280_1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}56418.h1
                  BLASTX
Method
NCBI GI
                  g3411152
BLAST score
                  191
E value
                   8.0e-15
                   54
Match length
% identity
                   (AF066050) thymidine kinase [Oryza sativa]
NCBI Description
                   32061
Seq. No.
                  266337 1.R1040
Contig ID
                  uC-gmrominsoy310d10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3335373
BLAST score
                  284
                  2.0e-25
E value
Match length
                  72
                  71
% identity
                   (AC003028) putative GTL1 protein [Arabidopsis thaliana].
NCBI Description
                  32062
Seq. No.
                  266337 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy125a08b1
```

BLASTX

Method

NCBI GI

g28589

```
NCBI GI
                   q3335373
                                                  *· <u>:</u>:
BLAST score
                   385
E value
                   3.0e-37
Match length
                   93
                   74
% identity
                   (AC003028) putative GTL1 protein [Arabidopsis thaliana]
NCBI Description
                   32063
Seq. No.
Contig ID
                   266356_1.R1040
5'-most EST
                   uC-gmropic012d12b1
Method
                   BLASTX
                   g1663541
NCBI GI
BLAST score
                   224
E value
                   2.0e-18
Match length
                   91
% identity
                   58
NCBI Description
                   (U55805) disease resistance protein homolog [Glycine max]
                   32064
Seq. No.
Contig ID
                   266428 1.R1040
5'-most EST
                   gsv701\overline{0}54626.h1
                   32065
Seq. No.
Contig ID --
                   266487 1.R1040
5'-most EST
                   jC-gmle01810018c01a2
Seq. No.
                   32066
Contig ID
                   266605 1.R1040
5'-most EST
                   epx701109042.h1
Method
                   BLASTX
NCBI GI
                   g3242071
BLAST score
                   285
E value
                   3.0e-25
Match length
                   163
                   42
% identity
NCBI Description
                   (AJ007289) myb-like protein [Arabidopsis thaliana]
Seq. No.
                   32067
Contig ID
                   266624 1.R1040
5'-most EST
                   gsv701055903.hl
Method
                   BLASTX
NCBI GI
                   g2827709
BLAST score
                   446
                   2.0e-44
E value
                   114
Match length
                   73
% identity
NCBI Description
                   (AL021684) predicted protein [Arabidopsis thaliana]
                   32068
Seq. No.
                   266713 1.R1040
Contig ID
5'-most EST
                   gsv701055205.hl
                   32069
Seq. No.
Contig ID
                   266809 1.R1040
5'-most EST
                   gsv701055203.hl
Method
                   BLASTN
```

NCBI GI

```
BLAST score
                   315
                   1.0e-177
E value
                   315
Match length
% identity
                   100
NCBI Description
                  Human messenger RNA for serum albumin (HSA)
                   32070
Seq. No.
Contig ID
                   266881 1.R1040
5'-most EST
                   uC-gmrominsoy219f09b1
                   32071
Seq. No.
                   266882 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810082f09a1
Method
                  BLASTX
NCBI GI
                   g4490316
BLAST score
                   242
E value
                   2.0e-20
Match length
                  123
                   43
% identity
                   (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32072
                   266933 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}55343.h1
Method
                  BLASTX
NCBI GI
                   g3551954
BLAST score
                  176
E value
                   1.0e-12
                  78
Match length
% identity
                   44
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                   32073
Seq. No.
                   267126 1.R1040
Contig ID
5'-most EST
                   gsv701055586.hl
Seq. No.
                   32074
                   267154 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220103a08a1
Method
                  BLASTX
NCBI GI
                  g3510254
BLAST score
                  148
                  2.0e-09
E value
                  41
Match length
% identity
NCBI Description
                   (AC005310) putative zinc transporter [Arabidopsis thaliana]
                  32075
Seq. No.
                  267155 1.R1040
Contig ID
5'-most EST
                  gsv701055657.hl
                  32076
Seq. No.
Contig ID
                  267175 1.R1040
                  uC-gmrominsoy072e01b1
5'-most EST
Method
                  BLASTX
```

g3334142

```
BLAST score
                   579
E value
                   6.0e-60
Match length
                   148
% identity
                   76
NCBI Description
                   CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
                   (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
                   >gi_2737892 (U59150) nucleolar protein AfCbf5p [Sartorya
                   fumigata]
                   32077
Seq. No.
Contig ID
                   267306 1.R1040
5'-most EST
                   fC-gmro700763939d3
Method
                   BLASTX
NCBI GI
                   q3201554
BLAST score
                   328
                   2.0e-30
E value
                   62
Match length
% identity
                   95
                   (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
                   32078
Seq. No.
                   267411 1.R1040
Contig ID
5'-most EST
                   gsv701\overline{0}55941.h1
Method ----
                   BLASTX
NCBI GI
                   g3688284
BLAST score
                   595
E value
                   8.0e-62
Match length
                   146
% identity
                   73
NCBI Description
                   (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
                   lanata]
                   32079
Seq. No.
                   267480 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910003g06a1
Seq. No.
                   32080
Contig ID
                   267608_1.R1040
5'-most EST
                   jC-qmro02910061c08a1
Method
                   BLASTX
                   g1857447
NCBI GI
BLAST score
                   251
E value
                   1.0e-21
Match length
                   110
% identity
                   47
                   (U82367) UDP-glucose glucosyltransferase [Solanum
NCBI Description
                   tuberosum]
                   32081
Seq. No.
Contig ID
                   267784_1.R1040
5'-most EST
                   zsg701126354.h1
Method
                   BLASTX
                   g4388832
NCBI GI
BLAST score
                   514
                   2.0e-52
E value
Match length
                   119
% identity
                   85
```

```
(AC006528) putative DNA replication licensing factor with
NCBI Description
                   an MCM family domain (prosite:PDOC00662) [Arabidopsis
                   thalianal
                   32082
Seq. No.
                   267856 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}08984.h1
                   32083
Seq. No.
Contig ID
                   267885_1.R1040
5'-most EST
                   gsv701\overline{0}56530.h1
Method
                   BLASTX
                   g3176671
NCBI GI
                   227
BLAST score
E value
                   7.0e-19
Match length
                   69
                   59
% identity
                   (AC004393) Contains similarity to hypothetical gene B0495.7
NCBI Description
                   gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis
                   thaliana]
                   32084
Seq. No.
                   267894 1.R1040
Contig ID
                   gsv701056543.h1
5'-most EST
                   32085
Seq. No.
Contig ID
                   267922 1.R1040
5'-most EST
                   epx701107501.h1
                   32086
Seq. No.
                   267929 1.R1040
Contig ID
                   jC-qmro02910048c01a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1346396
BLAST score
                   150
                   1.0e-09
E value
Match length
                   85
% identity
NCBI Description
                   PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
                   >gi 100913 pir S10930 probable receptor protein kinase (EC
                   2.7.1.-) precursor - maize >gi 22432 emb CAA36611 (X52384)
                   precursor protein (AA -26 to 791) [Zea mays]
                   >gi 22436 emb CAA47962 (X67733) receptor-like protein
                   kinase [Zea mays] >gi 226927 prf 1611404A receptor protein
                   kinase [Zea mays]
                   32087
Seq. No.
Contig ID
                   267936 1.R1040
5'-most EST
                   gsv701\overline{0}56591.h1
                   32088
Seq. No.
                   267989 1.R1040
Contig ID
5'-most EST
                   gsv701056662.hl
                   32089
Seq. No.
                   268024 1.R1040
Contig ID
                   qsv701\overline{0}56810.h1
5'-most EST
```

```
32090
Seq. No.
Contia ID
                    268048 1.R1040 -
5'-most EST
                    gsv701056739.hl
                    32091
Seq. No.
                    268093 1.R1040
Contig ID
5'-most EST
                    gsv701\overline{0}56795.h1
Method
                   BLASTX
NCBI GI
                    g2809251
BLAST score
                    650
E value
                    8.0e-81
Match length
                   179
                   80
% identity
NCBI Description
                    (AC002560) F21B7.20 [Arabidopsis thaliana]
                    32092
Seq. No.
                    268099 1.R1040
Contig ID
                   jC-gmro02910070f02a1
5'-most EST
                   32093
Seq. No.
                   268146_1.R1040
Contig ID
5'-most EST
                    epx701\overline{1}06688.h1
Method'
                   BLASTX
NCBI GI
                   q4455301
BLAST score
                    219
                                                             414 · · ·
E value
                    4.0e-18
                    59
Match length
% identity
                   81
NCBI Description
                    (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                   32094
                   268209 1.R1040
Contig ID
5'-most EST
                    asn701\overline{1}41115.h1
Method
                   BLASTX
NCBI GI
                   g2245034
BLAST score
                    409
                    4.0e-40
E value
                   119
Match length
% identity
                    67
NCBI Description
                    (Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]
                   32095
Seq. No.
                   268296 1.R1040
Contig ID
5'-most EST
                   cle700967859.h1
Method
                   BLASTX
NCBI GI
                   g2262178
BLAST score
                   140
E value
                   6.0e-09
                   59
Match length
% identity
                    (AC002329) putative Mlo-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32096
                   268350 1.R1040
Contig ID
                   hrw701056925.hl
5'-most EST
```

BLASTX

Method

```
NCBI GI
                   g2911276
BLAST score
                   138
E value
                   1.0e-08
Match length
                   64
                   45
% identity
NCBI Description
                   (U63631) LMW heat shock protein [Fragaria x ananassa]
Seq. No.
Contig ID
                   268351 1.R1040
5'-most EST
                   uC-gmrominsoy136g04b1
Seq. No.
                   268417 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}57018.h2
                   32099
Seq. No.
                   268438 1.R1040
Contig ID
                   hrw701057058.h2
5'-most EST
                   32100
Seq. No.
                   268504 1.R1040
Contig ID
                   hrw701057302.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1620016
BLAST score
                   189
E value ·
                   1.0e-102
Match length
                   205
                   98
% identity
                  Human heart mRNA for heat shock protein 90, partial cds
NCBI Description
                   32101
Seq. No.
                   268521 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}57327.h1
                   BLASTN
Method
NCBI GI
                   g34200
BLAST score
                   252
E value
                   1.0e-140
Match length
                   272
                   98
% identity
                   Human mRNA for ribosomal protein L35a
NCBI Description
                   >gi 4506638 ref_NM_000996.1_RPL35A Homo sapiens ribosomal
                   protein L35a (RPL35A) mRNA
                   32102
Seq. No.
                   268533 1.R1040
Contig ID
5'-most EST
                   hrw701057518.hl
Method
                   BLASTN
                   g28338
NCBI GI
BLAST score
                   446
                   0.0e+00
E value
Match length
                   545
% identity
NCBI Description
                   Human mRNA for cytoskeletal gamma-actin
                   >gi_4501886_ref_NM_001614.1_ACTG1_ Homo sapiens actin,
                   gamma 1 (ACTG1) mRNA
```

32103

Seq. No.

% identity

98

```
268549 1.R1040
Contig ID
                   hrw701057561.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1702923
BLAST score
                   194
E value
                   1.0e-105
Match length
                   268
% identity
                   99
NCBI Description
                   H.sapiens mRNA for p0071 protein
                   >gi 4505842 ref NM 003628.1 PKP4 Homo sapiens plakophilin
                   4 (PKP4) mRNA
                   32104
Seq. No.
Contig ID
                   268568 1.R1040
5'-most EST
                   zsq701129207.hl
                   BLASTN
Method
NCBI GI
                   q4506742
BLAST score
                   429
E value
                   0.0e + 00
Match length
                   429
                   100
% identity
                   Homo sapiens ribosomal protein S8 (RPS8) mRNA
NCBI Description
                   32105
Seq. No.
                   268570 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}57416.h1
                   BLASTN
Method
                   a31101
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
Match length
                   287
                   100
% identity
                   H.sapiens mRNA for protein homologous to elongation factor
NCBI Description
                   1-gamma from A.salina >gi_4503480_ref_NM_001404.1_EEF1G_
                   Homo sapiens eukaryotic translation elongation factor 1
                   gamma (EEF1G) mRNA
                   32106
Seq. No.
                   268615 1.R1040
Contig ID
5'-most EST
                   hrw701057504.hl
                   BLASTN
Method
NCBI GI
                   q598714
BLAST score
                   254
                   1.0e-141
E value
Match length
                   274
% identity
NCBI Description
                   Human HepG2 3' region cDNA, clone hmd3b09
Seq. No.
                   32107
                   268619 1.R1040
Contig ID
5'-most EST
                   hrw701057510.hl
                   BLASTN
Method
NCBI GI
                   q188855
BLAST score
                   257
E value
                   1.0e-143
Match length
                   277
```

E value

1.0e-34

```
NCBI Description Human mitochondrial specific single stranded DNA binding
                   protein mRNA, complete cds.
                   >gi_4507230_ref_NM_003143.1_SSBP_ Homo sapiens
                   single-stranded DNA-binding protein (SSBP), nuclear gene
                   encoding mitochondrial protein, mRNA
                   32108
 Seq. No.
                   268642_1.R1040
 Contig ID
 5'-most EST
                   jC-gmle01810072a01d1
Method
                   BLASTN
                   g1857236
NCBI GI
                   393
BLAST score
                   0.0e+00
E value
                   505
Match length
                   94
 % identity
NCBI Description
                   Human p97 mRNA, complete cds
                   >gi 4503538 ref NM 001418.1 EIF4G2 Homo sapiens eukaryotic
                   translation initiation factor 4 gamma, 2 (EIF4G2) mRNA
                   32109
Seq. No.
Contig ID
                   268644_1.R1040
 5'-most EST
                   hrw701057542.h1
                   BLASTN
Method
                   g4500180
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
Match length
                   264
                   98
 % identity
                   Homo sapiens mRNA; cDNA DKFZp586N0318 (from clone
NCBI Description
                   DKFZp586N0318)
Seq. No.
                   32110
                   268682 1.R1040
Contig ID
 5'-most EST
                   zsg701129177.hl
Method
                   BLASTN
NCBI GI
                   g23690
BLAST score
                   339
E value
                   0.0e + 00
Match length
                   339
                   100
 % identity
NCBI Description H.sapiens mRNA for 23 kD highly basic protein
Seq. No.
                   32111
                   268684 1.R1040
Contig ID
 5'-most EST
                   hrw701057604.hl
                   32112
Seq. No.
                   268692_1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220073e01a1
                   32113
Seq. No.
Contig ID
                   268708 1.R1040
· 5'-most EST
                   kl1701212504.h1
Method
                   BLASTX
NCBI GI
                   q1076315
BLAST score
                   361
```

5'-most EST

```
Match length
                  113
                  70
% identity
NCBI Description
                  cytochrome P450 - Arabidopsis thaliana
                  >gi_853719_emb_CAA60793_ (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
                  CYP90 protein [Arabidopsis thaliana]
Seq. No.
                  32114
                  268869 1.R1040
Contig ID
5'-most EST
                  hrw701057915.hl
Method
                  BLASTX
NCBI GI
                  q2245006
BLAST score
                  155
E value
                  1.0e-10
Match length
                  83
                  45
% identity
NCBI Description
                  (297341) hypothetical protein [Arabidopsis thaliana]
                  32115
Seq. No.
                  268870 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy276d09b1
Seq. No.
                  32116
                  268950 1.R1040 ....
Contig ID
5'-most EST
                  hrw701058033.hl
                  32117
Seq. No.
                  268983 1.R1040
Contig ID
5'-most EST
                  hrw701058092.hl
Method
                  BLASTN
NCBI GI
                  q1370187
BLAST score
                  230
                  1.0e-126
E value
Match length
                  354
                  92
% identity
NCBI Description
                  L.japonicus mRNA for small GTP-binding protein, RAB7D
Seq. No.
                  32118
                  269005 1.R1040
Contig ID
5'-most EST
                  hrw701058205.hl
Method
                  BLASTX
NCBI GI
                  q2618684
BLAST score
                  183
E value
                  8.0e-14
Match length
                  61
% identity
NCBI Description
                  (AC002510) putative
                  UDP-N-acetylglucosamine--dolichyl-phosphate
                  N-acetylglucosaminephosphotransferase [Arabidopsis
                  thaliana] >gi_3241947 (AC004625) putative
                  UDP-N-acetylglucosamine--dolichyl-phosphate
                  N-acetylglucosaminephosphotransferase [Arabidopsis
                  thalianal
Seq. No.
                  32119
                  269092 1.R1040
Contig ID
```

hrw701058318.hl

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   g2342719
BLAST score
                   141
E value
                   6.0e-09
Match length
                   87
% identity
                   39
                   (AC002341) SF16 protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32120
                   269096 1.R1040
Contig ID
                   hrw701058333.hl
5'-most EST
Seq. No.
                   32121
Contig ID
                   269119 1.R1040
5'-most EST
                   jsh701068477.hl
                   32122
Seq. No.
                   269197 1.R1040
Contig ID
5'-most EST
                   hrw701058652.hl
                   32123
Seq. No.
                   269250 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910051e04d1
Method - -
                   BLASTX
                   g3549660
NCBI GI
BLAST score
                   332
                   9.0e-31
E value
                   108
Match length
% identity
                   55
                   (AL031394) carbonate dehydratase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   32124
Seq. No.
                   269268 1.R1040
Contig ID
5'-most EST
                   g5057717
Seq. No.
                   32125
                   269308 1.R1040
Contig ID
                   hrw701058718.hl
5'-most EST
Method
                   BLASTX
                   q3135269
NCBI GI
BLAST score
                   252
E value
                   2.0e-21
Match length
                   159
% identity
                   45
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32126
Contig ID
                   269373 1.R1040
                   hrw701\overline{0}61721.h1
5'-most EST
Method
                   BLASTX
                   g1769556
NCBI GI
BLAST score
                   415
                   6.0e-41
E value
                   101
Match length
                   81
% identity
```

(U81158) Forsythia x intermedia

```
(+)-pinoresinol/(+)-lariciresinol reductase (PLR) protein,
complete sequence [Forsythia x intermedia]
```

32127 Seq. No. 269382 1.R1040 Contig ID 5'-most EST hrw701058832.hl Method BLASTN NCBI GI g530206 BLAST score 40 E value 3.0e-13 Match length 112 % identity 84 NCBI Description Glycine max heat shock protein (SB100) mRNA, complete cds 32128 Seq. No. 269384 1.R1040 Contig ID 5'-most EST hrw701058872.hl 32129 Seq. No. 269412 1.R1040 Contig ID 5'-most EST jC-gmle01810059g06d1 32130 Seq. No. 269432 1.R1040 -----Contig ID----5'-most EST hrw701059664.h1 Seq. No. 32131 269534 1.R1040 Contig ID 5'-most EST hrw701059062.hl 32132 Seq. No. 269565 1.R1040 Contig ID 5'-most EST epx701108592.hl 32133 Seq. No. 269571 1.R1040 Contig ID 5'-most EST hrw701059110.hl Seq. No. 32134 269620 1.R1040 Contig ID zsg701120003.h1 5'-most EST 32135 Seq. No. 269627 1.R1040 Contig ID hrw701059195.hl 5'-most EST 32136 Seq. No. 269658 1.R1040 Contig ID 5'-most EST $zsg701\overline{1}17393.h1$ Seq. No. 32137 269674 1.R1040 Contig ID hrw701059296.h1 5'-most EST

32138

269687 1.R1040

epx701105776.h1

Seq. No.

Contig ID

5'-most EST

Contig ID

5'-most EST

```
BLASTX
Method
                  q4220515
NCBI GI
                  451
BLAST score
                  6.0e-45
E value
                  153
Match length
                  57
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  32139
Seq. No.
                  269695 1.R1040
Contig ID
                  uC-gmflminsoy080h10b1
5'-most EST
Method
                  BLASTX
                  g2832629
NCBI GI
BLAST score
                   349
                   2.0e-32
E value
Match length
                   251
                   37
% identity
                   (ALO21711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                  thaliana]
                   32140
Seq. No.
                   269751 1.R1040
Contig ID
                   jsh701\overline{0}69189.h1
5'-most EST
                   BLASTX -
Method
                   g2244910
NCBI GI
                   144
BLAST score
                   1.0e-09
E value
Match length
                   52
% identity
                   46
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32141
                   269824 1.R1040
Contig ID
                   jsh701\overline{0}64879.h1
5'-most EST
Method
                   BLASTX
                  ·g101065
NCBI GI
                   139
BLAST score
                   1.0e-08
E value
Match length
                   95
% identity
NCBI Description rad4 protein - fission yeast (Schizosaccharomyces pombe)
                   32142
Seq. No.
                   269837 1.R1040
Contig ID
                   hrw701059564.hl
5'-most EST
                   BLASTX
Method
                   g4249385
NCBI GI
                   247
BLAST score
                   2.0e-21
E value
Match length
                   67
                   66
% identity
                   (AC005966) T2K10.11 [Arabidopsis thaliana]
NCBI Description
                   32143
Seq. No.
                   269879 1.R1040
```

hrw701059615.hl

Contig ID

```
32144
Seq. No.
                   269899 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910046g05d1
                   32145
Seq. No.
                   270055 1.R1040
Contig ID
5'-most EST
                   g5753406
Method
                   BLASTN
NCBI GI
                   g347456
BLAST score
                   73
E value
                   1.0e-32
Match length
                   250
                   17
% identity
NCBI Description
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP1) mRNA,
                   partial cds
Seq. No.
                   32146
                   270136 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}33623.h2
Method
                   BLASTX
                   g2281647
NCBI GI
BLAST score
                   216
E value
                   1.0e-17
Match length
                   83 --
% identity
                   52
                   (AF003104) AP2 domain containing protein RAP2.11
NCBI Description
                   [Arabidopsis thaliana]
                   32147
Seq. No.
                   270183 1.R1040
Contig ID
5'-most EST
                   g4313963
Method
                   BLASTX
                   g2541876
NCBI GI
BLAST score
                   195
E value
                   1.0e-14
Match length
                   119
% identity
                   39
NCBI Description
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
                   [Nicotiana tabacum]
                   32148
Seq. No.
                   270203 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy036g08b1
                   32149
Seq. No.
                   270224 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810028d01d1
Method
                   BLASTX
                   g3047118
NCBI GI
BLAST score
                   170
E value
                   5.0e-12
Match length
                   47
% identity
                   72
NCBI Description
                   (AF058919) No definition line found [Arabidopsis thaliana]
                   32150
Seq. No.
```

270250 1.R1040

Seq. No.

Contig ID

32157

270784 1.R1040

```
5'-most EST
                  hrw701060156.hl
Method
                   BLASTX
                   g3269301
NCBI GI
BLAST score
                   216
E value
                   1.0e-34
Match length
                   125
                   59
% identity
NCBI Description
                   (AL030978) putative protein [Arabidopsis thaliana]
                   32151
Seq. No.
                   270270 1.R1040
Contig ID
                   jC-gmf102220138d06d1
5'-most EST
Method
                   BLASTN
                   g170059
NCBI GI
BLAST score
                   200
E value
                   1.0e-108
                   290
Match length
% identity
                   95
                  Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete
NCBI Description
                   cds
Seq. No.
                   32152
                   270275_1.R1040
Contig ID
5'-most EST
                   epx701104266.hl
Method
                   BLASTX
NCBI GI
                   g4006868
BLAST score
                   187
E value
                   4.0e-14
Match length
                   43
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   32153
Seq. No.
                   270319 1.R1040
Contig ID
                  hrw701060263.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3242077
BLAST score
                   275
E value
                   1.0e-24
Match length
                   77
% identity
                   66
                   (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32154
                   270589 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071e12a1
Seq. No.
                   32155
Contig ID
                   270613 1.R1040
5'-most EST
                  uC-gmropic050e07b1
                   32156
Seq. No.
                   270712 1.R1040
Contig ID
5'-most EST
                  hrw701\overline{0}63328.h1
```



```
5'-most EST
                   hrw701060856.hl
Method
                   BLASTX
NCBI GI
                   g3128210
BLAST score
                   183
                    7.0e-14
E value
Match length
                   56
                    68
% identity
                    (AC004077) putative cytochrome P450 protein [Arabidopsis
NCBI Description
                    thaliana] >gi_3337378 (AC004481) putative cytochrome P450
                   protein [Arabidopsis thaliana]
                    32158
Seq. No.
                   270990 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy0001b04a1
                   32159
Seq. No.
Contig ID
                   271051 1.R1040
5'-most EST
                   asn701\overline{1}37356.h1
                   BLASTX
Method
                   q4522004
NCBI GI
BLAST score
                   190
                    1.0e-14
E value
Match length
                   53
                   70
% identity
                    (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    32160
Contig ID
                    271120 1.R1040
                   hrw701061322.h1
5'-most EST
                   32161
Seq. No.
                   271141 1.R1040
Contig ID
                   hrw701\overline{0}61352.h1
5'-most EST
                    32162
Seq. No.
                   271153 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}61372.h1
Method
                   BLASTX
NCBI GI
                    g3068704
BLAST score
                    414
                    9.0e-41
E value
Match length
                    118
% identity
                    66
                    (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                    32163
Seq. No.
                    271235 1.R1040
Contig ID
                   hrw701\overline{0}61486.h1
5'-most EST
                   32164
Seq. No.
                   271286 1.R1040
Contig ID
                   k11701\overline{2}02348.h1
5'-most EST
                   BLASTX
Method
                   g119095
NCBI GI ·
```

187

2.0e-14

BLAST score E value



67 Match length 57 % identity EMBRYONIC ABUNDANT PROTEIN PRECURSOR (CLONE USP LAMBDA NCBI Description VF30.1) >gi_82003_pir__S05471 embryonic abundant protein precursor (clone USP Vf30.1) - tick bean 32165 Seq. No. 271305 1.R1040 Contig ID 5'-most EST hrw701061582.hl 32166 Seq. No. 271365 1.R1040 Contig ID jC-gmro02910043g10d1 5'-most EST Method BLASTX g4249409 NCBI GI 251 BLAST score 2.0e-21 E value Match length 91 52 % identity NCBI Description (AC006072) putative sugar transporter [Arabidopsis thaliana] 32167 Seq. No. 271380 1.R1040 Contig ID 5'-most EST $k11701\overline{2}10123.h1$ Method BLASTX g3746063 NCBI GI BLAST score 170 6.0e-12 E value 54 Match length 57 % identity NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

32168 Seq. No.

271465 1.R1040 Contig ID asn701136564.hl 5'-most EST

Seq. No. 32169

271592 1.R1040 Contig ID 5'-most EST $hrw701\overline{0}62573.h1$

32170 Seq. No.

271607 1.R1040 Contig ID hrw701062009.h1 5'-most EST

32171 Seq. No.

271697 1.R1040 Contig ID

5'-most EST uC-gmrominsoy027f11b1

32172 Seq. No.

271757 1.R1040 Contig ID

5'-most EST jC-gmst02400072g10d1

Method BLASTX NCBI GI g3935173 BLAST score 271 3.0e-24 E value 74 Match length

Match length

134



```
% identity
                   (AC004557) F17L21.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32173
                   271773 1.R1040
Contig ID
                   hrw701062261.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q408793
BLAST score
                   270
E value
                   1.0e-150
Match length
                   278
% identity
                   99
NCBI Description
                   Glycine soja chloroplast 3-omega faty acid desaturase
                    (Fad3) mRNA, complete cds
Seq. No.
                   32174
                   271883 1.R1040
Contig ID
5'-most EST
                   hrw701\overline{0}62821.h1
Method
                   BLASTX
NCBI GI
                   g4262176
BLAST score
                   159
E value
                   3.0e-14
Match length
                   53
% identity
                   75
NCBI Description (AC005508) 18857 [Arabidopsis thaliana]
Seq. No.
                   32175
                   271990 1.R1040
Contig ID
                   hrw701\overline{0}62572.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510385
BLAST score
                   337
E value
                   1.0e-31
Match length
                   96
% identity
                   67
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32176
                   272015 1.R1040
Contig ID
                   hrw701062609.hl
5'-most EST
                   32177
Seq. No.
                   272032 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800032f03a1
                   32178
Seq. No.
Contig ID
                   272062_1.R1040
5'-most EST
                   jsh701\overline{0}66162.h1
Seq. No.
                   32179
                   272086 1.R1040
Contig ID
5'-most EST
                   hrw701062718.hl
Method
                   BLASTX
NCBI GI
                   g3355484
BLAST score
                   206
                   1.0e-29
E value
```

% identity 56
NCBI Description (AC004218) putative geranylgeranyl transferase type I beta
subunit [Arabidopsis thaliana]

 Seq. No.
 32180

 Contig ID
 272092_1.R1040

 5'-most EST
 hrw701062734.h1

Method BLASTX
NCBI GI g1931654
BLAST score 338
E value 6.0e-38
Match length 134
% identity 61

NCBI Description (U95973) BRCA1-associated RING domain protein isolog

[Arabidopsis thaliana]

Seq. No. 32181

Contig ID 272131 1.R1040 5'-most EST hrw701062820.h1

Seq. No. 32182 Contin ID 272154

Contig ID 272154_1.R1040 5'-most EST uC-gmropic038a06b1

Method BLASTX
NCBI GI g2373405
BLAST score 223
E value 3.0e-18

Match length 124 % identity 10

NCBI Description (D85194) no known genes showing a high homology to 4B-1

clone sequence were found in the EMBL database. Orf was 640 amino acid long and contained a proline and alanine repeat

[Arabidopsis thaliana]

Seq. No. 32184

Contig ID 272212 1.R1040 5'-most EST asn701140314.h1

Seq. No. 32185

Contig ID 272247_1.R1040 5'-most EST kl1701207262.h1

Seq. No. 32186

Contig ID 272272_1.R1040 5'-most EST asn701134541.h1

Method BLASTX
NCBI GI g3559816
BLAST score 297
E value 6.0e-27
Match length 78
% identity 72

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

```
32187
Seq. No.
                   272325 1.R1040
Contig ID
5'-most EST
                   hrw701063082.hl
Method
                   BLASTX
NCBI GI
                   g3047096
BLAST score
                   585
E value
                   1.0e-60
Match length
                   143
% identity
                   77
NCBI Description
                   (AF058826) similar to eukaryotic protein kinase domains
                   (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
                   32188
Seq. No.
                   272377 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910065c08d1
Method
                   BLASTX
                   q1370174
NCBI GI
BLAST score
                   271
E value
                   9.0e-24
Match length
                   63
% identity
                   79
NCBI Description
                   (Z73936) RAB1Y [Lotus japonicus]
                   32189
Seq. No.
Contig ID
                   272394 1.R1040
5'-most EST
                   jC-gmst02400077h05d1
Method
                   BLASTX
NCBI GI
                   q3395432
BLAST score
                   286
E value
                   1.0e-25
Match length
                   63
% identity
                   83
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32190
Seq. No.
Contig ID
                   272486 1.R1040
5'-most EST
                   hrw701\overline{0}63284.h1
                   32191
Seq. No.
                   272534 2.R1040
Contig ID
                   k11701\overline{2}11827.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3337367
BLAST score
                   128
E value
                   6.0e-17
Match length
                   77
                   61
% identity
NCBI Description
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
                   32192
Seq. No.
                   272641 1.R1040
Contig ID
5'-most EST
                   jsh701065193.h1
                   32193
Seq. No.
                   272710 1.R1040
Contig ID
5'-most EST
                   hrw701063586.hl
```

BLASTX

Method



```
NCBI GI
                   g4262183
BLAST score
                   246
                   7.0e-38
E value
Match length
                   111
% identity
                   70
                   (AC005508) 51434 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32194
Contig ID
                   272812_1.R1040
5'-most EST
                   jC-gmro02910020g11d1
Seq. No.
                   32195
Contig ID
                   272814 1.R1040
5'-most EST
                   dkc700967938.h1
Method
                   BLASTX
NCBI GI
                   q2435395
BLAST score
                   423
                   2.0e-41
E value -
Match length.
                   146
% identity
                   62
                   (U63550) pectate lyase [Fragaria x ananassa]
NCBI Description
                   32196
Seq. No.
                   272818 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy070c11b1
Method
                   BLASTX
NCBI GI
                   g3687248
                   307
BLAST score
                   5.0e-28
E value
Match length
                   90
                   59
% identity
                   (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32197
                   272830 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400077d05a1
Seq. No.
                   32198
                   273000 1.R1040
Contig ID
5'-most EST
                   jsh701063793.hl
Seq. No.
                   32199
Contig ID
                   273098 1.R1040
5'-most EST
                   k11701202633.hl
                   32200
Seq. No.
Contig ID
                   273108 1.R1040
5'-most EST
                   jsh701\overline{0}63934.h1
Method
                   BLASTX
NCBI GI
                   g2829925
BLAST score
                   458
```

.

BLAST score 458
E value 8.0e-46
Match length 131
% identity 66

NCBI Description (AC002291) Similar to dnaj-like protein, gp_Y11969_2230757 [Arabidopsis thaliana]

5'-most EST

 $q55089\overline{3}0$

```
32201
Seq. No.
                   273183_1.R1040
Contig ID
                    jsh701\overline{0}64044.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g571484
BLAST score
                   359
E value
                   1.0e-34
Match length
                   84
% identity
                   85
                    (U16727) peroxidase precursor [Medicago truncatula]
NCBI Description
                   32202
Seq. No.
                   273229_1.R1040
Contig ID
                   jsh701\overline{0}64102.h1
5'-most EST
Method
                   BLASTX
                   g3201541
NCBI GI
BLAST score
                   148
E value
                   9.0e-10
Match length
                   31
                   77
% identity
                    (AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
                   32203
Seq. No.
                   273375 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}65331.h1
Seq. No.
                   32204
                   273443 1.R1040
Contig ID
                   uC-gmflminsoy010c03b1
5'-most EST
                   32205
Seq. No.
                   273451 2.R1040
Contig ID
                   jsh701\overline{0}65694.h1
5'-most EST
                   BLASTX
Method
                   g4262173
NCBI GI
BLAST score
                   211
                   3.0e-17
E value
Match length
                   82
                   59
% identity
                   (AC005508) 3975 [Arabidopsis thaliana]
NCBI Description
                   32206
Seq. No.
                   273492 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220068d02a1
                   32207
Seq. No.
                   273547 1.R1040
Contig ID
5'-most EST
                   jC-gmf\(\bar{1}\)02220050f07d1
                   32208
Seq. No.
                   273621 1.R1040
Contig ID
5'-most EST
                   zsg701125691.hl
                   32209
Seq. No.
                   273637 1.R1040
Contig ID
```

```
Seq. No.
                   32210
                   273793 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy261e02b1
                   32211
Seq. No.
                   273816 1.R1040
Contig ID
                   g4437099
5'-most EST
Seq. No.
                   32212
                   273847 1.R1040
Contig ID
5'-most EST
                   g4396069
Seq. No.
                   32213
                   273853 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}65028.h1
                   32214
Seq. No.
                   273854 1.R1040
Contig ID
5'-most EST
                   g5688430
Method
                   BLASTX
NCBI GI
                   g625241
BLAST score
                   147
E value
                   2.0e-15
Match length
                   72
                   56
% identity
NCBI Description
                   inorganic pyrophosphatase (EC 3.6.1.1) - yeast
                   (Saccharomyces cerevisiae) >gi 536206 emb CAA84949_
                   (Z35880) ORF YBR011c [Saccharomyces cerevisiae]
Seq. No.
                   32215
Contig ID
                   273935 1.R1040
5'-most EST
                   jsh701065338.hl
                   32216
Seq. No.
                   273947_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910037b11a1
Seq. No.
                   32217
                   273950 1.R1040
Contig ID
5'-most EST
                   jC-gmr002910049c05d1
Seq. No.
                   32218
                   274011 1.R1040
Contig ID
5'-most EST
                   g55089<del>2</del>9
Method
                   BLASTN
NCBI GI
                   q255580
BLAST score
                   378
E value
                   0.0e + 00
Match length
                   398
% identity
                   small auxin up RNA gene cluster: orf 10A5 [Glycine
NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 646 nt]
                   32219
Seq. No.
                   274061 1.R1040
Contig ID
5'-most EST
                   jsh701065493.hl
```

BLASTX

Method

Contig ID

```
NCBI GI
                    q3540207
BLAST score
                    243
E value
                    6.0e-21
Match length
                    73
% identity
                    60
NCBI Description
                    (AC004260) Putative protein kinase [Arabidopsis thaliana]
Seq. No.
                    32220
                    274108 1.R1040
Contig ID
                    jsh701\overline{0}65431.h1
5'-most EST
Method
                    BLASTN
NCBI GI
                    q348719
BLAST score
                    83
E value
                    1.0e-38
                    211
Match length
                    85
% identity
NCBI Description
                   MtNMedicago truncatula protochlorophyllide reductase
                    homolque mRNA, complete cds
Seq. No.
                    274322 1.R1040
Contig ID
5'-most EST
                    zsq701121638.h1
Seq. No.
Contig ID
                    274338 1.R1040
5'-most EST
                    jsh701\overline{0}65764.h1
Seq. No.
                    32223
                    274344 1.R1040
Contig ID
5'-most EST
                    jsh701065774.h1
Method
                    BLASTX
NCBI GI
                    q730832
BLAST score
                    142
E value
                    1.0e-08
Match length
                    51
% identity
                    59
NCBI Description
                    8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)
                    (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965
                    probable proteinase inhibitor (Bowman-Birk) p322 - soybean
                   >gi_18748_emb_CAA78359_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk
                    Proteinase Inhibitor [Glycine max]
Seq. No.
                    32224
                    274361 1.R1040
Contig ID
5'-most EST
                    jsh701065804.h1
Method
                    BLASTX
NCBI GI
                    q3834306
BLAST score
                    152
E value
                    8.0e-10
Match length
                    36
% identity
NCBI Description
                    (AC005679) EST qb R65024 comes from this gene. [Arabidopsis
                    thaliana]
Seq. No.
                    32225
```

274433 1.R1040

Seq. No.

Contig ID

32234

274968 1.R1040



```
jC-qmle01810044b10a1
5'-most EST
                   32226
Seq. No.
                   274480 1.R1040
Contig ID
                   jsh701\overline{0}65988.h1
5'-most EST
                   BLASTX
Method
                   q3184285
NCBI GI
                  178
BLAST score
                   9.0e-13
E value
                   78
Match length
% identity
                   41
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32227
Seq. No.
                   274535 1.R1040
Contig ID
                   kwa701015687.hl
5'-most EST
Seq. No.
                   32228
                   274623 1.R1040
Contig ID
5'-most EST
                   jsh701066228.hl
Method
                   BLASTX
                   g2244732
NCBI GI
BLAST score
                   185
                   9.0e-14
E value
                   69
Match length
% identity
                   (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
NCBI Description
                   32229
Seq. No.
                   274653 1.R1040
Contig ID
                   jsh701066272.hl
5'-most EST
                   32230
Seq. No.
Contig ID
                   274795 1.R1040
5'-most EST
                   jC-gmro02910072c05a1
                   32231
Seq. No.
                   274810 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910070b12a1
Seq. No.
                   32232
                   274867 1.R1040
Contig ID
5'-most EST
                   jsh701066587.hl
Seq. No.
                   32233
                   274955 1.R1040
Contig ID
                   zsg701118382.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252632
BLAST score
                   339
                   6.0e-32
E value
Match length
                   92
% identity
                   (U95973) Barley Mlo protein isolog [Arabidopsis thaliana]
NCBI Description
```

```
5'-most EST
                   jC-gmle01810091f09a1
Method
                   BLASTX
NCBI GI
                   g2864618
BLAST score
                   231
E value
                   3.0e-19
Match length
                   85
% identity
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   275067 1.R1040
Contig ID
                   jsh701066875.hl
5'-most EST
                   32236
Seq. No.
                   275072 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810043a10a1
Method
                   BLASTX
                   g3096947
NCBI GI
BLAST score
                   186
E value
                   8.0e-14
Match length
                   83
% identity
                   54
NCBI Description
                   (Y16327) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana]
Seq. No.
                   32237
                   275094 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}66921.h1
Seq. No.
                   32238
Contig ID
                   275196 1.R1040
5'-most EST
                   jsh701067139.hl
                   32239
Seq. No.
                   275270_1.R1040
Contig ID
5'-most EST
                   zsg701122675.h1
Method
                   BLASTX
                   g3281868
NCBI GI
BLAST score
                   216
                   9.0e-18
E value
                   48
Match length
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   32240
Seq. No.
                   275366_1.R1040
Contig ID
5'-most EST
                   fC-qmse700754068d2
Method
                   BLASTX
                   g3785996
NCBI GI
BLAST score
                   334
E value
                   1.0e-35
Match length
                   125
% identity
                   41
                   (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
                   32241
Seq. No.
```

275367 1.R1040

Contig ID

```
5'-most EST
                   uC-gmflminsoy072f04b1
                   BLASTX
Method
NCBI GI
                   q3367571
BLAST score
                   360
                   3.0e-34
E value
Match length
                   116
% identity
                   61
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                   32242
Contig ID
                   275435 1.R1040
5'-most EST
                   jsh701067638.hl
                   32243
Seq. No.
Contig ID
                   275456 1.R1040
5'-most EST
                   jsh701\overline{0}67739.h1
                   32244
Seq. No.
                   275490 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68418.h1
                   32245
Seq. No.
Contig ID
                   275579 1.R1040
5'-most EST
                   jC-gmf102220054f05d1
Method
                   BLASTX
                   g1946355
NCBI GI
BLAST score
                   171
E value
                   4.0e-12
Match length
                   88
                   42
% identity
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                   32246
Contig ID
                   275588 1.R1040
5'-most EST
                   uC-gmflminsoy064g11b1
Method
                   BLASTX
NCBI GI
                   q3452263
BLAST score
                   734
                   4.0e-78
E value
Match length
                   150
% identity
                   91
NCBI Description
                   (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
                   thaliana]
Seq. No.
                   32247
Contig ID
                   275600 1.R1040
5'-most EST
                   jC-gmro02910023f06d1
Method
                   BLASTX
                   g4240122
NCBI GI
                   291
BLAST score
E value
                   2.0e-26
Match length
                   89
% identity
                   53
                  (AB007802) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                   32248
                   275623 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910064c02a1
Method
                   BLASTX
NCBI GI
                   g1082054
BLAST score
                   179
E value
                   4.0e-13
Match length
                   87
% identity
                   37
NCBI Description
                   (Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.
                   275677 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910019d06d1
Seq. No.
                   275689 1.R1040
Contig ID
                   jsh701\overline{0}68243.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1575699
BLAST score
                   541
                   1.0e-55
E value
Match length
                   125
% identity
                   (U70478) putative leucoanthocyanidin dioxygenase
NCBI Description
                   [Arabidopsis thaliana] >gi_3292813_emb_CAA19803_ (AL031018)
                   putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis
                   thaliana]
                   32251
Seq. No.
                   275701 1.R1040
Contig ID
                   jsh701\overline{0}68263.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2129854
BLAST score
                   178
E value
                   2.0e-14
Match length
                   63
% identity
                   early nodulin 8 precursor - alfalfa >gi_304037 (L18899)
NCBI Description
                   early nodulin [Medicago sativa]
Seq. No.
                   275895 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68541.h1
                   32253
Seq. No.
Contig ID
                   275898 1.R1040
5'-most EST
                   zsg701121326.hl
Method
                   BLASTN
NCBI GI
                   q2618600
BLAST score
                   37
E value
                   2.0e-11
Match length
                   41
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MDC12, complete sequence [Arabidopsis thaliana]

```
32254
Seq. No.
                   276134:1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}68942.h1
Method
                   BLASTX
NCBI GI
                   g2435406
BLAST score
                   284
E value
                   2.0e-25
Match length
                   123
% identity
NCBI Description
                   (U83490) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                   32255
                   276694 1.R1040
Contig ID
5'-most EST
                   jsh701\overline{0}69816.h1
Method
                   BLASTX
NCBI GI
                   q4218120
BLAST score
                   326
                   4.0e-30
E value
                   75
Match length
                   77
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   32256
Seq. No.
                   276694_2.R1040
Contig ID
                   jC-gmst02400006g10d1
5'-most EST
Method
                   BLASTX
                   g4218120
NCBI GI
                   371
BLAST score
                   1.0e-35
E value
Match length
                   92
% identity
                   72
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
                   32257
Seq. No.
Contig ID
                   276713 1.R1040 -
                   g5605703
5'-most EST
Method
                   BLASTX
                   g3341694
NCBI GI
BLAST score
                   244
                   2.0e-20
E value
Match length
                   116
                   44
% identity
                   (AC003672) PREG-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32258
Contig ID
                   276867_1.R1040
                   jsh701\overline{0}70084.h2
5'-most EST
Method
                   BLASTX
                   q746487
NCBI GI
BLAST score
                   185
                                  et.
E value
                   8.0e-14
Match length
                   76
% identity
                   45
```

NCBI Description (U23514) No definition line found [Caenorhabditis elegans]

5'-most EST

```
Seq. No.
                   32259
                   276986 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400004d04d1
Method
                   BLASTX
                   g1354849
NCBI GI
BLAST score
                   281
E value
                   5.0e-25
Match length
                   77
% identity
                   66
NCBI Description
                   (U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.
                   32260
                   277132 1.R1040
Contig ID
5'-most EST
                   jsh701070426.hl
Method
                   BLASTX
NCBI GI
                   g4218144
BLAST score
                   287
E value
                   2.0e-25
Match length
                   88
% identity
                   60
NCBI Description
                   (AJ132398) glutathione transferase, GST 10b [Arabidopsis
                   thaliana]
Seq. No.
                   32261
                   277244 1.R1040
Contig ID
5'-most EST
                   ek1700\overline{9}68205.h1
Method
                   BLASTX
NCBI GI
                   q4539394
BLAST score
                   139
                   8.0e-09
E value
Match length
                   78
                   12
% identity
NCBI Description
                   (AL035526) putative protein [Arabidopsis thaliana]
                   32262
Seq. No.
Contig ID
                   277333 1.R1040.
5'-most EST
                   k11701\overline{2}02324.h1
                   32263
Seq. No.
                   277349 1.R1040
Contig ID
5'-most EST
                   kl1701202346.h1
Method
                   BLASTX
                   g542058
NCBI GI
BLAST score
                   186
E value
                   2.0e-14
                   47
Match length
% identity
                   68
NCBI Description
                   HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
                   (X77136) HSR203J [Nicotiana tabacum]
                   32264
Seq. No.
                   277354 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}02353.h1
                   32265
Seq. No.
                   277441 1.R1040
Contig ID
```

 $jC-gmf\overline{1}02220142g03a1$

```
32266
Seq. No.
 Contig ID
                    277447 1.R1040
 5'-most EST
                    k11701\overline{2}13720.h1
 Method
                    BLASTX
                    g3859592
 NCBI GI
 BLAST score
                    267
E value
                    1.0e-23
Match length
                    73
 % identity
                    73
 NCBI Description
                     (AF104919) contains similarity to expansins [Arabidopsis
                    thaliana]
                    32267
 Seq. No.
                    277568 1.R1040
 Contig ID
 5'-most EST
                    k11701\overline{2}07518.h1
Method
                    BLASTX
                    g4056506
 NCBI GI
 BLAST score
                    140
                    9.0e-09
 E value
Match length
                    75
 % identity
                    36
                     (AC005896) nodulin-like protein [Arabidopsis thaliana]
 NCBI Description
                    32268
 Seq. No.
                    277591 1.R1040
 Contig ID
 5'-most EST
                    kl1701202657.hl
Method
                    BLASTX
                    g1076274
 NCBI GI
 BLAST score
                    183
                    7.0e-14
 E value
                    53
Match length
 % identity
                    62
                    cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
 NCBI Description
 Seq. No.
                    32269
                    277674 1.R1040
 Contig ID
 5'-most EST
                    k11701\overline{2}02770.h1
 Seq. No.
                    32270
                    277677 1.R1040
 Contig ID
                    k11701\overline{2}02774.h1
 5'-most EST
 Seq. No.
                    32271
                    277743 1.R1040
 Contig ID
                    k11701\overline{2}02883.h1
 5'-most EST
 Method
                    BLASTX
NCBI GI
                    g2191137
                    Ž90
 BLAST score
                    2.0e-26
E value
                    77
Match length
 % identity.
                     (AF007269) similar to the GDSL family of lipolytic enzymes
NCBI Description
                     [Arabidopsis thaliana]
 Seq. No.
                    32272
```

277750 1.R1040

Contig ID

```
5'-most EST
                   k11701202993.h1
                   32273
Seq. No.
                   277767 1.R1040
Contig ID
                   k11701\overline{2}02917.h1
5'-most EST
                   BLASTX
Method
                   q1669591
NCBI GI
BLAST score
                   361
E value
                   9.0e-35
                   90
Match length
% identity
                   73
                   (D88742) O-methyltransferase [Glycyrrhiza echinata]
NCBI Description
Seq. No.
                   32274
Contig ID
                   277777 1.R1040
                   k11701\overline{2}02933.h1
5'-most EST
Method
                   BLASTX
                   g3688284
NCBI GI
BLAST score
                   232
                   1.0e-19
E value
Match length
                   89
                   51
% identity
                    (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                   lanata]
                   32275
Seq. No.
Contig ID
                   277801 1.R1040
5'-most EST
                   g5753444
Method
                   BLASTX
                   g2832625
NCBI GI
BLAST score
                   152
                   1.0e-12
E value
                   91
Match length
% identity
                   56
                    (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   32276
Seq. No.
Contig ID
                   277804 1.R1040
                   k11701205008.h1
5'-most EST
                   32277
Seq. No.
                   277817 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}09742.h1
Method
                   BLASTX
                   q4056403
NCBI GI
BLAST score
                   343
                   3.0e-32
E value
Match length
                   124
% identity
                   56
                   (AD001673) lipoxygenase [Persea americana]
NCBI Description
Seq. No.
                   32278
                   277844 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}30384.h1
```

32279

277877 1.R1040

Seq. No.

Contig ID

% identity

63

```
5'-most EST
                   kl1701203134.h1
Seq. No.
                   32280
                   277878 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}03123.h1
                   32281
Seq. No.
                   277893 1.R1040
Contig ID
                   k11701\overline{2}14961.h1
5'-most EST
                   32282
Seq. No.
Contig ID
                   278003 1.R1040
                   k11701\overline{2}12941.h1
5'-most EST
                   32283
Seq. No.
Contig ID
                   278011 1.R1040
                   uC-gmrominsoy066a05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2262177
BLAST score
                   485
E value
                   1.0e-48
Match length
                   214
% identity
                   50
                   (AC002329) hypothetical protein similar to T18A10.3
NCBI Description
                   [Arabidopsis thaliana]
                   32284
Seq. No.
Contig ID
                   278018 1.R1040
5'-most EST
                   kl1701203338.hl
Method
                   BLASTX
NCBI GI
                   q4204277
BLAST score
                   409
E value
                   3.0e-40
Match length
                   98
% identity
NCBI Description
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32285
Contig ID
                   278040 1.R1040
5'-most EST
                   jC-gmro02800043a11a1
Method
                   BLASTX
NCBI GI
                   q2655098
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   108
% identity
NCBI Description
                   (AF023472) peptide transporter [Hordeum vulgare]
                   32286
Seq. No.
Contig ID
                   278093 1.R1040
5'-most EST
                   kl1701212102.hl
Method
                   BLASTX
NCBI GI
                   q4538930
BLAST score
                   306
E value
                   4.0e-28
Match length
                   99
```

```
NCBI Description (AL049483) putative peroxidase [Arabidopsis thaliana]
                  32287
Seq. No.
                  278112 1.R1040
Contig ID
                  uC-gmropic093g12b1
5'-most EST
                  BLASTX
Method
                  g3548806
NCBI GI
                  379
BLAST score
                  2.0e-36
E value
                  148
Match length
                   47
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32288
Contig ID
                   278116 1.R1040
5'-most EST
                   jC-gmro02910071a12a1
Method
                  BLASTX
NCBI GI
                   g2262111
BLAST score
                   528
                   8.0e-54
E value
Match length
                   178
                   59
% identity
                   (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   32289
                   278120 1.R1040
Contig ID
5'-most EST
                   kl1701212133.h1
Seq. No.
                   32290
                   278124 1.R1040
Contig ID
                   k11701\overline{2}03501.h2
5'-most EST
                   32291
Seq. No.
                   278157 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy057f04b1
                   BLASTX
Method
NCBI GI
                   g3201617
BLAST score
                   281
E value
                   6.0e-25
Match length
                   82
% identity
                  (AC004669) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32292
                   278162 1.R1040
Contig ID
5'-most EST
                   k11701204108.h1
                   BLASTX
Method
                   g2443890
NCBI GI
BLAST score
                   221
E value
                   2.0e-18
Match length
                   52
                   73
% identity
                   (AC002294) similar to NAM (gp X92205 1321924) and CUC2
NCBI Description
                   (gp_AB002560_1944132) proteins [Arabidopsis thaliana]
```

32293

Seq. No.

Match length

```
Contig ID
                   278178 1.R1040
5'-most EST
                   k11701\overline{2}03571.h2
                   BLASTX
Method
                   g1421741
NCBI GI
BLAST score
                   330
                   4.0e-31
E value
                   86
Match length
                   74
% identity
NCBI Description (U54770) cytochrome P450 homolog [Lycopersicon esculentum]
Seq. No.
                   32294
Contig ID
                   278242 1.R1040
5'-most EST
                   jC-gmro02910036e04d1
Method
                   BLASTX
NCBI GI
                   g2506139
BLAST score
                   217
E value
                   1.0e-17
Match length
                   61
                   67
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                   archain/delta-COP [Oryza sativa]
                   32295
Seq. No.
                   278295 1.R1040
Contig ID
                  g50581<del>9</del>0
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4262226
BLAST score
                   268
                   2.0e-23
E value
Match length
                   140
% identity
NCBI Description
                  (AC006200) putative protein kinase [Arabidopsis thaliana]
                   32296
Seq. No.
                   278332 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}03793.h2
                   BLASTX
Method
NCBI GI
                   q3641865
BLAST score
                   493
E value
                   6.0e-50
Match length
                   131
                   70
% identity
NCBI Description
                   (AJ011010) beta-galactosidase [Cicer arietinum]
Seq. No.
                   32297
                   278335 1.R1040
Contig ID
                   k11701203881.hl
5'-most EST
Seq. No.
                   32298
                   278394 1.R1040
Contig ID
                   jC-gmst02400041b06a1
5'-most EST
Method
                   BLASTX
                   g3249103
NCBI GI
BLAST score
                   347
                   8.0e-33
E value
                   134
```

NCBI Description

```
% identity
                   (AC003114) Contains similarity to membrane-associated
NCBI Description
                   salt-inducible protein homolog TMO21BO4.10 gb_2191192 from
                   A. thaliana BAC gb AF007271. [Arabidopsis thaliana]
                   32299
Seq. No.
                   278470 1.R1040
Contig ID
                   jC-gmro02910005a11d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193284
BLAST score
                   285
E value
                   2.0e-25
                   70
Match length
                   76
% identity
                   (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                   32300
Seq. No.
                   278512 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}04057.h1
                   32301 -
Seq. No.
                   278535 1.R1040
Contig ID
                   k11701\overline{2}04114.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q867691
BLAST score
                   210
E value
                   5.0e-17
Match length
                   84
                   49
% identity
                   (M19735) beta-hexosaminidase beta-subunit [Homo sapiens]
NCBI Description
Seq. No.
                   32302
                   278571 1.R1040
Contig ID
5'-most EST
                   zsg701121108.hl
                   32303
Seq. No.
                   278574 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}04184.h1
Method
                   BLASTX
NCBI GI
                   g3360289
BLAST score
                   429
                   3.0e-42
E value
Match length
                   164
% identity
                   (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   1 [Zea mays]
                   32304
Seq. No.
Contig ID
                   278627 1.R1040
5'-most EST
                   epx701\overline{1}08916.h1
Method
                   BLASTX
                   g4098647
NCBI GI
                   346
BLAST score
                   1.0e-32
E value
Match length
                   86
% identity
                   (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
```

thaliana] 32305 Seq. No. Contig ID 278652 1.R1040 $k11701\overline{2}04312.h2$ 5'-most EST 32306 Seq. No. 278697 1.R1040 Contig ID 5'-most EST $k11701\overline{2}04367.h2$ 32307 Seq. No. Contig ID 278737 1.R1040 $k11701\overline{2}12025.h1$ 5'-most EST 32308 Seq. No. 278744 1.R1040 Contig ID $k11701\overline{2}04431.h2$ 5'-most EST 32309 Seq. No. 278746 2.R1040 Contiq ID 5'-most EST $k11701\overline{2}12792.h1$ 32310 Seq. No. 278751 1.R1040 Contig ID 5'-most EST $k11701\overline{2}04438.h2$ Method BLASTX NCBI GI g4454467 999 BLAST score 1.0e-109 E value 250 Match length 77 % identity (AC006234) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 32311 278761 1.R1040 Contig ID epx701105670.hl 5'-most EST Method BLASTX NCBI GI g544250 BLAST score 258 2.0e-22 E value 61 Match length 77 % identity ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) NCBI Description >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana 32312 Seq. No. 278764 1.R1040 Contig ID $k11701\overline{2}11424.h1$ 5'-most EST

Seq. No. 32313

Contig ID 278808_1.R1040 5'-most EST kl1701204518.h2

Seq. No. 32314

Contig ID 278811_1.R1040 5'-most EST kl1701204522.h2

```
Method
                   BLASTX
NCBI GI
                   g4371292
BLAST score
                   167
                   5.0e-12
E value
Match length
                   69
% identity
                   54
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32315
Seq. No.
                   278862 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910062f07d1
                   32316
Seq. No.
                   278940 1.R1040
Contig ID
                   k11701\overline{2}04694.h1
5'-most EST
Method
                   BLASTX
                   g3269287
NCBI GI
                   147
BLAST score
E value
                   3.0e-09
Match length
                   113
                   34
% identity
                   (AL030978) GH3 like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32317
                   278965 1.R1040
Contig ID
5'-most EST
                   uC-gmropic110c12b1
Seq. No.
                   32318
Contig ID
                   278999 1.R1040
                   k11701\overline{2}04795.h1
5'-most EST
                   32319
Seq. No.
                   279082 1.R1040
Contig ID
                   k11701\overline{2}07154.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g529353
BLAST score
                   419
                   8.0e-49
E value
Match length
                   159
% identity
NCBI Description
                   (U12757) diphenol oxidase [Acer pseudoplatanus]
                   32320
Seq. No.
                   279116 1.R1040
Contig ID
5'-most EST
                   k11701204975.h1
Method
                   BLASTX
NCBI GI
                   g3426038
BLAST score
                   597
                   6.0e-62
E value
Match length
                   176
                   66
% identity
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32321
Seq. No.
                   279440 1.R1040
Contig ID
```

kl1701205461.h1

5'-most EST

```
Seq. No.
                   32322
                   279480 1.R1040
Contig ID
5'-most EST
                   uC-gmropic108a02b1
                                                                       rise 1
                   32323
Seq. No.
                   279503 1.R1040
Contig ID
                   zsq701125331.h1
5'-most EST
                   BLASTX
Method
                   g4538980
NCBI GI
BLAST score
                   155
                   4.0e-10
E value
Match length
                   74
                   38
% identity
                   (AL049487) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   279593 1.R1040
Contiq ID
5'-most EST
                   kl1701205651.h1
Seq. No.
                   32325
                   279910 1.R1040
Contig ID
                   k11701\overline{2}06114.h1
5'-most EST
Seq. No.
                   32326
                   279992 1.R1040
Contig ID
                   k11701\overline{2}06234.h1
5'-most EST
Seq. No.
                   32327
Contig ID
                   279994 1.R1040
5'-most EST
                   g5509328
Seq. No.
                   32328
Contig ID
                   280031 1.R1040
5'-most EST
                   jC-gmro02910012f01a1
Method
                   BLASTX
NCBI GI
                   g3643608
BLAST score
                   230
E value
                   6.0e-19
Match length
                   71
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32329
                   280049 1.R1040
Contig ID
5'-most EST
                   q5509307
                   32330
Seq. No.
Contig ID
                   280088 1.R1040
5'-most EST
                   jC-gmro02910003b06a1
Method
                   BLASTX
NCBI GI
                   g2344901
BLAST score
                   444
E value
                   3.0e-44
Match length
                   133
% identity
                   68
NCBI Description
                   (AC002388) serine/threonine protein kinase isolog
```

[Arabidopsis thaliana]

```
Seq. No.
                    32331
                    280284 1.R1040
Contig ID
5'-most EST
                    k11701206653.h1
                    32332
Seq. No.
                    280303 1.R1040
Contig ID
                    k11701\overline{2}06652.h1
5'-most EST
                    32333
Seq. No.
                    280332 1.R1040
Contig ID
                    zsg701130154.hl
5'-most EST
Method
                    BLASTX
                    g4079632
NCBI GI
                    465
BLAST score
                    2.0e-46
E value
Match length
                    117
                    79
% identity
                    (AJ131722) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    32334
Seq. No.
                    280355_1.R1040
Contig ID
5'-most EST
                    jC-gmst02400045h09a1
                    32335
Seq. No.
                    280357 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}06724.h1
                    32336
Seq. No.
                    280566 1.R1040
Contig ID
                    k11701\overline{2}07117.h1
5'-most EST
                    32337
Seq. No.
                    280630 1.R1040
Contig ID
                    kl1701209969.hl
5'-most EST
                    32338
Seq. No.
                    280651 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}07230.h1
                    32339
Seq. No.
                    280681 1.R1040
Contig ID
                    k11701\overline{2}07272.h1
5'-most EST
                    32340
Seq. No.
                    280689 1.R1040
Contig ID
                    kl1701207292.hl
5'-most EST
                    32341
Seq. No.
                    280795_1.R1040
Contig ID
5'-most EST
                    jC-gmf102220126g09a1
                    32342
Seq. No.
                    280812 1.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy120e10b1
```

32343

Seq. No.

NCBI Description

```
Contig ID
                  280837 1.R1040
                  uC-gmflminsoy003c12b1
5'-most EST.
Method
                  BLASTX
                  g4218011
NCBI GI
                  770
BLAST score
                  4.0e-82
E value
                  200
Match length
                  72
% identity
                  (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi_4309721_gb_AAD15491_ (AC006439) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
                  32344
Seq. No.
                  280906 1.R1040
Contig ID
                  uC-gmflminsoy109b08b1
5'-most EST
Method
                  BLASTX
                  g2133437
NCBI GI
BLAST score
                  219
                  7.0e-18
E value
                  100
Match length
                  47
% identity
                  RNA polymerase II second largest chain RPB2 - Euplotes
NCBI Description
                  octocarinatus (SGC9) >gi 2654279 emb CAA47069_ (X66453)
                  DNA-directed RNA polymerase [Euplotes octocarinatus]
                  32345
Seq. No.
                  280913 1.R1040
Contig ID
5'-most EST
                  k11701207655.h1
Method
                  BLASTX
NCBI GI
                  q3776559
BLAST score
                  409
E value
                  3.0e-40
Match length
                  97
% identity
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  32346
Contig ID
                  280934 1.R1040
5'-most EST
                  epx701109379.hl
Seq. No.
                  32347
                  280949 1.R1040
Contig ID
                  kl1701207867.h1
5'-most EST
Seq. No.
                  32348
                  280958 1.R1040
Contig ID
5'-most EST
                  k11701\overline{2}09323.h1
Method
                  BLASTX
                  g3924597
NCBI GI
BLAST score
                  138
                  1.0e-08
E value
Match length
                  87
% identity
```

(AF069442) putative oxidoreductase [Arabidopsis thaliana]

NCBI Description

```
32349
Seg. No.
Contig ID
                   281016 1.R1040
                   jC-gmro02910004a10d1
5'-most EST
Method
                   BLASTX
                   g2244973
NCBI GI
BLAST score
                   413
                   3.0e-40
E value
                   193
Match length
                   40
% identity
                   (Z97340) similarity to extensin class 1 protein
NCBI Description
                   [Arabidopsis thaliana]
                   32350
Seq. No.
Contig ID
                   281054 1.R1040
5'-most EST
                   k11701\overline{2}08323.h1
Method
                   BLASTX
NCBI GI
                   g2342735
BLAST score
                   162
                   2.0e-11
E value
Match length
                   49
% identity
NCBI Description
                   (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32351
Contig ID
                   281129 1.R1040
                   k11701207975.h1
5'-most EST
Seq. No.
                   32352
Contig ID
                   281132 1.R1040
5'-most EST
                   jC-gmle01810018a08a2
                   32353
Seq. No.
Contig: ID
                   281150 1.R1040
                   k11701\overline{2}08002.h1
5'-most EST
                   32354
Seq. No.
Contig ID
                   281183 1.R1040
5'-most EST
                   kl1701208043.hl
Method
                   BLASTX
NCBI GI
                   q4204297
BLAST score
                   519
E value
                   6.0e-53
Match length
                   106
                   92
% identity
                   (AC003027) ADK1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32355
                   281226 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}08104.h1
Method
                   BLASTX
                   g3150412
NCBI GI
BLAST score
                   231
                   2.0e-19
E value
Match length
                   67
% identity
```

(AC004165) putative Fe(II) transport protein [Arabidopsis

```
thaliana] >gi_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]
```

```
Seq. No.
                    32356
                    281256 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}08136.h1
                    32357
Seq. No.
Contig ID
                    281280 1.R1040
5'-most EST
                    kl1701208165.hl
                    32358
Seq. No.
                    281382_1.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy154a05b1
Seq. No.
                    32359
                    281409 1.R1040
Contig ID
                    k11701\overline{2}08332.h1
5'-most EST
Seq. No.
                    32360
Contig ID
                    281441_1.R1040
5'-most EST
                    k11701\overline{2}08373.h1
                    32361
Seq. No.
Contig ID
                    281462 1.R1040
5'-most EST
                    k11701\overline{2}15446.h1
                    32362
Seq. No.
                    281545 1.R1040
Contig ID
5'-most EST
                    uC-gmronoir030e01b1
                    32363
Seq. No.
                    281681_1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}08708.h1
                    32364
Seq. No.
Contig ID
                    281683 1.R1040
5'-most EST
                    k11701\overline{2}12911.h1
                    BLASTX
Method
                    g1619602
NCBI GI
BLAST score
                    235
E value
                    7.0e-20
Match length
                    53
                    87
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                    32365
Seq. No.
Contig ID
                    281705 1.R1040
5'-most EST
                    k11701\overline{2}08747.h1
Method
                    BLASTX
NCBI GI
                    g3115374
BLAST score
                    483
E value
                    1.0e-48
Match length
                    106
```

NCBI Description (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

86

% identity

```
32366
Seq. No.
                    281719 1.R1040
Contig ID
                    kl1701209188.hl
5'-most EST
                    32367
Seq. No.
                    281749 1.R1040
Contig ID
5'-most EST
                    epx701\overline{1}04434.h1
                    32368
Seq. No.
                    281796 1.R1040
Contig ID
5'-most EST
                    kl1701209567.hl
                    32369
Seq. No.
                    281813 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}08908.h1
Method
                    BLASTX
                    g3077640
NCBI GI
BLAST score
                    228
E value
                    3.0e-19
Match length
                    79
% identity
                    59
                    (AJ223151) O-methyltransferase [Prunus dulcis]
NCBI Description
                    32370
Seq. No.
                    281891_1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}09045.h1
                    32371
Seq. No.
                    281920 1.R1040
Contig ID
                    k11701209102.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g1685005
BLAST score
                    199
                    9.0e-16
E value
Match length
                    51
                    73
% identity
NCBI Description
                    (U32644) immediate-early salicylate-induced
                    glucosyltransferase [Nicotiana tabacum]
                    32372
Seq. No.
                    281921 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}09103.h1
Seq. No.
                    32373
                    281959 1.R1040
Contig ID
                    epx701\overline{1}03727.h1
5'-most EST
Method
                   BLASTX
                    g1076331
NCBI GI
BLAST score
                    306
                    5.0e-34
E value
                    96
Match length
                    74
% identity
NCBI Description
                   histidine transport protein - Arabidopsis thaliana
                   >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                   1-1 [Arabidopsis thaliana] >gi 744157_prf__2014244A His
```

transporter [Arabidopsis thaliana]

```
32374
Seq. No.
                    281977 1.R1040
Contig ID
5'-most EST
                    kl1701209177.hl
                    32375
Seq. No.
                    282020 1.R1040
Contig ID
                    k11701\overline{2}09233.h1
5'-most EST
Seq. No.
                    32376
                    282027 1.R1040
Contig ID
                    k11701\overline{2}12080.h1
5'-most EST
                    32377
Seq. No.
                    282180 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}14205.h1
                    32378
Seq. No.
                    282325 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}09656.h1
                    32379
Seq. No.
Contig ID
                    282326 1.R1040 ~
5'-most EST
                    g4293821
Method
                    BLASTX
                    q2981463
NCBI GI
BLAST score
                    118
                    5.0e-09
E value
                    93
Match length
% identity
                    (AF052663) gamma-tubulin interacting protein [Xenopus
NCBI Description
                    laevis]
                    32380
Seq. No.
Contig ID
                    282347 1.R1040
                    asn701140632.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4235430
BLAST score
                    239
E value
                    3.0e-20
Match length
                    69
                    68
% identity
NCBI Description
                    (AF098458) latex-abundant protein [Hevea brasiliensis]
                    32381
Seq. No.
                    282379 1.R1040
Contig ID
5'-most EST
                    k11701\overline{2}14478.h1
Seq. No.
                    32382
                    282402 1.R1040
Contig ID
                    k11701\overline{2}13719.h1
5'-most EST
                    32383
Seq. No.
                    282420 1.R1040
Contig ID
                    k11701\overline{2}13504.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4220491
BLAST score
                    202
```

5'-most EST

Method

```
7.0e-16
E value
Match length
                   103
                   42
% identity
NCBI Description
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32384
                   282442 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}09829.h1
Seq. No.
                   32385
Contig ID
                   282521 1.R1040
5'-most EST
                   k11701\overline{2}11385.h1
                   32386
Seq. No.
Contig ID
                   282528 1.R1040
5'-most EST
                   k11701\overline{2}09951.h1
Method
                   BLASTX
                   g3128186
NCBI GI
BLAST score
                   164
E value
                   8.0e-12
Match length
                   56
% identity
                   54
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32387
Seq. No.
                   282552 1.R1040
Contig ID
                   k11701\overline{2}11063.h1
5'-most EST
                   32388
Seq. No.
                   282554 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}09976.h1
                   BLASTX
Method
NCBI GI
                   g1351303
BLAST score
                   334
E value
                   3.0e-31
Match length
                   92
% identity
                   70
NCBI Description
                   INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
                   >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                   [Arabidopsis thaliana]
                   32389
Seq. No.
                   282616 1.R1040
Contig ID
5'-most EST
                   k11701210061.h1
Method
                   BLASTX
NCBI GI
                   g4454012
                   212
BLAST score
                   6.0e-17
E value
Match length
                   86
% identity
NCBI Description
                   (AL035396) Pollen-specific protein precursor like
                   [Arabidopsis thaliana]
                   32390
Seq. No.
Contig ID
                   282630 1.R1040
```

kl1701210079.hl

BLASTX

```
q3024871
NCBI GI
BLAST score
                   223
                   2.0e-18
E value
Match length
                   83
                   55
% identity
                   HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                   >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                   32391
Seq. No.
Contig ID
                   282712 1.R1040
5'-most EST
                   k11701\overline{2}10189.h1
Method
                   BLASTX
NCBI GI
                   q4490297
BLAST score
                   188
                   7.0e-14
E value
Match length
                   113
                   42
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   32392
Seq. No.
                   282735 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}10560.h1
                   32393
Seq. No.
                   282742 1.R1040
Contig ID
5'-most EST
                   k11701210229.h1
                   BLASTX
Method
                   g3128199
NCBI GI
                   207
BLAST score
                   9.0e-17
E value
Match length
                   57
% identity
                   (AC004521) putative proteinase [Arabidopsis thaliana]
NCBI Description
                   32394
Seq. No.
Contig ID
                   282755 1.R1040
                   k11701\overline{2}10252.h1
5'-most EST
                   32395
Seq. No.
                   282926 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy164d02b1
Method
                   BLASTX
                   g1708863
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
Match length
                   53
% identity
                   ACYL-[ACYL-CARRIER-PROTEIN] -- UDP-N-ACETYLGLUCOSAMINE
NCBI Description
                   O-ACYLTRANSFERASE (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)
                   >gi_1262294 (U51683) LpxA [Brucella abortus]
                   32396
Seq. No.
Contig ID
                   283013 1.R1040
5'-most EST
                   uC-gmrominsoy158g11b1
                   BLASTX
Method
NCBI GI
                   g2827141
```

NCBI Description

```
BLAST score
                        394
    E value
                        5.0e-38
    Match length
                        86
    % identity
                        83
    NCBI Description
                        (AF027173) cellulose synthase catalytic subunit
                        [Arabidopsis thaliana]
                        32397
    Seq. No.
    Contig ID
                        283040 1.R1040
colors -most EST
                        k11701\overline{2}10762.h1
                        32398
    Seq. No.
                        283158 1.R1040
    Contig ID
    5'-most EST
                        jC-gmst02400051e11d1
                        32399
    Seq. No.
                        283287 1.R1040
    Contig ID
                        k11701\overline{2}11109.h1
    5'-most EST
    Method
                        BLASTX
    NCBI GI
                        g3928150
    BLAST score
                        433
    E value
                        6.0e-43
    Match length
                        103
                        75
    % identity
    NCBI Description
                        (AJ131049) hypothetical protein [Cicer arietinum]
    Seq. No.
                        32400
                        283386 1.R1040
    Contig ID
    5'-most EST
                        k11701\overline{2}11250.h1
    Seq. No.
                        32401
    Contig ID
                        283461 1.R1040
    5'-most EST
                        k11701\overline{2}11360.h1
                        32402
    Seq. No.
                        283489 1.R1040
    Contig ID
    5'-most EST
                        g42980\overline{2}6
    Method
                        BLASTX
    NCBI GI
                        g3874440
    BLAST score
                        169
    E value
                        1.0e-11
    Match length
                        107
    % identity
                        33
                        (Z81038) Similarity to Bovine NADH-ubiquinone
    NCBI Description
                        oxidoreducatse B8 subunit (SW:Q02370) [Caenorhabditis
                        elegans]
                        32403
    Seq. No.
                        283563 1.R1040
    Contig ID
                        g4300673
    5'-most EST
    Method
                        BLASTX
                        g4099092
    NCBI GI
    BLAST score
                        426
    E value
                        6.0e-42
    Match length
                        140
    % identity
```

(U83179) unknown [Arabidopsis thaliana]

```
Seq. No.
                   32404
                   283571 1.R1040
Contig ID
                   jC-gmle01810006e04a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2809251
BLAST score
                   916
E value
                   7.0e-99
Match length
                   305
% identity
                   56
NCBI Description
                   (AC002560) F21B7.20 [Arabidopsis thaliana]
Seq. No.
                   32405
Contig ID
                   283700 1.R1040
5'-most EST
                   jC-qmle01810089a12a1
Method
                   BLASTX
                   g3819699
NCBI GI
BLAST score
                   373
E value
                   1.0e-41
Match length
                   197
% identity
                   51
                   (AJ009609) BnMAP4K alpha2 [Brassica napus]
NCBI Description
                   32406
Seq. No.
                   283704 1.R1040
Contig ID
5'-most EST
                   g5126825
                   32407
Seq. No.
                   283729 1.R1040
Contig ID
5'-most EST
                   kl1701211749.hl
                   32408
Seq. No.
                   283838 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220080a01a1
                   32409
Seq. No.
Contig ID
                   283930 1.R1040
5'-most EST
                   k11701\overline{2}12503.h1
Seq. No.
                   32410
                   283964 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy162e03b1
Seq. No.
                   32411
                   283988 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}12094.h1
Seq. No.
                   32412
Contig ID
                   284071 1.R1040
5'-most EST
                   kl1701212210.hl
Method
                   BLASTX
NCBI GI
                   g2346966
BLAST score
                   220
                   7.0e-18
E value
                   56
Match length
% identity
                   68
                   (AB004871) CPC [Arabidopsis thaliana]
NCBI Description
```

>gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 32413

Contig ID 284077 1.R1040

5'-most EST jC-gmle01810050a05a1

Method BLASTX
NCBI GI g3355486
BLAST score 193
E value 6.0e-15
Match length 51
% identity 63

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 284124 1.R1040 5'-most EST kl1701212277.h1

Seq. No. 32415

Contig ID 284193 1.R1040

5'-most EST uC-gmrominsoy046e07b1

32414

Seq. No. 32416

Contig ID 284214 1.R1040 5'-most EST kl1701212403.h1

Seq. No. 32417

Contig ID 284244_1.R1040 5'-most EST kl1701212684.h1

Method BLASTX
NCBI GI g3885329
BLAST score 339
E value 3.0e-32
Match length 78
% identity 82

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 32418

Contig ID 284423 1.R1040

5'-most EST uC-gmflminsoy071a07b2

Seq. No. 32419

Contig ID 284428_1.R1040 5'-most EST asn701143228.h1

Seq. No. 32420

Contig ID 284450_1.R1040

5'-most EST jC-gmle01810054a10a1

Seq. No. 32421

Contig ID 284511_1.R1040 5'-most EST epx701107757.h1

Seq. No. 32422

Contig ID 284560 1.R1040

5'-most EST uC-gmflminsoy025c12b1

Method BLASTX

```
g2352492
NCBI GI
BLAST score
                   520
                   7.0e-53
E value
Match length
                   125
                   75
% identity
NCBI Description
                    (AF005047) transport inhibitor response 1 [Arabidopsis
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   32423
Seq. No.
                   284660 1.R1040
Contig ID
5'-most EST
                   epx701108257.h1
                   32424
Seq. No.
Contig ID
                   284705 1.R1040
                   epx701109068.hl
5'-most EST
                   32425
Seq. No.
                   284768 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy007b12b1
                   32426
Seq. No.
                   284798 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910039h06a1
                   32427
Seq. No.
                   284824 1.R1040
Contig ID
5'-most EST
                   k11701213216.h1
                   32428
Seq. No.
                   284855 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}21725.h1
                   32429
Seq. No.
                   284880 1.R1040
Contig ID
5'-most EST
                   jC-gmr002910050e09d1
Seq. No.
                   32430
                   284889 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220092d01a1
                   32431
Seq. No.
Contig ID
                   285001 1.R1040
5'-most EST
                   uC-gmrominsoy033d10b1
                   BLASTX
Method
NCBI GI
                   g2459412
BLAST score
                   172
E value
                    6.0e-12
                   103
Match length
                    43
% identity
                    (AC002332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                   32432
Seq. No.
                   285042 1.R1040
Contig ID
                   jC-gmro02910002a07a1
5'-most EST
```

32433

Seq. No.

Match length

94

```
285049 1.R1040
Contig ID
5'-most EST
                   q5509313
Method
                   BLASTX
NCBI GI
                   q2864625
BLAST score
                   320
                   2.0e-29
E value
                   92
Match length
                   67
% identity
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   32434
                   285172 1.R1040
Contig ID
                   k11701\overline{2}13667.h1
5'-most EST
                   32435
Seq. No.
                   285185_2.R1040
Contig ID
5'-most EST
                   jC-gmst02400066b03d1
                   32436
Seq. No.
                   285304 1.R1040
Contig ID
5'-most EST
                   uC-gmropic015d09b1
Method
                   BLASTN
                   g3869068
NCBI GI
BLAST score
                   64
E value
                   3.0e-27
                   300
Match length
% identity
                   80
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MDC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   32437
                   285340 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}13890.h1
Method
                   BLASTX
NCBI GI
                   g2569940
BLAST score
                   264
                   1.0e-27
E value
Match length
                   136
% identity
                   50
NCBI Description
                   (Y15194) GRS protein [Arabidopsis thaliana]
                   32438
Seq. No.
Contig ID
                   285365 1.R1040
5'-most EST
                   zsg701\overline{1}22787.h1
Seq. No.
                   32439
                   285400 1.R1040
Contig ID
5'-most EST
                   zsg701125845.hl
Seq. No.
                   32440
Contig ID
                   285447 1.R1040
5'-most EST
                   kl1701214043.h1
Method
                   BLASTX
NCBI GI
                   g2160166
BLAST score
                   288
                   4.0e-26
E value
```

```
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   32441
Seq. No.
                   285508 1.R1040
Contig ID
                   jC-gmf\overline{1}02220112g07d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2583123
BLAST score
                   470
E value
                   4.0e-47
Match length
                   115
                   78
% identity
                   (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                   thalianal
                   32442
Seq. No.
                   285606 1.R1040
Contig ID
5'-most EST
                   kl1701214241.h1
                   32443
Seq. No.
                   285676 1.R1040
Contig ID
                   k11701\overline{2}14344.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2894600
                   215
BLAST score
E value
                   1.0e-17
Match length
                   51
                   67
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   32444
Seq. No.
                   285699 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}14351.h1
                   BLASTX
Method
                   g1711382
NCBI GI
BLAST score.
                   176
E value
                   5.0e-13
Match length
                   55
                   51
% identity
                   SET PROTEIN >qi 940889 (U30470) SET [Drosophila
NCBI Description
                   melanogaster]
Seq. No.
                   32445
                   285750 1.R1040
Contig ID
                   jC-gmle01810084h09a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4185507
BLAST score
                   866
                   2.0e-93
E value
Match length
                   216
                   70
% identity
                   (AF100163) EZA1 [Arabidopsis thaliana]
NCBI Description
                   32446
Seq. No.
                   285774 1.R1040
Contig ID
```

asn701140406.hl

5'-most EST

```
32447
Seq. No.
                   285827 1.R1040
Contig ID
                   uC-gmropic017h02b1
5'-most EST
Method
                   BLASTX
                   q1076758
NCBI GI
BLAST score
                   528
                   6.0e-54
E value
                   131
Match length
% identity
                   76
                   heat-shock protein precursor - rye >gi_2130093_pir__S65776
NCBI Description
                   heat-shock protein, 82K, precursor - rye
                   >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
                   32448
Seq. No.
Contig ID
                   285852 1.R1040
5'-most EST
                   k11701\overline{2}14562.h1
Method
                   BLASTX
                   g4151319
NCBI GI
BLAST score
                   147
E value
                   1.0e-09
                   30
Match length
                   93
% identity
                   (AF089084) putative auxin efflux carrier protein; AtPIN1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   32449
                   285872 1.R1040
Contig ID
                   kl1701214554.h1
5'-most EST
                   32450
Seq. No.
                   285905 1.R1040
Contig ID
                   uC-gmflminsoy072d01b1
5'-most EST
Method
                   BLASTX
                   g3763934
NCBI GI
BLAST score
                   230
                   4.0e-19
È value
Match length
                   109
% identity
                   47
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32451
                   285926 1.R1040
Contig ID
                   k11701\overline{2}14620.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2827637
BLAST score
                   200
                   3.0e-15
E value
                   185
Match length
% identity
NCBI Description
                   (AL021636) putative protein [Arabidopsis thaliana]
                   32452
Seq. No.
                   285927 1.R1040
Contig ID
                   k11701215491.h1
5'-most EST
```

32453

Seq. No.

```
Contig ID
                   285962 1.R1040
5'-most EST
                   jC-gmf102220050g02a1
Method
                   BLASTX
NCBI GI
                   g3786000
BLAST score
                   262
E value
                   1.0e-22
Match length
                   108
                   45
% identity
NCBI Description
                   (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32454
                   286210 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}14989.h1
Method
                   BLASTX
NCBI GI
                   a3142303
BLAST score
                   161
                   3.0e-11
E value
                   88
Match length
% identity
                   39
NCBI Description
                   (AC002411) Strong similarity to MRP-like ABC transporter
                   gb_U92650 from A. thaliana and canalicular multi-drug
                   resistance protein gb_L49379 from Rattus norvegicus.
                   [Arabidopsis thaliana]
Seq. No.
                   32455
                   286282 1.R1040
Contig ID
5'-most EST
                   kl1701215347.h1
                   32456
Seq. No.
                   286323 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}15149.h1
                   32457
Seq. No.
                   286343 1.R1040
Contig ID
5'-most EST
                   k11701\overline{2}15175.h1
Seq. No.
                   32458
Contig ID
                   286388 1.R1040
5'-most EST
                   kl1701215237.h1
Method
                   BLASTX
                   g3738324
NCBI GI
BLAST score
                   237
E value
                   3.0e-20
Match length
                   88
                   50
% identity
                   (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
NCBI Description
                   32459
Seq. No.
                   286478 1.R1040
Contig ID
5'-most EST
                   g5605942
Seq. No.
                   32460
                   286527 1.R1040
Contig ID
                   asn701139270.h1
5'-most EST
                   32461
Seq. No.
```

286548 1.R1040

Contig ID

```
5'-most EST
                  kl1701215463.hl
Method
                  BLASTX
NCBI GI
                  g4544473
BLAST score
                  263
E value
                  3.0e-23
Match length
                  71
                  39
% identity
                  (AC006580) putative mei2 protein [Arabidopsis thaliana]
NCBI Description
                  32462
Seq. No.
                  286554 1.R1040
Contig ID
5'-most EST
                  kl1701215470.hl
Method
                  BLASTX
                  g1174718
NCBI GI
BLAST score
                  381
E value
                  2.0e-36
                  93
Match length
                  78
% identity
                  PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
NCBI Description
                  >gi 322579 pir JQ1674 receptor protein kinase TMK1 (EC
                  2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
                   (L00670) protein kinase [Arabidopsis thaliana]
                  32463
Seq. No.
                  286584 1.R1040
Contig ID
5'-most EST
                  epx701108777.hl
Seq. No.
                  32464
                  286651 1.R1040
Contig ID
5'-most EST
                  epx701103856.hl
                  32465
Seq. No.
Contig ID
                  286661 1.R1040
5'-most EST
                  epx701\overline{1}05166.h1
                  32466 '
Seq. No.
                  286670 1.R1040
Contig ID
5'-most EST
                  asn701137942.h1
Method
                  BLASTX
NCBI GI
                  g2979558
BLAST score
                  148
                  8.0e-10
E value
                  38
Match length
% identity
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32467
                  286690 1.R1040
Contig ID
5'-most EST
                  epx701103939.hl
                  32468
Seq. No.
Contig ID
                  286748 1.R1040
5'-most EST
                  epx701104058.hl
Method
                  BLASTX
NCBI GI
                  g4049350
BLAST score
                  217
                  2.0e-17
E value
```

BLAST score

279

```
73
Match length
                   56
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   32469
Seq. No.
                   286798 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy023h11b1
                   BLASTN
Method
NCBI GI
                   g3046855
BLAST score
                   70
E value
                   4.0e-31
Match length
                   266
                   82
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   32470
                   286902 1.R1040
Contig ID
5'-most. EST
                   epx701\overline{1}05832.h1
Seq. No.
                   32471
                   286902 2.R1040
Contig ID
5'-most EST
                   epx701\overline{1}04610.h1
Seq. No.
                   32472
                   286981 1.R1040
Contig ID
5'-most EST
                   epx701104381.hl
                   BLASTX
Method
                   g2558938
NCBI GI
                   569
BLAST score
E value
                   2.0e-58
Match length
                   228
% identity
                   54
                   (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   32473
Seq. No.
Contig ID
                   287162 1.R1040
5'-most EST
                   jC-gmf102220089c10a1
                   32474
Seq. No.
Contig ID
                   287311 1.R1040
5'-most EST
                   uC-gmrominsoy213h02b1
Method
                   BLASTX
NCBI GI
                   g2252840 -:
BLAST score
                   179
                   3.0e-13
E value
                   80
Match length
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                   32475
                   287456_1.R1040
Contig ID
5'-most EST
                   asn701136070.hl
                   BLASTX
Method
                   g3286691
NCBI GI
```

5'-most EST

```
E value
                  8.0e-25
                  87
Match length
                  57
% identity
                  (AJ007450) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32476
                  287634 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400067h03a1
                  32477
Seq. No.
                  287636 1.R1040
Contig ID
5'-most EST
                  zsg701118226.h1
                  32478
Seq. No.
                  287730 1.R1040
Contig ID
5'-most EST
                  zsq701118519.hl
                  BLASTX
Method
NCBI GI
                  q3805765
BLAST score
                  564
                  6.0e-58
E value
Match length
                  156
% identity
NCBI Description
                   (AC005693) putative protein kinase [Arabidopsis thaliana]
                  32479
Seq. No.
                  287766 1.R1040
Contig ID
5'-most EST
                  epx701105492.h1
Seq. No.
                  32480
                  287772 1.R1040
Contig ID
                  jC-gmro02910059a04d1
5'-most EST
Seq. No.
                  32481
Contig ID
                  287868 1.R1040
5'-most EST
                  epx701105637.h1
Method
                  BLASTX
NCBI GI
                  g4454459
BLAST score
                  605
E value
                  5.0e-63
Match length
                  147
% identity
                  79
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32482
Contig ID
                  287932 1.R1040
5'-most EST
                  jC-gmro02910009d05a1
Method
                  BLASTX
NCBI GI
                  g4544451
BLAST score
                  622
E value
                  5.0e-65
                  147
Match length
% identity
NCBI Description
                  (AC006592) unknown protein [Arabidopsis thaliana]
                  32483
Seq. No.
Contig ID
                  287960 1.R1040
```

uC-gmrominsoy028d03b1

```
32484
Seq. No.
                   288006 1.R1040
Contig ID
5'-most EST
                   zsg701121033.hl
                   32485
Seq. No.
                   288048 1.R1040
Contig ID
                   epx701105890.hl
5'-most EST
Seq. No.
                   32486
                   288051_1.R1040
Contig ID
                   epx701\overline{1}05893.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4432814
BLAST score
                   397
E value
                   7.0e-39
                   103
Match length
                   73
% identity
                   (AC006593) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32487
Seq. No.
                   288190 1.R1040
Contig ID
                   epx701106079.hl
5'-most EST
                   32488
Seq. No.
                   288200 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220079a03a1
                   BLASTX
Method
                   g2244753
NCBI GI
                   450
BLAST score
                   8.0e-45
E value
Match length
                   118
% identity
                   69
                    (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32489
Seq. No.
                   288218 1.R1040
Contig ID
5'-most EST
                   956768\overline{4}3
Seq. No.
                   32490
                   288258 1.R1040
Contig ID
                   jC-gmf\overline{1}02220081b07d1
5'-most EST
Seq. No.
                   32491
                   288325 1.R1040
Contig ID
5'-most EST
                   epx701106274.h1
                   BLASTX
Method
NCBI GI
                   g3914621
                   151
BLAST score
                   8.0e-10
E value
                   129
Match length
% identity
                   12
                   RAN GTPASE ACTIVATING PROTEIN 1 >gi 2062660 (U88155)
NCBI Description
                   RanGTPase activating protein [Xenopus laevis]
                   32492
Seq. No.
```

288425 1.R1040

Contig ID

```
jC-gmle01810078c08a1
5'-most EST
                   BLASTN
Method
                   q169036
NCBI GI
BLAST score
                   46
                   7.0e-17
E value
                   70
Match length
                   91
% identity
                   Pisum sativum L. aldolase gene, 3' end cds
NCBI Description
                   32493
Seq. No.
Contig ID
                   288482 1.R1040
5'-most EST
                   jC-gmro02910002a06d1
Seq. No.
                   32494
                   288502 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}06518.h1
Method
                   BLASTX
                   g585084
NCBI GI
BLAST score
                   153
                   6.0e-10
E value
Match length
                   56
                   57
% identity
                   ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)
NCBI Description
                   >gi_543383_pir__S40780 translation elongation factor G,
                   mitochondrial - rat >gi_310102 (L14684) elongation factor G
                   [Rattus norvegicus]
Seq. No.
                   32495
                   288655 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}06718.h1
                   BLASTX
Method -
NCBI GI
                   q4559371
BLAST score
                   160
                   8.0e-11
E value
                   58
Match length
                   53
% identity .
                   (AC006585) putative peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32496
                   288657 1.R1040
Contig ID
5'-most EST
                   epx701106822.h1
Method
                   BLASTX
NCBI GI
                   q3114573
BLAST score
                   314
                   3.0e-29
E value
Match length
                   92
% identity
                   (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
NCBI Description
                   piperita]
Seq. No.
                   32497
                   288876 1.R1040
Contig ID
5'-most EST
                   epx701107014.h1
Seq. No.
                   32498
                   289043 1.R1040
Contig ID
5'-most EST
                   uC-qmropic037d09b1
```

```
Method
                    BLASTX
                    g2191151
 NCBI GI
 BLAST score
                    509
 E value
                    1.0e-51
Match length
                    125
                    77
 % identity
NCBI Description
                    (AF007269) contains similarity to membrane associated
                    salt-inducible protein [Arabidopsis thaliana]
 Seq. No.
                    32499
 Contig ID
                    289209 1.R1040
 5'-most EST
                    uC-gmrominsoy235h10b1
 Seq. No.
                    32500
                    289209 2.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy265a01b1
 Seq. No.
                    32501
                    289273 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810009h03a1
                    32502
Seq. No.
Contig ID
                    289320 1.R1040
                    zsg701\overline{1}25287.h1
 5'-most EST
Method
                    BLASTX
NCBI GI
                    g1706885
BLAST score
                    146
                    2.0e-09
E value
Match length
                    78
 % identity
                    45
NCBI Description
                    FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR
                    (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) >gi 1345106
                    (U33557) folylpolyglutamate synthetase precursor [Mus
                   musculus]
Seq. No.
                    32503
                    289429_1.R1040
Contig ID
 5'-most EST
                    epx701107838.hl
                    32504
Seq. No.
                    289501 1.R1040
Contig ID
 5'-most EST
                    g5606214
Seq. No.
                    32505
                    289548 1.R1040
Contig ID
 5'-most EST
                    epx701108027.h1
Seq. No.
                    32506
Contig ID
                    289662_1.R1040
 5'-most EST
                    uC-gmrominsoy029a12b1
Seq. No.
                    32507
Contig ID
                    289665 1.R1040
 5'-most EST
                    epx701\overline{1}08193.h1
Seq. No.
                    32508
```

289680 1.R1040

Contig ID

5'-most EST epx701108215.hl 32509 Seq. No. Contig ID 289746 1.R1040 uC-gmflminsoy018a03b1 5'-most EST 32510 Seq. No. Contig ID 289836_1.R1040 5'-most EST epx701108410.hl 32511 Seq. No. 290042 1.R1040 Contig ID $epx701\overline{1}08718.h1$ 5'-most EST 32512 Seq. No. 290092 1.R1040 Contig ID 5'-most EST epx701108782.hl Seq. No. 32513 290127 1.R1040 Contig ID 5'-most EST $epx701\overline{1}08896.h1$ 32514 Seq. No. 290151 1.R1040 Contig ID 5'-most EST $epx701\overline{1}08876.h1$ Seq. No. 32515 290182_1.R1040 Contig ID 5'-most EST uC-gmrominsoy0001h07al 32516 Seq. No. Contig ID 290193 1.R1040 zsg701118973.hl 5'-most EST Method BLASTX NCBI GI g3420801 BLAST score 211 E value 7.0e-17 Match length 67 % identity 61 (AF081066) IAA-amino acid hydrolase homolog ILL3 NCBI Description [Arabidopsis thaliana] 32517 Seq. No. 290213 1.R1040 Contig ID 5'-most EST uC-gmflminsoy021g01b1 BLASTX Method NCBI GI g3914020 BLAST score 282 E value 4.0e-25 Match length 111 50 % identity (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR NCBI Description (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi 1561641 emb CAA69388 (Y08211) mandelonitrile lyase

4947

· .

[Prunus dulcis]

32518

Seq. No.

5'-most EST

```
290367 1.R1040
Contig ID
                   epx701\overline{1}09171.h1
5'-most EST
                   32519
Seq. No.
                   290387 1.R1040
Contig ID
                   uC-gmflminsoy081h06b1
5'-most EST
                   32520
Seq. No.
Contig ID
                   290399 1.R1040
                   epx701109213.hl
5'-most EST
                   32521
Seq. No.
                   290538 1.R1040
Contig ID
                   epx701109416.hl
5'-most EST
                   BLASTX
Method
                   q4164145
NCBI GI
                   306
BLAST score
                   7.0e-28
E value
                   114
Match length
                   48
% identity
                   (AB012205) gibberelin 3beta-hydroxylase [Lactuca sativa]
NCBI Description
                   32522
Seq. No.
                   290570 1.R1040
Contig ID
5'-most EST
                   epx701\overline{1}09489.h1
Method
                   BLASTX
                   g2289003
NCBI GI
                   699
BLAST score
                   7.0e-74
E value
                   179
Match length
                   76
% identity
                   (ACO02335) membrane transporter D1 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   32523
Seq. No.
                   290580 1.R1040
Contig ID
                   jC-gmle01810025a06a1
5'-most EST
Method
                   BLASTX
                   g2961352
NCBI GI
                   250
BLAST score
                   3.0e-21
E value
                   58
Match length
% identity
                   74
                   (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32524
                   290699 1.R1040
Contig ID
5'-most EST
                   epx701110431.h1
                   32525
Seq. No.
                   290758 1.R1040
Contig ID
                   epx701109965.hl
5'-most EST
Seq. No.
                   32526
                   290812 1.R1040
Contig ID
```

uC-qmropic042c05b1

```
32527
Seq. No.
Contig ID
                   290842 1.R1040
                   jC-gmf\(\bar{1}\)02220054f08d1
5'-most EST
Method
                   BLASTX
                   g2129755
NCBI GI
BLAST score
                   433
                   7.0e-43
E value
                   103
Match length
% identity
                   83
NCBI Description
                   tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis
                   thaliana >gi_619753 (U18993) tryptophan synthase alpha
                   chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp
                   synthase:SUBUNIT=alpha [Arabidopsis thaliana]
                   32528
Seq. No.
                   290888 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810030g01a2
Method
                   BLASTX
NCBI GI
                   g2062173
BLAST score
                   502
E value
                   3.0e-51
                   103
Match length
                   95
% identity
                   (AC001645) cell division protein FtsH isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   32529
                   290900 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy047c01b1
                   32530
Seq. No.
                   291084 1.R1040
Contig ID
5'-most EST
                   g5058010
                   32531
Seq. No.
                   291208 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910041017a1
Method
                   BLASTX
                   g4314358
NCBI GI
BLAST score
                   527
E value
                   2.0e-53
                   318
Match length
                   42
% identity
NCBI Description
                   (AC006340) putative kinesin heavy chain protein
                   [Arabidopsis thaliana]
                   32532
Seq. No.
Contig ID
                   291237 1.R1040
                   uC-gmrominsoy167h04b1
5'-most EST
Method
                   BLASTX
                   g2827549
NCBI GI
BLAST score
                   691
                   7.0e-73
E value
Match length
                   146
                   89
% identity
                   (AL021635) glycoprotein endopeptidase - like protein
NCBI Description
```

[Arabidopsis thaliana]

```
32533
Seq. No.
                   291410 1.R1040
Contig ID
                   fjg700968435.hl
5'-most EST
                   32534
Seq. No.
                   291488 1.R1040
Contig ID
                   asn701142644.hl
5'-most EST
                   32535
Seq. No.
Contig ID
                   291513 1.R1040
5'-most EST
                   kwa701015563.hl
                   32536
Seq. No.
                   291556 1.R1040
Contig ID
5'-most EST
                   kwa701015625.hl
                   BLASTN
Method
                   q510875
NCBI GI
BLAST score
                   100
E value
                   4.0e-49
                   209
Match length
                   94
% identity
NCBI Description
                   P.vulgaris PvME1 gene
                   32537
Seq. No.
                   291569 1.R1040
Contig ID
5'-most EST
                   fC-gms\overline{t}700893503d3
                   32538
Seq. No.
                   291651 1.R1040
Contig ID
                   zsg701\overline{1}17506.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3220021
                   98
BLAST score
                   2.0e-10
E value
                   85
Match length
                   41
% identity
                   (U57828) lipase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32539
                   291661 1.R1040
Contig ID
5'-most EST
                   uC-gmropic047e09b1
                   32540
Seq. No.
                   291667 1.R1040
Contig ID
5'-most EST
                   zsg701117441.h1
Method
                   BLASTX
                   g2984333
NCBI GI
                   193
BLAST score
E value
                   1.0e-14
                   58
Match length
% identity
                   (AE000774) Na(+) dependent transporter (Sbf family)
NCBI Description
                   [Aquifex aeolicus]
                   32541
Seq. No.
```

291833_1.R1040

Contig ID

```
jC-gmro02910022b05a1
5'-most EST
                   BLASTX
Method
                   a586021
NCBI GI
BLAST score
                   134
                   1.0e-09
E value
Match length
                   64
                   55
% identity
                   PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION
NCBI Description
                   PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation
                   protein - Bacillus subtilis >gi_467442_dbj_BAA05288_
                   (D26185) stage V sporulation [Bacillus subtilis]
                   >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant
                   blocks spore coat formation (stage V sporulation) [Bacillus
                   subtilis]
Seq. No.
                   32542
                   291866 1.R1040
Contig ID
5'-most EST
                   zsq701\overline{1}25639.h1
Method
                   BLASTX
NCBI GI
                   g1055161
BLAST score
                   159
                   1.0e-10
E value
Match length
                   134
% identity
NCBI Description
                   (U40029) similar to human 100 kDa coactivator (U22055)
                   [Caenorhabditis elegans]
Seq. No.
                   32543
                   291952 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy030a06b1
                   32544
Seq. No.
                   292089 1.R1040
Contig ID
5'-most EST
                   g4396380
                   32545
Seq. No.
Contig ID
                   292298 1.R1040
                   zsg701118524.h1
5'-most EST
Method
                   BLASTX
                   g2959781
NCBI GI
BLAST score
                   490
                   9.0e-60
E value
Match length
                   159
% identity
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   32546
Seq. No.
Contig ID
                   292303 1.R1040
5'-most EST
                   zsg701126941.hl
Method
                   BLASTX
NCBI GI
                   q3152559
BLAST score
                   504
E value
                   3.0e-51
Match length
                   127
                   70
% identity
NCBI Description
                   (AC002986) Similarity to A. thaliana gene product
```

F21M12.20, gb AC000132. EST gb Z25651 comes from this gene.

[Arabidopsis thaliana] Seq. No. 32547 Contig ID 292433_1.R1040 5'-most EST zsg701118711.h1

Seq. No. 32548

Contig ID 292454 1.R1040 5'-most EST zsg701118744.h1

Seq. No. 32549

Contig ID 292499_1.R1040 5'-most EST zsg701118805.h1

Method BLASTX
NCBI GI g2384671
BLAST score 664
E value 8.0e-70
Match length 166
% identity 77

NCBI Description (AF012657) putative potassium transporter AtKT2p

[Arabidopsis thaliana]

Seq. No. 32550

Contig ID 292509 1.R1040 5'-most EST zsg701118818.h1

Method BLASTX
NCBI GI g1777312
BLAST score 393
E value 4.0e-38
Match length 100
% identity 75

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 32551

Contig ID 292534_1.R1040 5'-most EST asn701135674.h1

Seq. No. 32552

Contig ID 292677 1.R1040 5'-most EST zsg701119045.h1

Method BLASTN
NCBI GI g3702736
BLAST score 34
E value 2.0e-09
Match length 42
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRI1, complete sequence [Arabidopsis thaliana]

Seq. No. 32553

Contig ID 292690_1.R1040

5'-most EST uC-gmflminsoy064g10b1

Seq. No. 32554

Contig ID 292737_1.R1040 5'-most EST zsg701119132.h1

Contig ID

```
Method
                   BLASTX
                   g4337192
NCBI GI
BLAST score
                   273
                   8.0e-24
E value
Match length
                   54
                   89
% identity
                   (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32555
Seq. No.
                   292857 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}19308.h1
                   32556
Seq. No.
                   292873 1.R1040
Contig ID
                   zsg701\overline{1}19326.h1
5'-most EST
                   BLASTX
Method
                   g2244755
NCBI GI
BLAST score
                   354
                   6.0e-34
E value
                   89
Match length
                   70
% identity
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   32557
Seq. No.
                   292889 1.R1040
Contig ID
5'-most EST
                   zsg701119350.hl
Method
                   BLASTX
                   g2191139
NCBI GI
BLAST score
                   143
                   9.0e-09
E value
                   52
Match length
                   50
% identity
                   (AF007269) A IG002N01.19 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   32558
Seq. No.
                   293078 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810072a02a1
                   BLASTX
Method
                   g4038592
NCBI GI
                   555
BLAST score
                   8.0e-57
E value
Match length
                   162
% identity
                   (Y10403) RNA-directed RNA polymerase [Lycopersicon
NCBI Description
                   esculentum]
                   32559
Seq. No.
                   293232 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy031f07b1
Seq. No.
                   32560
                   293252 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910070b07a1
                   32561
Seq. No.
                   293291 1.R1040
```

```
zsg701119966.hl
5'-most EST
                  BLASTX
Method
                  q544075
NCBI GI
BLAST score
                  542
                  1.0e-55
E value
                  148
Match length
% identity
                   68
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                   (P102) >gi_486768_pir__S35312 coatomer complex chain beta'
                   - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
                   [Bos taurus]
                   32562
Seq. No.
                   293335 1.R1040
Contig ID
                   zsg701\overline{1}20037.h1
5'-most EST
Method
                   BLASTX
                   q1171429
NCBI GI
BLAST score
                   668
                   2.0e-70
E value
                   138
Match length
                   57
% identity
                   (U44028) CKC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32563
                   293394 1.R1040
Contig ID
                   g5057754
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2959324
BLAST score
                   245
                   1.0e-20
E value
Match length
                   61
% identity
                   (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   32564
Seq. No.
                   293453 1.R1040
Contig ID
                   zsg701120212.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3176723
BLAST score
                   188
                   6.0e-17
E value
Match length
                   104
                   46
% identity
                   (AC002392) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   32565
Seq. No.
                   293526 1.R1040
Contig ID
                   jC-gmst02400055h08a1
5'-most EST
                   32566
Seq. No.
                   293613 1.R1040
Contig ID
                   jC-gmst02400058h07a1
5'-most EST
                   32567
Seq. No.
                   293725 1.R1040
Contig ID
```

zsq701126009.hl

5'-most EST

BLAST score

235

```
Seq. No.
                   32568
Contig ID
                   293779 1.R1040
5'-most EST
                   zsg701120654.h1
                   BLASTX
Method
                   g1663537
NCBI GI
                   240
BLAST score
                   4.0e-20
E value
Match length
                   151
% identity
                   39
                   (U55803) disease resistance protein homolog [Glycine max]
NCBI Description
                   32569
Seq. No.
                   293817 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220103h08a1
Method
                   BLASTX
                   g1077569
NCBI GI
BLAST score
                   346
                   1.0e-32
E value
                   164
Match length
                   41
% identity
                   probable membrane protein YDR109c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi 747884 emb CAA88663 (Z48758) unknown
                   [Saccharomyces cerevisiae]
                   32570
Seq. No.
                   293829 1.R1040
Contig ID
5'-most EST
                   zsg701120720.hl
Method
                   BLASTX
NCBI GI
                   g2960364
BLAST score
                   330
E value
                   9.0e-31
Match length
                   127
% identity
                   46
NCBI Description
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
Seq. No.
                   32571
                   293899 1.R1040
Contig ID
5'-most EST
                   zsg701122101.h1
Method
                   BLASTX
NCBI GI
                   g2735017
BLAST score
                   290
E value
                   2.0e-26
Match length
                   97
% identity
                   58
NCBI Description
                   (U82481) KI domain interacting kinase 1 [Zea mays]
Seq. No.
                   32572
Contig ID
                   293959 1.R1040
5'-most EST
                   zsg701129661.h1
Seq. No.
                   32573
Contig ID
                   293970 1.R1040
5'-most EST
                   asn701140095.hl
Method
                   BLASTX
NCBI GI
                   q4493908
```

Match length

% identity

79

```
E value
                   6.0e-20
                   87
Match length
                   45
% identity
                   (AL034558) predicted using hexExon; MAL3P2.30 (PFC0305w),
NCBI Description
                   Putative homologue of Human EB1, len: 511 aa; Similarity to
                   Human EB1 protein. H.sapiens EB1 protein (TR:Q156910) BLAST
                   Score: 325, sum P(2) = 6.2e-35; 46% identity in
                   32574
Seq. No.
Contig ID
                   294089 1.R1040
5'-most EST
                   zsg701121057.hl
                   32575
Seq. No.
                   294097 1.R1040
Contig ID
5'-most EST
                   zsg701121068.hl
Method
                   BLASTN
NCBI GI
                   q3046856
                   45
BLAST score
                   3.0e-16
E value
Match length
                   164
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXI22, complete sequence [Arabidopsis thaliana]
                   32576
Seq. No.
                   294135 1.R1040
Contig ID
                                      20 1/2
                   zsg701\overline{1}21119.h1
5'-most EST
Seq. No.
                   32577
                   294144 1.R1040
Contig ID
                   uC-gmflminsoy098b03b1
5'-most EST
                   32578
Seq. No.
Contig ID
                   294184 1.R1040
5'-most EST
                   g4437061
Method
                   BLASTX
                   g2497539
NCBI GI
BLAST score
                   336
E value
                   3.0e-31
Match length
                   120
% identity
                   56
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703
NCBI Description
                   (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                   32579
                   294184 2.R1040
Contig ID
                   jC-gmle01810031e07d1
5'-most EST
                   32580
Seq. No.
Contig ID
                   294246 1.R1040
                   zsg701\overline{1}30122.h1
5'-most EST
Method
                   BLASTX
                   g3927831
NCBI GI
                   391
BLAST score
                   3.0e-38
E value
                   96
```

```
NCBI Description
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                   thaliana]
                   32581
Seq. No.
                   294291 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy089a05b1
Seq. No.
                   294292 1.R1040
Contig ID
5'-most EST
                   jC-gmf\(\bar{1}\)02220090c08d1
                   32583
Seq. No.
Contig ID
                   294295 1.R1040
5'-most EST
                   zsq701121395.h1
Method
                   BLASTX
NCBI GI
                   q3033399
BLAST score
                   144
                   3.0e-09
E value
Match length
                   56
% identity
                   52
NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]
                   32584
Seq. No.
                   294333 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy275f03b1
Method
                   BLASTN
                   q886099
NCBI GI
BLAST score
                   36
E value
                   9.0e-11
Match length
                   67
                   97
% identity
NCBI Description
                  Glycine max putative water channel protein (Pip1) mRNA,
                   complete cds
                   32585
Seq. No.
                   294406 2.R1040
Contig ID
5'-most EST
                   zsg701121561.hl
Method
                   BLASTN
                  g22073
NCBI GI
BLAST score
                   54
E value
                   1.0e-21
Match length
                   58
% identity
                   98
NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region
                   32586
Seq. No.
                   294438 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy120e03b1
Method
                   BLASTX
NCBI GI
                   q3289002
BLAST score
                   166
E value
                   6.0e-12
Match length
                   89
% identity
                   23
                  (AF073522) CRP1 [Zea mays]
NCBI Description
```

32587

Seq. No.

5'-most EST

```
Contig ID
                   294475 1.R1040
5'-most EST
                   jC-gmle01810075g03a1
Seq. No.
                   294632 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy175g11b1
Method
                   BLASTX
NCBI GI
                   g2062169
BLAST score
                   438
                   1.0e-43
E value
Match length
                   107
                   53
% identity
                   (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   32589
Seq. No.
                   294645 1.R1040
Contig ID
5'-most EST
                   zsq701122111.h1
                   32590
Seq. No.
                   294753_1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}22347.h1
Method
                   BLASTX
NCBI GI
                   g4415924
BLAST score
                   316
E value
                   2.0e-29
Match length
                   95
                   60
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   32591
Seq. No.
Contig ID
                   294755 1.R1040
5'-most EST
                   zsg701122354.hl
Seq. No.
                   32592
Contig ID
                   294820 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220084h03a1
                   32593
Seq. No.
                   294859 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}22569.h1
                   32594
Seq. No.
                   294893 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy031g12b1
Method
                   BLASTN
NCBI GI
                   g169048
BLAST score
                   226
E value
                   1.0e-124
Match length
                   378
                   90
% identity
NCBI Description Pea farnesyltransferase beta-subunit mRNA, complete cds
                   32595
Seq. No.
                   295073 1.R1040
Contig ID
```

zsg701122936.hl

, <u>}</u>

Method.

```
32596
Seq. No.
                  295099 1.R1040
Contig ID .
5'-most EST
                  uC-gmflminsoy002b02b1
Method
                  BLASTX
                  g3335349
NCBI GI
BLAST score
                  413
E value
                  2.0e-40
Match length
                  117
% identity
                   (AC004512) Similar to gb_U46691 putative chromatin
NCBI Description
                  structure regulator (SUPT6H) from Homo sapiens. ESTs
                  gb T42908, gb_AA586170 and gb_AA395125 come from this gene.
                  [Arabidopsis thaliana]
                  32597
Seq. No.
                  295114 1.R1040
Contig ID
5'-most EST
                  zsg701122991.h1
                  BLASTX
Method
NCBI GI
                  g3063458
BLAST score
                  339
                  1.0e-31
E value
Match length
                  132
                  51
% identity
                  (AC003981) F22013.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  32598
                  295156 1.R1040
Contig ID
                  jC-gmst02400071e12a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4314365
BLAST score
                  331
E value
                  1.0e-30
Match length
                  207
                  43
% identity
                   (AC006340) putative copia-like retrotransposon Hopscotch
NCBI Description
                   [Arabidopsis thaliana]
                  32599
Seq. No.
                  295212 1.R1040
Contig ID
                  zsg701123250.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4544407
BLAST score
                  271
E value
                  3.0e-24
                  73
Match length
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  32600
Seq. No.
                  295220 1.R1040
Contig ID
                  zsg701123155.hl
5'-most EST
                  32601
Seq. No.
                  295235 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy320d06b1
```

BLASTX

NCBI Description

```
q3549626
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
Match length
                   108
% identity
                   41
                   (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
                   32602
Seq. No.
Contig ID
                   295278_1.R1040
5'-most EST
                   zsg701123256.hl
                   BLASTX
Method
NCBI GI
                   g2583120
BLAST score
                   153
                   1.0e-09
E value
                   170
Match length
                   15
% identity
                   (AC002387) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   32603
Seq. No.
Contig ID
                   295335 1.R1040
                   asn701140185.hl
5'-most EST
                   32604
Seq. No.
                   295367 1.R1040
Contig ID
5'-most EST
                   zsg701123470.h1
Seq. No.
                   32605
                   295386 1.R1040
Contig ID
                   zsg701\overline{1}23392.h1
5'-most EST
                   32606
Seq. No.
Contig ID
                   295405 1.R1040
                   zsq701\overline{1}23417.h1
5'-most EST
                   32607
Seq. No.
                   295413 1.R1040
Contig ID
                   jC-gms\(\overline{t}\)02400039a12a1
5'-most EST
Method
                   BLASTX
                   g3107903
NCBI GI
BLAST score
                   257
                   5.0e-22
E value
Match length
                   65
% identity
                   (D83719) polycomb-like protein [Daucus carota]
NCBI Description
                   32608
Seq. No.
                   295471 1.R1040
Contig ID
                   uC-gmropic021b08b1
5'-most EST
Method
                   BLASTX
                   q3980384
NCBI GI
BLAST score
                   259
E value
                   3.0e-22
Match length
                   124
                   42
% identity
                   (AC004561) hypothetical protein [Arabidopsis thaliana]
```

```
32609
Seq. No.
                   295614 1.R1040
Contig ID
5'-most EST
                   zsq701123679.h1
Seq. No.
                   32610
                   295641 1.R1040
Contig ID
5'-most EST
                   zsq701123866.hl
Seq. No.
                   32611
                   295713 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400065h01d1
Method
                   BLASTX
NCBI GI
                   q1055162
BLAST score
                   194
E value
                   8.0e-15
Match length
                   130
% identity
                   38
NCBI Description
                   (U40029) coded for by C. elegans cDNA yk16b1.3; coded for
                   by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA
                   yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by
                   C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA
                   yk7e12.5; co
Seq. No.
                   32612
Contig ID
                   295725 1.R1040
5'-most EST
                   zsq701123841.h1
Seq. No.
                   32613
                   295776 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}23912.h1
Seq. No.
                   32614
                   295821_1.R1040
Contig ID
5'-most EST
                   asn701142424.hl
Method
                   BLASTX
NCBI GI
                   q4191786
BLAST score
                   225
E value
                   2.0e-18
Match length
                   52
% identity
NCBI Description
                   (AC005917) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32615
                   295846 1.R1040
Contig ID
5'-most EST
                   zsg701124006.hl
Seq. No.
                   32616
                   295873 1.R1040
Contig ID
5'-most EST
                   zsg701124036.hl
Seq. No.
                   32617
Contig ID
                   295891 1.R1040
5'-most EST
                   jC-qmle01810044a06a1
Method
                   BLASTX
NCBI GI
                   q4263778
BLAST score
                   342
E value
                   4.0e-32
```

NCBI GI

```
92
Match length
                    66.
% identity
                    (AC006068) putative serine carboxypeptidase II [Arabidopsis
NCBI Description
                    thalianal
                    32618
Seq. No.
                    295909 1.R1040
Contig ID
5'-most EST
                    zsg701\overline{1}24081.h1
                    32619
Seq. No.
Contig ID
                    295913 1.R1040
                   uC-gmflminsoy044c03b1
5'-most EST
Seq. No.
                    32620
Contig ID
                    295978 1.R1040
                    jC-gmro02800028f06a1
5'-most EST
                    32621
Seq. No.
                    296187 1.R1040
Contig ID
5'-most EST
                   g5606708
Seq. No.
                   32622
                    296282_1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400074g01a1
                    32623
Seq. No.
                    296308 1.R1040
Contig ID
5'-most EST
                    zsg701\overline{1}24740.h1
                    32624
Seq. No.
                   296345 1.R1040
Contig ID
5'-most EST
                   uC-gmropic104e02b1
Method
                   BLASTX
NCBI GI
                    g1553133
BLAST score
                    234
E value
                    3.0e-19
Match length
                   161
% identity
                    19
                    (U64722) actin-fragmin kinase [Physarum polycephalum]
NCBI Description
                    32625
Seq. No.
Contig ID
                    296424 1.R1040
5'-most EST
                    zsq701\overline{1}27390.h1
Method
                   BLASTX
                   g2194117
NCBI GI
BLAST score
                    301
E value
                    1.0e-27
Match length
                    99
                    60
% identity
                    (AC002062) Strong similarity to Arabidopsis receptor
NCBI Description
                   protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]
Seq. No.
                    32626
                   296435 1.R1040
Contig ID
                   g4307200
5'-most EST
Method
                   BLASTX
```

g1171429

```
BLAST score
                   477
E value
                   6.0e-48
Match length
                   147
% identity
                   47
                   (U44028) CKC [Arabidopsis thaliana]
NCBI Description
                   32627
Seq. No.
                   296489 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}25024.h1
                   32628
Seq. No.
                   296554 1.R1040
Contig ID
5'-most EST
                   uC-gmropic096g05b1
                   32629
Seq. No.
                   296671_1.R1040
Contig ID
5'-most EST
                   zsg701125390.h1
Method
                   BLASTX
NCBI GI
                   g2213600
BLAST score
                   213
E value
                   5.0e-17
Match length
                   117
                   43
% identity
                   (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32630
                   296679 1.R1040
Contig ID
5'-most EST
                   943972\overline{18}
                   32631
Seq. No.
                   296872 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy100b07b1
Method
                   BLASTX
NCBI GI
                   g3892709
BLAST score
                   235
                   1.0e-19
E value
Match length
                   114
% identity
                   (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   32632
Seq. No.
                   296904 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220143c12a1
Method
                   BLASTX
NCBI GI
                   g2811226
BLAST score
                   497
                   3.0e-50
E value
Match length
                   142
                   69
% identity
NCBI Description
                   (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
                   32633
Seq. No.
                   296914 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}33289.h1
```

32634

Seq. No.

```
297000 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy079g06b1
Seq. No.
                   32635
                   297192 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810030h05a2
                   32636
Seq. No.
Contig ID
                   297261 1.R1040
5'-most EST
                   zsg701126236.hl
                   32637
Seq. No.
                   297333 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy256d12b1
Method
                   BLASTX
                   g4204302
NCBI GI
BLAST score
                   143
E value
                   7.0e-09
                            . . .
Match length
                   41
                   66
% identity
NCBI Description
                   (AC003027) Hypothetical protein [Arabidopsis thaliana]
                   32638
Seq. No.
                   297447 1.R1040
Contig ID
5'-most EST
                   uC-gmropic012f02b1
Seq. No.
                   32639
                   297574_1.R1040
Contig ID
5'-most EST
                   jC-gmf102220051a08a1
Method
                   BLASTX
                   g4001805
NCBI GI
BLAST score
                   130
E value
                   8.0e-12
Match length
                   122
                   36
% identity
NCBI Description
                   (AF041476) BAF53a [Mus musculus]
Seq. No.
                   32640
Contig ID
                   297593 1.R1040
5'-most EST
                   fC-gmro700561647w1
Method
                   BLASTX
NCBI GI
                   g4510406
BLAST score
                   373
E value
                   2.0e-35
Match length
                   110
% identity
NCBI Description
                   (AC006587) putative protein kinase [Arabidopsis thaliana]
                   32641
Seq. No.
                   297594 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810090d01a1
Method
                   BLASTX
                   g3157943
NCBI GI
BLAST score
                   141
                   1.0e-14
E value
Match length
                   98
```

50

% identity

```
(AC002131) Contains similarity to BAP31 protein gb X81816
NCBI Description
                   from Mus musculus. [Arabidopsis thaliana]
Seq. No.
                   32642
                   297722 1.R1040
Contig ID
                   zsq701\overline{1}27004.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2341032
BLAST score
                   305
                   4.0e-28
E value
Match length
                   92
% identity
                   65
                   (AC000104) EST gb ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   32643
                   297777 1.R1040
Contig ID
5'-most EST
                   uC-gmropic111d05b1
                   32644
Seq. No.
                   297877_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy241e08b1
                   32645
Seq. No.
Contig ID
                   297936 1.R1040
5'-most EST
                   zsg701127433.h1
                   32646
Seq. No.
                   298080 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy018e06b1
Method
                   BLASTX
                   g3885342
NCBI GI
                   398
BLAST score
E value
                   1.0e-38
Match length
                   105
% identity
                   (ACO05623) putative DNA polymerase [Arabidopsis thaliana]
NCBI Description
                   32647
Seq. No.
Contig ID
                   298227 1.R1040
5'-most EST
                   uC-gmrominsoy199e07b1
Method
                   BLASTX
NCBI GI
                   q1663648
BLAST score
                   300
E value
                   3.0e-27
Match length
                   151
% identity
                   46
NCBI Description
                   (U75321) chromaffin granule ATPase II homolog [Mus
                  musculus]
                   32648
Seq. No.
                   298291 1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}29887.h1
                   32649
Seq. No.
```

298312 1.R1040

uC-gmropic101d09b1

Contig ID 5'-most EST

```
32650
Seq. No.
Contig ID
                    298361 1.R1040
5'-most EST
                    zsg701127922.hl
                    32651
Seq. No.
                    298637 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy115b09b1
                    32652
Seq. No.
                    298705 1.R1040
Contig ID
5'-most EST
                    zsg701128652.hl
                   BLASTX
Method
NCBI GI
                    a3176726
BLAST score
                    361
                    9.0e-35
E value
                    91
Match length
                    75
% identity
NCBI Description
                    (AC002392) putative serine proteinase [Arabidopsis
                    thaliana]
                   32653
Seq. No.
                   298721_1.R1040
Contig ID
                   asn701\overline{1}34467.h1
5'-most EST
Method
                   BLASTX
                   g3080450
NCBI GI
BLAST score
                   185
E value
                    4.0e-14
                   79
Match length
                    49
% identity
                    (AL022605) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    32654
Seq. No.
                   298826_1.R1040
Contig ID
5'-most EST
                   zsg701\overline{1}29278.h1
                   BLASTN
Method
NCBI GI
                   g35589
BLAST score
                   272
                   1.0e-151
E value
Match length
                   272
                   100
% identity
                   Human pancreatic polypeptide (PP) and icosapeptide precursor
NCBI Description
                   >gi 4506032 ref NM 002722.1 PPY Homo sapiens pancreatic
                   polypeptide (PPY) mRNA
                   32655
Seq. No.
Contig ID
                   298841_1.R1040
5'-most EST
                   zsg701\overline{1}29285.h1
Method
                   BLASTN
NCBI GI
                   q177828
                   293
BLAST score
                   1.0e-164
E value
Match length
                   293
% identity
                   100
                   Human alpha-1-antitrypsin mRNA, complete cds
NCBI Description
```

32656

Seq. No.

```
298844 1.R1040
Contig ID
5'-most EST
                   zsq701128941.h1
Method
                   BLASTN
                                                 1. July -
NCBI GI
                   g32417
BLAST score
                   238
E value
                   1.0e-131
Match length
                   477
% identity
                   66
NCBI Description
                   Human Hp2 gene fragment for haptoglobin alpha- and
                   beta-chain
                   32657
Seq. No.
                   298852 1.R1040
Contiq ID
5'-most EST
                   zsg701129141.hl
Method
                   BLASTN
NCBI GI
                   g182429
BLAST score
                   614
E value
                   0.0e + 00
Match length
                   622
% identity
                   100
NCBI Description
                   Human fibrinogen beta-chain mRNA, partial cds
Seq. No.
                   32658
Contig ID
                   298859 1.R1040
5'-most EST
                   zsg701128965.hl
Method
                   BLASTN
                   q183269
NCBI GI
BLAST score
                   424
E value
                   0.0e + 00
Match length
                   460
% identity
                   98
NCBI Description
                   Human glucagon mRNA, complete cds.
                   >gi_4503944_ref_NM_002054.1_GCG_ Homo sapiens glucagon
                   (GCG) mRNA
Seq. No.
                   32659
Contig ID
                   298861_1.R1040
5'-most EST
                   zsg701128967.h1
Method
                   BLASTN
NCBI GI
                   q183269
BLAST score
                   231
E value
                   1.0e-127
Match length
                   235
% identity
                   100
NCBI Description
                   Human glucagon mRNA, complete cds.
                   >gi_4503944_ref_NM_002054.1_GCG_ Homo sapiens glucagon
                   (GCG) mRNA
Seq. No.
                   32660
                   298865 1.R1040
Contig ID
                   zsg701\overline{1}28973.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q189583
BLAST score
                   269
E value
                   1.0e-150
Match length
                   281
```

99

% identity

Method

NCBI GI

BLASTN

g34753

```
NCBI Description Human prealbumin mRNA, complete cds
Seq. No.
                   32661
                   298891 1.R1040
Contig ID
                   zsg701129086.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g28589
BLAST score
                   229
E value
                   1.0e-126
                   252
Match length
                   98
% identity
                  Human messenger RNA for serum albumin (HSA)
NCBI Description
Seq. No.
                   298896 1.R1040
Contig ID
5'-most EST
                   zsg701129017.hl
Seq. No.
                   32663
                   298925 1.R1040
Contig ID
5'-most EST
                   zsq701129119.hl
Method
                   BLASTN
NCBI GI
                   q1490418
BLAST score
                   272
E value
                   1.0e-152
Match length
                   284
% identity
                   33
NCBI Description
                  Human ubiquitin gene, complete cds
Seq. No.
                   32664
                   298944_1.R1040
Contig ID
5'-most EST
                   zsg701129095.hl
Method
                   BLASTN
NCBI GI
                   q24444
BLAST score
                   281
E value
                   1.0e-157
Match length
                   285
% identity
                   100
NCBI Description
                  Human mRNA for alphal-acid glycoprotein (orosomucoid)
                   32665
Seq. No.
Contig ID
                   298950 1.R1040
5'-most EST
                   zsq701129107.h1
Method
                  BLASTN
NCBI GI
                   g288104
BLAST score
                   298
E value
                   1.0e-167
Match length
                   302
% identity
                   100
NCBI Description
                  H.sapiens mRNA for 4-hydroxyphenylpyruvate dioxygenase
                   >gi 4504476 ref NM 002150.1 HPD Homo sapiens
                   4-hydroxyphenylpyruvate dioxygenase (HPD) mRNA
Seq. No.
                   32666
                   298958 1.R1040
Contig ID
5'-most EST
                   zsg701129116.hl
```

Contig ID

```
BLAST score
                   276
 E value
                   1.0e-154
Match length
                   280
 % identity
                   100
NCBI Description
                   Human MRL3 mRNA for ribosomal protein L3 homologue ( MRL3 =
                   mammalian ribosome L3 )
Seq. No.
                   32667
Contig ID
                   298963 1.R1040
5'-most EST
                   zsg701129122.h1
Seq. No.
                   32668
Contig ID
                   298982 1.R1040
5'-most EST
                   zsg701129148.hl
Method
                   BLASTN
NCBI GI
                   g32429
BLAST score
                   487
E value
                   0.0e + 00
Match length
                   503
% identity
                   99
NCBI Description
                   Human mRNA FOR haptoglobin alpha 1S (Hpa 1S)
Seq. No.
                   32669
Contig ID
                   299015 1.R1040
5'-most EST
                   zsg701129187.h1
Method
                   BLASTN
                                                                          :7
NCBI GI
                   g4503714
BLAST score
                   300
E value
                   1.0e-168
Match length
                   300
% identity
                   100
NCBI Description
                   Homo sapiens fibrinogen, gamma polypeptide (FGG) mRNA
Seq. No.
                   32670
Contig ID
                   299031 1.R1040
5'-most EST
                   zsg701129234.h1
                                                                      . 11
Method
                   BLASTN
NCBI GI
                   g34312
BLAST score
                   288
E value
                   1.0e-161
Match length
                   296
% identity
                   99
NCBI Description Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)
Seq. No.
                   32671
Contig ID
                  299058 1.R1040
5'-most EST
                  zsg701129264.h1
Method
                  BLASTN
NCBI GI
                  g452047
BLAST score
                  189
E value
                  1.0e-102
Match length
                  261
% identity
                  93
NCBI Description Homo sapiens HnRNP F protein mRNA, complete cds
Seq. No.
                  32672
```

299172 1.R1040

5'-most EST

```
5'-most EST
                   g5666766
Seq. No.
                   32673
                   299202 1.R1040
Contig ID
5'-most EST
                   zsg701129448.h1
Method
                   BLASTX
NCBI GI
                   g3036819
BLAST score
                   518
E value
                   1.0e-52
Match length
                   143
% identity
                   72
NCBI Description
                   (AJ000058) MCM3 homolog [Arabidopsis thaliana]
Seq. No.
                   32674
Contig ID
                   299220 1.R1040
                   jC-gmro02910066a05a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4056489
BLAST score
                   144
E value
                   8.0e-09
Match length
                   104
% identity
                   36
NCBI Description
                   (AC005896) putative white protein [Arabidopsis thaliana]
Seq. No.
                   32675
                   299233 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy119a01b1
Method
                   BLASTX
NCBI GI
                   g2979554
BLAST score
                   381
E value
                   7.0e-37
Match length
                   115
% identity
                   61
                   (AC003680) CDC4 like protein [Arabidopsis thaliana]
NCBI Description
                   32676
Seq. No.
Contig ID
                   299340 1.R1040
5'-most EST
                   uC-gmflminsoy028b04b1
Seq. No.
                   32677
                   299404 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy179b12b1
                   BLASTX
Method
                   g2827635
NCBI GI
BLAST score
                   775
E value
                   1.0e-82
Match length
                   199
% identity
                   75
NCBI Description
                   (AL021636) predicted protein [Arabidopsis thaliana]
                   32678
Seq. No.
                   299425 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy047f11b1
                   32679
Seq. No.
                   299453 1.R1040
Contig ID
```

zsg701129776.hl

*...

```
32680
Seq. No.
                    299497 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy008e06b1
Seq. No.
                    299503 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy070c08b1
Seq. No.
                    299510 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910059h07a1
Seq. No.
                    299526 1.R1040
Contig ID
5'-most EST
                    q55098\overline{5}2
                    32684
Seq. No.
Contig ID
                    299542 1.R1040
5'-most EST
                    g56062<del>6</del>7
Method
                    BLASTX
NCBI GI
                    q2853087
BLAST score
                    327
E value
                    3.0e-30
Match length
                    95
% identity
NCBI Description
                    (AL021768) putative protein [Arabidopsis thaliana]
                    32685
Seq. No.
                    299573 1.R1040
Contig ID
5'-most EST
                    q5677178
                    BLASTX
Method
NCBI GI
                    q4204281
BLAST score
                    203
E value
                    1.0e-15
Match length
                   99
% identity
                    38
NCBI Description
                    (AC004146) Hypothetical protein [Arabidopsis thaliana]
                    32686
Seq. No.
Contig ID
                    299740 1.R1040
5'-most EST
                    zsq701\overline{1}30174.h1
                    32687
Seq. No.
                    299806 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy138c10b1
Seq. No.
                    32688
                   299932 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}31393.h1
Method
                   BLASTX
NCBI GI
                   a3201541
BLAST score
                   312
E value
                   1.0e-28
Match length
                   128
% identity
NCBI Description
                    (AJ005077) TCTR2 protein [Lycopersicon esculentum]
```

```
32689
Seq. No.
                   299992 1.R1040
Contig ID
                   asn701130596.hl
5'-most EST
Method
                   BLASTX
                   q3005931
NCBI GI
BLAST score
                   187
E value
                   2.0e-14
Match length
                   68
% identity
                   53
                   (AJ005016) ABC transporter [Homo sapiens]
NCBI Description
                   32690
Seq. No.
                   300357 1.R1040
Contig ID
5'-most EST
                   asn701133603.h2
                   32691
Seq. No.
                   300814 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy238b11b1
Method
                   BLASTX
NCBI GI
                   q1771381
BLAST score
                   155
E value
                   2.0e-10
Match length
                   81
                   42
% identity
                   (X95877) phosphoinositide-specific phospholipase C
NCBI Description
                   [Nicotiana rustica]
Seq. No.
                   32692
Contig ID
                   300869 1.R1040
5'-most EST
                   jC-gmst02400071c02a1
Method
                   BLASTX
NCBI GI
                   q1785851
BLAST score
                   152
E value
                   8.0e-10
Match length
                   83
% identity
                   36
NCBI Description
                   (D50692) c-myc binding protein [Homo sapiens]
                   >gi 2443310 dbj BAA22408 (AB007191) AMY-1 [Homo sapiens]
Seq. No.
                   32693
Contig ID
                   300980 1.R1040
5'-most EST
                   asn701132877.hl
                   32694
Seq. No.
                   301112 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy022e04b1
Method
                   BLASTX
NCBI GI
                   g1703168
BLAST score
                   219
E value
                   7.0e-18
Match length
                   121
% identity
NCBI Description
                   BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN
                   BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA
                   LARGE CHAIN) (AP105A) >gi_482950_pir_B32105 clathrin-associated protein complex 2, beta chain minor
```

```
component - rat >gi 203113 (M77245) beta'-chain clathrin
                  associated protein complex AP-1 [Rattus norvegicus]
                  32695
Seq. No.
                  301114 1.R1040
Contig ID
5'-most EST
                  asn701133063.h1
Method
                  BLASTX
NCBI GI
                  q542058
BLAST score
                  161
                  3.0e-11
E value
                  52
Match length
                  58
% identity
                  HSR203J protein - common tobacco >gi_444002 emb CAA54393
NCBI Description
                  (X77136) HSR203J [Nicotiana tabacum]
Seq. No.
                  32696
                  301138 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910017g12a1
Method
                  BLASTX
NCBI GI
                  q3242728
BLAST score
                  321
E value
                  1.0e-29
Match length
                  152
% identity
NCBI Description
                  (AC003040) unknown protein [Arabidopsis thaliana]
Seq. No.
                  32697
                  301157 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy080c03b1
Seq. No.
                  32698
                  301243 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910068b05a1
Method
                  BLASTX
NCBI GI
                  q3860008
BLAST score
                  361
E value
                  3.0e-34
Match length
                  152
% identity
                  47
NCBI Description
                  (AF091085) unknown [Homo sapiens]
Seq. No.
                  32699
Contig ID
                  301343 1.R1040
                  asn701133624.h2
5'-most EST
                  32700
Seq. No.
```

```
Contig ID
                  301346 1.R1040
5'-most EST
                  asn701141925.hl
Method
                  BLASTX
NCBI GI
                  q2739168
BLAST score
                  260
E value
                  1.0e-22
Match length
                  119
% identity
NCBI Description
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
```

tabacum]

NCBI Description

```
32701
Seq. No.
                   301475 1.R1040
Contig ID
                   asn701134307.hl
5'-most EST
                   32702
Seq. No.
                   301478 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}33646.h2
Method
                   BLASTN
                   g1675195
NCBI GI
BLAST score
                   102
                   3.0e-50
E value
                   240
Match length
                   86
% identity
                   Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   32703
Seq. No.
                   301559 1.R1040
Contig ID
                   asn701133893.hl
5'-most EST
                   32704
Seq. No.
                   301589 1.R1040
Contig ID
                   asn701134088.hl
5'-most EST
Seq. No.
                   32705
                   301649 1.R1040
Contig ID
                   asn701134301.h1
5'-most EST
                   32706
Seq. No.
                   301683 1.R1040
Contig ID
                   jC-gmf\(\bar{1}\)02220077a05d1
5'-most EST
                   BLASTX
Method
                   g3184282
NCBI GI
BLAST score
                   296
E value
                   8.0e-27
Match length
                   70
% identity
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32707
                   301807 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy075h04b1
                   32708
Seq. No.
                   301842 1.R1040
Contig ID
5'-most EST
                   asn701134632.h2
                   32709
Seq. No.
                   301863 1.R1040
Contig ID
                   asn701134657.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2979562
BLAST score
                   339
                   1.0e-31
E value
                   124
Match length
% identity
                   (AC003680) unknown protein [Arabidopsis thaliana]
```

Contig ID

```
thaliana]
                   32710
Seq. No.
                   302092 1.R1040
Contig ID
5'-most EST
                   asn701135586.h1
Seq. No.
                   32711
                   302099 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}35090.h1
Seq. No.
                   32712
                   302312 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810059c05a1
Method
                   BLASTX
NCBI GI
                   g3335378
BLAST score
                   459
E value
                   8.0e-46
Match length
                   139
% identity
                   69
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
                   32713
Seq. No.
                   302548 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910074b09a1
Method
                   BLASTX
NCBI GI
                   q2134102
BLAST score
                   506
E value
                   3.0e-51
                   193
Match length
% identity
                   60
NCBI Description
                   kinesin-like protein 1 - African clawed frog
                   >gi 562793 emb CAA57539 (X82012) kinesin-like protein 1
                   [Xenopus laevis]
                   32714
Seq. No.
                   302584 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910012c04a1
Seq. No.
                   32715
                   302605 1.R1040
Contig ID
                   asn701136918.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2618698
BLAST score
                   301
E value
                   1.0e-27
Match length
                   91
% identity
NCBI Description
                   (AC002510) unknown protein [Arabidopsis thaliana]
                   32716
Seq. No.
                   302655 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy074b12b1
Seq. No.
                   32717
```

>qi 3386623 (AC004665) unknown protein [Arabidopsis

302702 1.R1040

```
5'-most EST
                   uC-gmrominsoy099h04b1
Method
                   BLASTN
NCBI GI
                   g938299
                   130
BLAST score
E value
                   8.0e-67
                   311
Match length
% identity
                   85
NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)
                   32718
Seq. No.
                   302746 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}36609.h1
Method
                   BLASTX
NCBI GI
                   g2245065
BLAST score
                   232
E value
                   1.0e-19
Match length
                   64
                   23
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                   32719
Seq. No.
                   302890 1.R1040
Contig ID
5'-most EST
                   q5126428
Seq. No.
                   32720
                   302893 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910010h07a1
                   32721
Seq. No.
                   302931 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810035a08a2
Method
                   BLASTX
NCBI GI
                   g2529707
BLAST score
                   276
E value
                   3.0e-32
Match length
                   158 ·
% identity
                   48
NCBI Description
                   (AF001434) Hpast [Homo sapiens]
Seq. No.
                   32722
                   302992 1.R1040
Contig ID
5'-most EST
                   asn701136856.h1
Seq. No.
                   32723
                   303018 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}36911.h1
Seq. No.
                   32724
                   303157 1.R1040
Contig ID
5'-most EST
                   uC-gmropic110e02b1
Method
                   BLASTX
NCBI GI
                   q1363484
BLAST score
                   251
E value
                   1.0e-21
Match length
                   64
% identity
                   75
NCBI Description IAA13 protein - Arabidopsis thaliana >gi 972929 (U18415)
```

```
32725
Seq. No.
                    303183 1.R1040
Contig ID
                    asn701137293.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1480014
BLAST score
                    151
E value
                    4.0e-10
Match length
                    36
% identity
                    89
                    (D78493) putative delta subunit of ATP synthase [Brassica
NCBI Description
Seq. No.
                    32726
                    303196 1.R1040
Contig ID
5'-most EST
                    q42981\overline{5}2
Method
                   BLASTX
NCBI GI
                    q3176709
BLAST score
                    259
                    2.0e-22
E value
Match length
                   130
% identity
                    (AC002392) putative anthranilate
NCBI Description
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                -: thaliana]
                    32727
Seq. No.
                    303210 1.R1040
Contig ID
5'-most EST
                    jC-qmf102220086d12a1
                    32728
Seq. No.
                    303300 1.R1040
Contig ID
                    uC-gmrominsoy028c03b1
5'-most EST
Method
                   BLASTX
                    g114974
NCBI GI
BLAST score
                    382
E value
                    8.0e-37
Match length
                    110
                    66
% identity
NCBI Description
                   NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
                   >gi_67491_pir_GLJY31 beta-glucosidase (EC 3.2.1.21)
                   precursor (clone TRE361) - white clover >gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
                    [Trifolium repens]
Seq. No.
                    32729
Contig ID
                    303343 1.R1040
5'-most EST
                    jC-gmro02910023d09a1
Method
                   BLASTX
NCBI GI
                   q2289003
BLAST score
                   143
E value
                   1.0e-08
Match length
                   46
% identity
                   63
NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis
```

IAA13 [Arabidopsis thaliana] >qi 2459414 (AC002332) auxin

inducible protein, IAA13 [Arabidopsis thaliana]

thaliana]

Seq. No. 32730 303579 1.R1040 Contig ID uC-gmropic024c03b1 5'-most EST 32731 Seq. No. Contig ID 303593 1.R1040 5'-most EST jC-gmle01810091d08a1 Method BLASTX NCBI GI q3252806 BLAST score 305 E value 9.0e-28 Match length 139 % identity 45 (AC004705) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. Contig ID 303869 1.R1040 5'-most EST jC-gmro02910016b06d1 32733 Seq. No. 304041 1.R1040 Contig ID 5'-most EST jC-qmf102220067a12a1 Seq. No. 32734 304136 1.R1040 Contig ID 5'-most EST uC-qmropic024d05b1 Method BLASTX NCBI GI q4263718 BLAST score 670 1.0e-70 E value Match length 154 % identity (AC006223) putative DNA topoisomerase III beta [Arabidopsis NCBI Description thaliana] 32735 Seq. No. 304179 1.R1040 Contig ID jC-gmro02910001c02a1 5'-most EST BLASTX Method g4512665 NCBI GI BLAST score 181 3.0e-13 E value Match length 53 % identity 64 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana] >gi 4544472 gb AAD22379.1 AC006580_11 (AC006580) unknown protein [Arabidopsis thaliana] 32736 Seq. No. 304211 1.R1040 Contiq ID

5'-most EST jC-qmst02400025f08a1

32737 Seq. No.

304306 1.R1040 Contig ID

5'-most EST g4396105

5'-most EST

```
32738
Seq. No.
                   304410 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy229f12b1
Seq. No.
                   32739
                   304594 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810066h11a1
Method
                   BLASTX
NCBI GI
                   g140496
BLAST score
                   157
E value
                   2.0e-10
                   132
Match length
% identity
                   32
NCBI Description
                   HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION
                   >gi_83226_pir__S19457 probable membrane protein YCR044c -
                   yeast (Saccharomyces cerevisiae) >qi 1907186 emb CAA42292
                   (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]
Seq. No.
                   32740
                   304629 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}39693.h1
Method
                   BLASTX
NCBI GI
                   q1929998
BLAST score
                   306
E value
                   1.0e-27
Match length
                   145
% identity
                   (U77463) NADPH-dependent HC-toxin reductase [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   32741
                   304693 1.R1040
Contig ID
                   jC-gmle01810064g04d1
5'-most EST
                   32742
Seq. No.
                   304803 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}40503.h1
                   32743
Seq. No.
                   304927 1.R1040
Contig ID
5'-most EST
                   asn701140133.hl
                   32744
Seq. No.
                   304937 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy120c02b1
Method
                   BLASTX
NCBI GI
                   q4220524
BLAST score
                   272
E value
                   3.0e-24
Match length
                   92
% identity
NCBI Description
                   (AL035356) putative protein [Arabidopsis thaliana]
                   32745
Seq. No.
                   305124 1.R1040
Contig ID
```

 $asn701\overline{1}40533.h1$

```
Method
                   BLASTX
NCBI GI
                   q4262167
BLAST score
                   509
E value
                   1.0e-51
Match length
                   116
% identity
                   83
NCBI Description
                   (AC005275) putative LRR receptor-linked protein kinase
                   [Arabidopsis thaliana]
                   32746
Seq. No.
                   305156 1.R1040
Contig ID
5'-most EST
                   asn701140683.hl
                   32747
Seq. No.
                   305323 1.R1040
Contig ID
                   jC-gmro02910006c08a1
5'-most EST
                   BLASTN
Method
                   g347454
NCBI GI
BLAST score
                   80
E value
                   6.0e-37
                   237
Match length
                   40
% identity
NCBI Description
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
                   end
                   32748
Seq. No.
                   305661 1.R1040
Contig ID
                   asn701\overline{1}41506.h1
5'-most EST
Method
                   BLASTX
                   g4416307
NCBI GI
BLAST score
                   308
                   4.0e-28
E value
                   104
Match length
                   53
% identity
                   (AF105716) hypothetical protein [Zea mays]
NCBI Description
Seq. No.
                   32749
                   305791 1.R1040
Contig ID
5'-most EST
                   q4397239
Method
                   BLASTN
                   g169348
NCBI GI
BLAST score
                   50
E value
                   4.0e-19
Match length
                   212
% identity
                   86
                   P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'
NCBI Description
                   32750
Seq. No.
                   305867_1.R1040
Contig ID
                   asn701\overline{1}41850.h1
5'-most EST
                   32751
Seq. No.
                   305957 1.R1040
Contig ID
                   g4396382
5'-most EST
```

32752 .

Seq. No.

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306078 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400076b03d1
Method
                   BLASTX
NCBI GI
                   g2262159
BLAST score
                   155
E value
                   3.0e-10
Match length
                   46
% identity
NCBI Description
                   (AC002329) predicted protein similar to S.pombe protein
                   C5H10.03 [Arabidopsis thaliana]
Seq. No.
                   32753
                   306142 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400049q11d1
Method
                   BLASTX
NCBI GI
                   g3493367
BLAST score
                   156
E value
                   3.0e-10
Match length
                   44
% identity
                   (AB017159) citrate synthase [Daucus carota]
NCBI Description
Seq. No.
                   32754
Contig ID
                   306384 1.R1040
5'-most EST
                   uC-qmrominsoy053h02b1
Method
                   BLASTX
NCBI GI
                   q4263722
BLAST score
                   364
                   8.0e-35
E value
                   126
Match length
% identity
                   56
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                   32755
Seq. No.
                   306544 1.R1040
Contig ID
5'-most EST
                   asn701\overline{1}42952.h2
Method
                   BLASTX
NCBI GI
                   q1176529
BLAST score
                   327
                   3.0e-30
E value
                   138
Match length
% identity
                   HYPOTHETICAL 100.9 KD PROTEIN C34E10.3 IN CHROMOSOME III
NCBI Description
                   >gi 500726 (U10402) C34E10.3 gene product [Caenorhabditis
                   elegans]
Seq. No.
                   32756
Contig ID
                   306582 1.R1040
5'-most EST
                   q43137\overline{15}
Method
                   BLASTX
                   q3861153
NCBI GI
BLAST score
                   311
E value
                   2.0e-28
Match length
                   111
% identity
                   54
                   (AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)
NCBI Description
                   [Rickettsia prowazekii]
```

32757 Seq. No.

306594 1.R1040 Contig ID 5'-most EST asn701143167.hl

32758 Seq. No.

Contig ID 306662 1.R1040 5'-most EST uC-gmropic015h12b1

32759 Seq. No.

306703 1.R1040 Contig ID

5'-most EST uC-gmrominsoy173e03b1

Method BLASTX NCBI GI q4103635 222 BLAST score 5.0e-18 E value Match length 112 38 % identity

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

32760 Seq. No.

306825 1.R1040 Contig ID

5'-most EST jC-gmf102220050a02d1

Seq. No. 32761

306827 1.R1040 Contig ID

5'-most EST jC-qmf102220050a03d1

Method BLASTX NCBI GI q417576 BLAST score 144 5.0e-09 E value Match length 71 % identity 45

NCBI Description

60S RIBOSOMAL PROTEIN YL16A >gi_322960_pir__S28944 ribosomal protein L6.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_218509_dbj_BAA01077_ (D10225) ribosomal

protein YL16 [Saccharomyces cerevisiae]

>gi_914877_emb_CAA86505_ (Z46373) YL16a gene, len: 176, CAI: 0.64, R16A_YEAST_Q02326 60S ribosomal protein YL16A

[Saccharomyces cerevisiae]

32762 Seq. No.

306837 1.R1040 Contig ID

5'-most EST $jC-gmf\overline{1}02220050a10d1$

Seq. No. 32763

306839 1.R1040 Contig ID

5'-most EST jC-gmf102220050a12a1

32764 Seq. No.

306841 1.R1040 Contig ID

5'-most EST $jC-qmf\overline{1}02220050b01d1$

Method BLASTX NCBI GI g2341032 BLAST score 263 8.0e-23 E value Match length 93

```
% identity
                   (AC000104) EST qb ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   32765
Seq. No.
                   306850 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220050b07a1
Seq. No.
                   32766
                   306873 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810092g03d1
Method
                   BLASTX
NCBI GI
                   q3152583
BLAST score
                   229
E value
                   6.0e-19
Match length
                   90
% identity
NCBI Description
                   (AC002986) Contains similarity to inhibitor of apoptosis
                   protein gb_U45881 from D. melanogaster. [Arabidopsis
                   thaliana]
Seq. No.
                   32767
Contig ID
                   306888 1.R1040
5'-most EST
                   jC-gmle01810050c02d1
Method
                   BLASTN
NCBI GI
                   a2351071
BLAST score
                   40
E value
                   5.0e-13
Match length
                   116
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MVA3, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   306910 1.R1040
5'-most EST
                   jC-qmf102220050e04d1
Seq. No.
                   306923 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810036e03d1
Seq. No.
                   306925 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400065e10d1
Seq. No.
                   306932 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220050f05d1
Seq. No.
                   306944 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220050f11d1
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   379
                   0.0e+00
E value
Match length
                   483
```

5'-most EST

```
% identity
NCBI Description
                   Tobacco chloroplast genome DNA
                   32773
Seq. No.
                   306951 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810050f02d1
Seq. No.
                   32774
                   306972 1.R1040
Contig ID
                   jC-gmf102220050h03a1
5'-most EST
Method
                   BLASTX
                   g3668077
NCBI GI
BLAST score
                   125
E value
                   3.0e-09
Match length
                   67
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32775
                   306975 1.R1040
Contig ID
                                                                          21 ....
5'-most EST
                   jC-gmle01810050h04d1
Method
                   BLASTX
NCBI GI
                   q2447013
BLAST score
                   167
E value
                   1.0e-11
Match length
                   63
                   52
% identity
                   (D37949) defective F1F0-ATPase alpha subunit precursor
NCBI Description
                   [Saccharomyces cerevisiae]
Seq. No.
                   32776
                   307016 1.R1040
Contig ID
                   jC-gmle01810051b05d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3033392
BLAST score
                   283
E value
                   3.0e-25
Match length
                   85
                   65
% identity
                   (AC004238) putative translation initiation factor
NCBI Description
                   EIF-2B-epsilon subunit [Arabidopsis thaliana]
                   32777
Seq. No.
                   307024 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220051b10d1
                   BLASTN
Method
                   g3319365
NCBI GI
BLAST score
                   77
E value
                   5.0e-35
Match length
                   193
% identity
NCBI Description
                   Arabidopsis thaliana BAC T24M8
                   32778
Seq. No.
                   307035 1.R1040
Contig ID
```

jC-gmle01810051c06d1

```
32779
Seq. No.
                   307047 1.R1040
Contig ID
                   jC-gmf\(\bar{1}\)02220051d01d1
5'-most EST
                   BLASTX
Method
                   g3047125
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   38
% identity
                   76
NCBI Description
                   (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                   32780
                   307063 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810051e12d1
Seq. No.
                   307078 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810067b08d1
Seq. No.
                   32782
                   307091 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220051f04d1
Method
                   BLASTX
NCBI GI
                   q4512682
BLAST score
                   306
E value
                   6.0e-28
Match length
                   71
% identity
NCBI Description
                   (AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32783
                   307097 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810051f07d1
                   32784
Seq. No.
Contig ID
                   307115 1.R1040
5'-most EST
                   jC-gmle01810051g07d1
Seq. No.
                   32785
                   307126 1.R1040
Contiq ID
5'-most EST
                   uC-qmflminsoy014e07b1
Method
                   BLASTX
NCBI GI
                   q2244816
BLAST score
                   753
E value
                   6.0e-80
Match length
                   248
% identity
                   27
NCBI Description
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
                   32786
Seq. No.
                   307129 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220051h03a1
Method
                   BLASTX
NCBI GI
                   q1652745
BLAST score
                   184
                   3.0e-13
E value
```

156

Match length

5'-most EST

```
% identity
NCBI Description
                   (D90908) hypothetical protein [Synechocystis sp.]
                   32787
Seq. No.
                   307143 1.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220051h12a1
Seq. No.
                   32788
                   307153 1.R1040
Contig ID
                   jC-gmf\overline{1}02220052a07a1
5'-most EST
                   BLASTX
Method
                   q2317910
NCBI GI
BLAST score
                   405
E value
                   2.0e-45
                   152
Match length
% identity
                   60
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]
Seq. No.
                   32789
                   307154 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810052a07d1
                   32790
Seq. No.
                   307159 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220052a10d1
                   32791
Seq. No.
                   307219 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073f06d1
Method
                   BLASTX
NCBI GI
                   q3336894
BLAST score
                   207
E value
                   2.0e-16
Match length
                   85
% identity
NCBI Description
                   (AJ225049) Hsp20.2 protein [Lycopersicon peruvianum]
                   32792
Seq. No.
                   307247 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220052q01d1
Seq. No.
                   307271 1.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220052h04a1
Seq. No.
                   307273 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810052h05d1
Seq. No.
                   32795
                   307275 1.R1040
Contig ID
5'-most EST
                   iC-qmf102220052h06d1
                   32796
Seq. No.
                   307282 1.R1040
Contig ID
```

jC-gmf102220052h11a1

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Seq. No.
                    32797
 Contig ID
                    307288 1.R1040
 5'-most EST
                    jC-gmf\overline{1}02220053a02d1
 Seq. No.
                    32798
 Contig ID
                    307327 1.R1040
 5'-most EST
                    jC-gmf102220053c03a1
 Method
                    BLASTX
 NCBI GI
                    q1903357
 BLAST score
                    496
 E value
                    4.0e-50
Match length
                    140
 % identity
                    63
 NCBI Description
                    (AC000104) Strong similarity to Arabidopsis 2A6
                    (gb_X83096). [Arabidopsis thaliana]
Seq. No.
                    32799
                    307357 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220053e01a1
Seq. No.
                    32800
Contig ID
                    307358 1.R1040
5'-most EST
                    jC-gmle01810053e01d1
Seq. No.
                    32801
Contig ID
                    307361 1.R1040
5'-most EST
                   g5126430
Method
                   BLASTX
NCBI GI
                   g3063691
BLAST score
                   329
E value
                   3.0e-43
Match length
                   107
% identity
NCBI Description
                    (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   32802
Contig ID
                   307361 2.R1040
5'-most EST
                   jC-gmle01810053e03a1
Seq. No.
                   32803
                   307363 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220053e04d1
Seq. No.
                   32804
Contig ID
                   307380 1.R1040
5'-most EST
                   jC-gmle01810053a07d1
Seq. No.
                   32805
Contig ID
                   307383 1.R1040
5'-most EST
                   jC-gmle01810053b10d1
Seq. No.
                   32806
Contig ID
                   307387 1.R1040
5'-most EST
                   jC-gmf102220053f07d1
Seq. No.
                   32807
Contig ID
```

307397 1.R1040

```
5'-most EST
                   jC-gmle01810053b07d1
                   32808
Seq. No.
                   307419 1.R1040
Contig ID
5'-most EST
                   jC-gmf\(\bar{1}\)02220053h04d1
Seq. No.
                   32809
                   307422 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy002d08b1
                   32810
Seq. No.
                   307434 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy100b10b1
Method
                   BLASTX
NCBI GI
                   g4262239
BLAST score
                   444
                   7.0e-44
E value
Match length
                   145
% identity
                   63
NCBI Description
                   (AC006200) putative membrane transporter [Arabidopsis
                   thaliana]
                   32811
Seq. No.
                   307434 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810002f05d1
                   32812
Seq. No.
                   307453 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220054b03d1
                   32813
Seq. No.
                   307485 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220054d04a1
Seq. No.
                   32814
                   307521 1.R1040
Contig ID
5'-most EST
                   jC-qmfl02220054f03d1
                   32815
Seq. No.
                   307527 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810047q12d1
Seq. No.
                   32816
                   307529 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810080h02d1
Seq. No.
                   32817
                   307561 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810054h07d1
                   32818
Seq. No.
                   307611 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810055c11a1
Seq. No.
                   32819
                   307641 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220055e11d1
```

5'-most EST

Chestan I

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32820
Seq. No.
                   307675 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810055h01d1
Seq. No.
                   32821
                   307704_1.R1040
Contig ID
                   jC-gmf\overline{1}02220056a07d1
5'-most EST
                   32822
Seq. No.
                   307722 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220056b09a1
                   32823
Seq. No.
                   307725 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810056b11d1
Seq. No.
                   32824
                   307756 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400040b11d1
Seq. No.
                   32825
                   307770 1.R1040
Contig ID
5'-most EST
                   uC-gmropic029b11b1
Seq. No.
                   32826
                   307781 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220056f02d1
Seq. No.
                   32827
                   307801 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810057g05d1
Seq. No.
                   32828
                   307803 1.R1040
Contig ID
                   jC-gmf\(\bar{1}\)02220057b02d1
5'-most EST
                   32829
Seq. No.
                   307824 1.R1040
Contig ID
5'-most EST
                   q5677492
                   32830
Seq. No.
                   307825 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810056h12d1
Method
                   BLASTX
NCBI GI
                   g1483218
BLAST score
                   275
E value
                   3.0e-24
                   73
Match length
% identity
                   (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
                   32831
Seq. No.
                   307833 1.R1040
Contig ID
```

jC-gmle01810057a06d1

```
32832
Seq. No.
                   307882 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910033f12d1
                   32833
Seq. No.
Contig ID
                   307890 1.R1040
5'-most EST
                   uC-gmflminsoy055h09b1
Method
                   BLASTX
NCBI GI
                   g2648588
BLAST score
                   294
E value
                   2.0e-26
Match length
                   156
% identity
                   41
NCBI Description
                   (AE000968) Glu-tRNA amidotransferase, subunit A (gatA-1)
                   [Archaeoglobus fulgidus]
                   32834
Seq. No.
                   307909 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810057f06d1
Seq. No.
                   32835
                   307936 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220057h06d1
Seq. No.
                   32836
                   307971 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910036f01d1
                   32837
Seq. No.
                   307995 1.R1040
Contig ID
                   jC-gmf102220058g10a1
5'-most EST
                   32838
Seq. No.
                   307997 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400046h02d1
                   32839
Seq. No.
                   307997 2.R1040
Contig ID
5'-most EST
                   jC-qmf102220101g05d1
Seq. No.
                   32840
                   308004_1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220059b01d1
                   32841
Seq. No.
                   308017 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy212a10b1
Method
                   BLASTX
NCBI GI
                   g2894560
BLAST score
                   563
E value
                   7.0e-58
Match length
                   187
% identity
                   (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32842
```

308039 1.R1040

Contig ID

Contig ID

```
5'-most EST
                   jC-qmf102220080a03d1
                BLASTX
Method
NCBI GI
                   g3335372
BLAST score
                  216
                   3.0e-17
E value
Match length
                   65
% identity
NCBI Description
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.
                  32843
                  308044 1.R1040
Contig ID
                  uC-gmflminsoy049b06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4467146
BLAST score
                  761
                   2.0e-84
E value
                  203
Match length
% identity
                  70
NCBI Description
                   (AL035540) galactosidase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  32844
                  308046 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220060e12a1
Method
                  BLASTX
NCBI GI
                  q3152614
BLAST score
                  258
E value
                   5.0e-22
Match length
                  163
% identity
                   45
NCBI Description
                   (AC004482) unknown protein [Arabidopsis thaliana]
Seq. No.
                  32845
                  308057 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400044e05d1
Seq. No.
                  32846
                  308067 1.R1040
Contig ID
5'-most EST
                  g5688407
Seq. No.
                  32847
                  308070 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220060h12a1
Method
                  BLASTX
NCBI GI
                  q3420057
BLAST score
                  653
E value
                  2.0e-68
Match length
                  197
% identity
NCBI Description
                   (AC004680) putative ABC transporter [Arabidopsis thaliana]
Seq. No.
                  308176 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220061f03a1
                  32849
Seq. No.
```

308235 1.R1040

NCBI GI

```
5'-most EST
                   g5605735
                   32850
Seq. No.
Contig ID
                   308252 1.R1040
5'-most EST
                   jC-gmf102220062b04a1
Seq. No.
                   32851
Contig ID
                   308273 1.R1040
5'-most EST
                   jC-gmro02910047g01d1
                   32852
Seq. No.
                   308292 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220127g02a1
Method
                   BLASTX
                   g2864613
NCBI GI
BLAST score
                   142
E value
                   1.0e-08
                   103
Match length
                   33
% identity
                   (AL021811) S-receptor kinase -like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor
                   kinase-like protein [Arabidopsis thaliana]
Seq. No.
                   32853
                   308325 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220062h03d1
Seq. No.
                   32854
                   308368 1.R1040
Contig ID
                   jC-gmf\overline{1}02220063b11d1
5'-most EST
Seq. No.
                   32855
                   308385 1.R1040
Contig ID
5'-most EST
                   fC-gmle700555329d3
Seq. No.
                   32856
                   308427 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220063e08d1
Seq. No.
                   32857
                   308476_1.R1040
Contig ID
5'-most EST
                   uC-gmronoir068e09b1
                   BLASTX
Method
NCBI GI
                   g3287695
BLAST score
                   293
E value
                   2.0e-26
Match length
                   100
% identity
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                   thaliana]
                   32858
Seq. No.
                   308543 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063f06d1
Method
                   BLASTX
```

g419760

```
BLAST score
                     249
                     2.0e-22
E value
Match length
                     70
% identity
                     47
NCBI Description
                     P-glycoprotein atpgpl - Arabidopsis thaliana
                     >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
                     [Arabidopsis thaliana]
Seq. No.
                     32859
                     308567 1.R1040
Contig ID
5'-most EST
                     jC-qmf102220065c03d1
Seq. No.
                     32860
                     308581 1.R1040
Contig ID
                     jC-qmf\overline{1}02220065c12d1
5'-most EST
Seq. No.
                     32861
                     308638 1.R1040
Contig ID
5'-most EST
                     jC-qmf102220137a08a1
Seq. No.
                     32862
Contig ID
                     308687 1.R1040
                     jC-gmf\overline{1}02220067e06a1
5'-most EST
Method
                     BLASTX
NCBI GI
                    q2244831
BLAST score
                     246
E value
                     8.0e-21
Match length
                     129
% identity
                     47
NCBI Description
                     (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                     32863
                     308730 1.R1040
Contig ID
5'-most EST
                     g57536<u>2</u>6
Seq. No.
                     32864
                     308779 1.R1040
Contig ID
5'-most EST
                     jC-qmf102220068d06d1
                     32865
Seq. No.
Contig ID
                     308848 1.R1040
5'-most EST
                     jC-gmro02910047h07d1
Method
                    BLASTX
NCBI GI
                     q1708971
BLAST score
                    215
E value
                     3.0e-17
Match length
                     60
% identity
NCBI Description
                     (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                     (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                    >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                     (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                     serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
```

[Prunus serotina]

NCBI GI

```
Seq. No.
                   32866
                   308893 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220069c07a1
Method
                   BLASTX
NCBI GI
                   q4006915
                   203
BLAST score
E value
                   1.0e-15
Match length
                   121
% identity
                   38
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   32867
                   308914 1.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220139b01d1
Method
                   BLASTX
NCBI GI
                   g2979548
BLAST score
                   328
E value
                   2.0e-30
Match length
                   119
% identity
                   49
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   32868
Contig ID
                   308930 1.R1040
5'-most EST
                   jC-qmle01810078e09d1
Seq. No.
                   308935 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810035a04d1
Seq. No.
                   32870
                   308949 1.R1040
Contig ID
5'-most EST
                   uC-gmropic066e06b1
Seq. No.
                   32871
                   308953 1.R1040
Contig ID -
5'-most EST
                   jC-gmst02400011f01a1
Method
                   BLASTX
NCBI GI
                   a3941543
BLAST score
                   256
E value
                   5.0e-22
Match length
                   69
% identity
                   70
NCBI Description
                   (AF069497) pelota [Arabidopsis thaliana]
                   >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                   [Arabidopsis thaliana]
                   32872
Seq. No.
                   308972 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220069h08a1
Seq. No.
                   32873
                   309054 1.R1040
Contig ID
                   jC-qmf\overline{1}02220070f01d1
5'-most EST
Method
                   BLASTX
```

q4454464



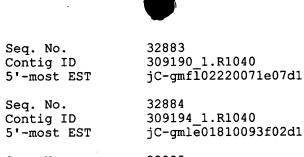
```
BLAST score
                   384
                   5.0e-37
E value
Match length
                   91
                   81
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   32874
Seq. No.
                   309063 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220070f06a1
                   32875
Seq. No.
                   309095 1.R1040
Contig ID
                   jC-qmf102220070h05d1
5'-most EST
                   32876
Seq. No.
                   309118 1.R1040
Contig ID
                   jC-gmf\overline{1}02220071a10a1
5'-most EST
Seq. No.
                   32877.
                   309121 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400025a11d1
Seq. No.
                   32878
                   309133 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220071b06a1
Seq. No.
                   32879
                   309159 1.R1040
Contig ID
5'-most EST
                   g4299702
Seq. No.
                   32880
                   309164 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220071d02a1
Method
                   BLASTX
NCBI GI
                   q2262100
BLAST score
                   749
E value
                   1.0e-79
Match length
                   192
% identity
                   72
NCBI Description
                   (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                   32881
                   309174 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy071h11b2
Method
                   BLASTX
NCBI GI
                   q3445204
BLAST score
                   344
E value
                   3.0e-32
                   86
Match length
% identity
                   (AC004786) putative GTP-binding protein [Arabidopsis
NCBI Description
```

Seq. No. 32882

Contig ID 309176_1.R1040

5'-most EST $jC-gmf\overline{1}02220071d07a1$

thaliana]



 Seq. No.
 32885

 Contig ID
 309202_1.R1040

 5'-most EST
 jC-gmst02400031b02d1

 Seq. No.
 32886

 Contig ID
 309222_1.R1040

 5'-most EST
 jC-gmf102220071g06d1

 Method
 BLASTN

 NCBI GI
 g3413321

 BLAST score
 42

BLAST score 42 E value 2.0e-14 Match length 102 % identity 85

NCBI Description M.sativa PG3 gene

Seq. No. 32888
Contig ID 309252_1.R1040
5'-most EST jC-gmfl02220071h11a1

 Seq. No.
 32889

 Contig ID
 309298_1.R1040

 5'-most EST
 jC-qmf102220072d01d1

Seq. No. 32890 Contig ID 309304 1.R1040

5'-most EST jC-gmf102220072c08a1

 Seq. No.
 32891

 Contig ID
 309308 1.R1040

 5'-most EST
 jC-gmf102220092g12d1

 Seq. No.
 32892

 Contig ID
 309331_1.R1040

 5'-most EST
 jC-gmf102220072e02d1

 Seq. No.
 32893

 Contig ID
 309335_1.R1040

 5'-most EST
 jC-gmfl02220072e04d1

 Seq. No.
 32894

 Contig ID
 309351_1.R1040

 5'-most EST
 jC-gmf102220072f06a1

 Method
 BLASTX

 NCBI GI
 g3281861

 BLAST score
 195

Seq. No.

32904

```
6.0e-15
E value
Match length
                   90
% identity
                    46
                    (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   32895
Seq. No.
                   309375 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220081h01a1
Seq. No.
                   32896
                   309389 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220072h12a1
Seq. No.
                   32897
                   309401 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220073c10a1
                   32898
Seq. No.
Contig ID
                   309420 1.R1040
5'-most EST
                   jC-gmf102220073b08a1
Seq. No.
                   309447 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220073d01d1
Seq. No.
                   32900
                   309452 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220073d04a1
Method
                   BLASTX
NCBI GI
                   q2244890
BLAST score
                   221
E value
                   6.0e-18
Match length
                   119
% identity
NCBI Description
                    (Z97338) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   32901
                   309455 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220073d07d1
Seq. No.
                   32902
                   309458 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220073f05a1
Method
                   BLASTX
NCBI GI
                   q3152592
BLAST score
                   190
E value
                   6.0e-15
Match length
                   52
% identity
                   75
NCBI Description
                    (AC002986) Contains similarity to 8A-2V protein gb Y10496
                   from Mus musculus. [Arabidopsis thaliana]
                   32903
Seq. No.
                   309473 1.R1040
Contig ID
5'-most EST
                   q43004\overline{2}1
```

Seq. No.

Contig ID

```
Contig ID
                   309476 1.R1040
5'-most EST
                   jC-qmf102220073e12d1
Seq. No.
                   32905
                   309541 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220075a07d1
                   32906
Seq. No.
Contig ID
                   309602 1.R1040
5'-most EST
                  jC-gmst02400001d10d1
                   32907
Seq. No.
                   309621 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910050b11d1
                   32908
Seq. No.
                   309638 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220075h10d1
Method
                   BLASTX
                   g1655536
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
Match length
                   39
% identity
                   79
                   (Y09095) chloride channel [Arabidopsis thaliana]
NCBI Description
                   >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
                   32909
Seq. No.
                   309662 1.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220077b01d1
                   32910
Seq. No.
                   309678 1.R1040
Contig ID
                   jC-gmf102220076d05a1
5'-most EST
Method
                   BLASTX
                   g2618701
NCBI GI
BLAST score
                   394
                   5.0e-38
E value
                   150
Match length
% identity
                   60
NCBI Description
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
                   32911
Seq. No.
                   309706 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810072a06d1
Seq. No.
                   32912
Contig ID
                   309731 1.R1040
5'-most EST
                   jC-qmf102220077a07d1
                   32913
Seq. No.
                   309743 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220078q09a1
```

309773_1.R1040

5'-most EST

```
5'-most EST
                    jC-gmro02910075a06d1
Method
                    BLASTN
NCBI GI
                    g168214
BLAST score
                    107
E value
                    8.0e-53
Match length
                    290
% identity
                    85
NCBI Description
                    Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A
                    reductase (hmgr3) mRNA, complete cds
Seq. No.
                    32915
Contig ID
                    309786 1.R1040
5'-most EST
                    jC-gmf102220077d05a1
Method
                    BLASTX
NCBI GI
                    g4314356
BLAST score
                    299
E value
                    7.0e-27
Match length
                    144
% identity
                    43
NCBI Description
                    (AC006340) putative anthocyanidin-3-glucoside
                   rhamnosyltransferase [Arabidopsis thaliana]
Seq. No.
                    32916·
                   309805 1.R1040 ···
Contig ID
5'-most EST
                   jC-gmf102220077f05a1
Seq. No.
                   32917
                   309806 1.R1040
Contig ID
5'-most EST
                   jC-gmf\(\overline{1}\)02220077e06d1
Seq. No.
                   32918
                   309826_1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220077f08d1
Seq. No.
                   32919
                   309849 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220077h01a1
Seq. No.
                   32920
Contig ID
                   309902 1.R1040
5'-most EST
                   uC-gmrominsoy260b11b1
Seq. No.
                   32921
Contig ID
                   309959 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220079b01d1
Seq. No.
                   32922
Contig ID
                   309969 1.R1040
5'-most EST
                   jC-qmf102220080h02d1
Seq. No.
                   32923
Contig ID
                   310019 1.R1040
5'-most EST
                   g5175497
Seq. No.
                   32924
Contig ID
                   310076_1.R1040
```

 $jC-gms\overline{t}02400017f07d1$



```
BLASTX
Method
NCBI GI
                   g1497987
BLAST score
                   142
                   1.0e-08
E value
                   82
Match length
% identity
                   33
NCBI Description
                   (U62798) SCARECROW [Arabidopsis thaliana]
Seq. No.
                   32925
                   310101 1.R1040
Contig ID
                   jC-gmst02400060a07d1
5'-most EST
                   32926
Seq. No.
                   310110 1.R1040
Contig ID
                   jC-qmf102220080b01a1
5'-most EST
                   32927
Seq. No.
                   310178 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220080f07d1
Seq. No.
                   32928
                   310181 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220080f09d1
Seq. No.
                   32929
                   310202 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400018e07d1
Seq. No.
                   32930
                   310351 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220082b07d1
                   32931
Seq. No.
                   310364 1.R1040
Contig ID
5'-most EST
                   q42602\overline{4}8
Method
                   BLASTX
NCBI GI
                   q4218120
BLAST score
                   209
E value
                   2.0e-16
Match length
                   53
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   32932
Contig ID
                   310399 1.R1040
5'-most EST
                   jC-qmf\overline{1}02220083b01d1
```

Seq. No. 32933

Contig ID 310406 1.R1040

5'-most EST jC-gmf102220083a11a1

Seq. No. 32934

Contig ID 310418 1.R1040

5'-most EST $jC-gmf\overline{10}2220083d12a1$

Seq. No. 32935



310446 1.R1040 Contig ID jC-gmf102220094a12a15'-most EST 32936 Seq. No. 310447 1.R1040 Contig ID jC-gmf102220083e02a1 5'-most EST Method BLASTX NCBI GI g2702268 BLAST score 588 E value 6.0e-61 Match length 163 % identity 64 NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana] 32937 Seq. No. Contig ID 310451 1.R1040 5'-most EST $jC-gmf\overline{1}02220083h10a1$ 32938 Seq. No. 310452 1.R1040 Contig ID 5'-most EST jC-gmf\(\overline{1}\)02220083f08a1 32939 Seq. No. 310465 4.R1040 Contig ID 5'-most EST jC-gmf102220099f03a1 Seq. No. 32940 310479 1.R1040 Contig ID $jC-gmf\overline{1}02220083g08a1$ 5'-most EST 32941 Seq. No. 310505 1.R1040 Contig ID 5'-most EST jC-gmf102220083h12d1 32942 Seq. No. 310511 1.R1040 Contig ID $jC-gmf\overline{1}02220101f11d1$ 5'-most EST Seq. No. 32943 310554 1.R1040 Contig ID $jC-gmf\overline{1}02220084e02d1$ 5'-most EST 32944 Seq. No. Contig ID 310579 1.R1040 5'-most EST jC-gmf102220084h09d1 32945 Seq. No. 310587 1.R1040 Contig ID 5'-most EST jC-gmf102220112d07d1 32946 Seq. No. Contig ID 310593_1.R1040 jC-gmst02400020h09a1 5'-most EST BLASTX Method

g3201611

2.0e-23

270

NCBI GI

E value

BLAST score



Match length 96 3 61

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 32947

Contig ID 310603 1.R1040

5'-most EST jC-gmst02400031a12d1

Method BLASTX
NCBI GI g3287857
BLAST score 379
E value 3.0e-36
Match length 105
% identity 69

NCBI Description 3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA

DEHYDROGENASE) (BHBD) >gi 1209052 (U32229) HbdA

[Bradyrhizobium japonicum]

Seq. No. 32948

Contig ID 310605 1.R1040

5'-most EST $jC-gmf\overline{1}02220115b11d1$

Method BLASTX
NCBI GI g1345132
BLAST score 186
E value 7.0e-14
Match length 55
% identity 69

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 32949

Contig ID 310623 1.R1040

5'-most EST jC-gmf102220085c01a1

Seq. No. 32950

Contig ID 310640_1.R1040

Seq. No. 32951

Contig ID 310654 1.R1040

5'-most EST $jC-gmf\overline{1}02220085f04d1$

Seq. No. 32952

Contig ID 310665 1.R1040

5'-most EST jC-gmf102220085h03d1

Seq. No. 32953

Contig ID 310684_1.R1040

5'-most EST jC-gmf102220090b10d1

Method BLASTX
NCBI GI g2529663
BLAST score 195
E value 7.0e-15
Match length 66
% identity 53

NCBI Description (AC002535) putative lysophospholipase [Arabidopsis



thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

32954 Seq. No.

310685 1.R1040 Contig ID $jC-gmf\overline{1}02220085h10a1$ 5'-most EST

32955 Seq. No.

Contig ID

310702 1.R1040 jC-gmf102220088b06a1

5'-most EST BLASTX Method

g2618686 NCBI GI 406 BLAST score 1.0e-39 E value 136 Match length 54

% identity

(AC002510) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

32956

Contig ID

310717 1.R1040

5'-most EST

jC-gmf\(\bar{1}\)02220086f09a1

Seq. No.

32957

Contig ID

310727 1.R1040 -

5'-most EST

jC-gmf102220086b08d1

Seq. No.

32958

Contig ID

310737 1.R1040

5'-most EST

jC-qmro02910019e03d1

Seq. No.

32959

Contig ID

310772 1.R1040

5'-most EST

jC-qmf\(\bar{1}\)02220086d10d1

Method NCBI GI BLASTX g4512664

BLAST score

290

E value

4.0e-26

Match length

64

% identity

NCBI Description

(AC006931) putative ribose phosphate pyrophosphokinase

[Arabidopsis thaliana]

>qi 4544471 gb AAD22378.1 AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.

32960

Contig ID

310805 1.R1040

5'-most EST

jC-gmle01810028f10d1

Seq. No.

32961

Contig ID

310890 1.R1040

5'-most EST

jC-gmle01810049e02d1

Seq. No.

32962

Contig ID

310906 1.R1040

5'-most EST

jC-qmfl02220089b05d1

Seq. No.

32963

```
310921 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220089c03a1
Method
                   BLASTX
NCBI GI
                   g731400
BLAST score
                   159
                   1.0e-10
E value
                   171
Match length
                   6
% identity
                   VACUOLAR PROTEIN 8 >gi_1077594_pir__S50446 hypothetical
NCBI Description
                   protein YEL013w - yeast (Saccharomyces cerevisiae)
                   >gi 602380 (U18530) Yel013wp [Saccharomyces cerevisiae]
                   32964
Seq. No.
                   310922 1.R1040
Contig ID
                   jC-gmf\overline{1}02220089c03d1
5'-most EST
Seq. No.
                   32965
                   310970 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220089e12a1
                   32966
Seq. No.
Contig ID
                   310999 1.R1040
                   jC-gmst02400003a01d1
5'-most EST
Method
                   BLASTX
                   g4063751
NCBI GI
BLAST score
                   154
E value
                   4.0e-10
Match length
                   58
                   50
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510409 gb AAD21495.1 (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   32967
Seq. No.
                   311016 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220112h12d1
                   32968
Seq. No.
Contig ID
                   311042_1.R1040
5'-most EST
                   jC-gmle01810073e12d1
Method
                   BLASTN
NCBI GI
                   g1707656
BLAST score
                   43
E value
                   7.0e-15
                   206
Match length
                   91
% identity
                   P.sativum mRNA for DnaJ-like protein
NCBI Description
                   32969
Seq. No.
                   311050 1.R1040
Contig ID
                   jC-gmf\overline{1}02220090e07a1
5'-most EST
                   32970
Seq. No.
Contig ID
                   311053 1.R1040
                   jC-gmf102220090d07d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455250
```

```
206
BLAST score
                    3.0e-16
E value
                    61
Match length
% identity
                    64
                    (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                    32971
Seq. No.
                    311086 1.R1040
Contig ID
5'-most EST
                    jC-gmf\overline{1}02220091g03a1
Method
                   BLASTX
NCBI GI
                   q4371280
                    211
BLAST score
                    8.0e-17
E value
                    48
Match length
                   88
% identity
NCBI Description
                    (AC006260) hypothetical protein [Arabidopsis thaliana]
                   32972
Seq. No.
                   311095 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220090d04d1
                   32973
Seq. No.
                   311120 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220090e09d1
Seq. No.
                   32974
Contig ID
                   311139 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220090f08d1
Seq. No.
                   32975
                    311162 1.R1040
Contig ID
5'-most EST
                  -jC-qmf\bar{1}02220090q09d1
                   32976
Seq. No.
                   311208 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220091b09a1
Seq. No.
                   32977
                   311256 1.R1040
Contig ID
                   jC-gmf\overline{1}02220091e09a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3176709
BLAST score
                    457
                   1.0e-45
E value
                   150
Match length
% identity
NCBI Description
                    (AC002392) putative anthranilate
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
                   32978
Seq. No.
                   311269 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800042d06d1
                   BLASTX
Method
NCBI GI
                   g3355471
BLAST score
                   180
```

5.0e-13

E value

4.55

```
Match length
                   44
% identity
                   68
NCBI Description
                   (AC004218) putative lysophospholipase [Arabidopsis
                   thaliana]
                   32979
Seq. No.
                   311330 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400008h07d1
Seq. No.
                   32980
                   311347 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220092d03d1
Method
                   BLASTN
NCBI GI
                   q1044867
BLAST score
                   43
E value
                   8.0e-15
Match length
                  . 47
                   98
% identity
                   Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)
NCBI Description
                   32981
Seq. No.
                   311372 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220092f05d1
Method
                   BLASTX
NCBI GI
                   q4538965
BLAST score
                   172
E value
                   1.0e-12
Match length
                   69
% identity
                   54
                   (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   32982
                   311377 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220092f12a1
Method
                   BLASTX
NCBI GI
                   g4530126
BLAST score
                   604
                   1.0e-62
E value
                  210
Match length
% identity
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                   32983
Seq. No.
                   311380 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220092g02d1
Method
                   BLASTX
NCBI GI
                   q4101626
BLAST score
                   402
E value
                   8.0e-39
Match length
                   89
% identity
NCBI Description
                   (AF005096) desaturase/cytochrome b5 protein [Ricinus
                   communis]
                   32984
Seq. No.
```

311396 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   jC-qmf102220092h06d1
Method
                   BLASTX
NCBI GI
                   q3004564
BLAST score
                   175
E value
                   2.0e-12
Match length
                   67
% identity
                   54
NCBI Description
                    (AC003673) putative receptor Ser/Thr protein kinase
                    [Arabidopsis thaliana]
Seq. No.
                   32985
                   311418 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220093b03d1
Seq. No.
                   32986
                   311508 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220094f12d1
                   32987
Seq. No.
                   311510 1.R1040
Contig ID
                   jC-gmf\overline{1}02220096d02a1
5'-most EST
Seq. No.
                   32988
                   311524 1.R1040 ·
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220094d01d1
                   32989
Seq. No.
                   311527 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220094b10d1
Seq. No.
                   32990
                   311559 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220094f01d1
                   32991
Seq. No.
Contig ID
                   311577 1.R1040
5'-most EST
                   jC-gmf102220094e08d1
                   32992
Seq. No.
                   311625 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220094h07d1
                   32993
Seq. No.
                   311659 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220096c07a1
Seq. No.
                   32994
                   311670 1.R1040
Contig ID
                   jC-gms\overline{t}02400068e03d1
5'-most EST
                   32995
Seq. No.
                   311698 1.R1040
Contig ID
                   jC-gmro02800043f09a1
5'-most EST
                   32996
Seq. No.
                   311717 1.R1040
Contig ID
```

n

uC-gmrominsoy201h09b1

Contig ID

```
32997
Seq. No.
                   311792 1.R1040
Contig ID
                   jC-gmf\overline{1}02220133h10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3341978
BLAST score
                   171
E value
                   5.0e-12
                   100
Match length
% identity
                   43
                   (AF044603) cytokinin oxidase [Zea mays]
NCBI Description
                   32998
Seq. No.
                   311805 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220139a10d1
Method
                   BLASTX
NCBI GI
                   g4314378
BLAST score
                   147
E value
                   3.0e-09
Match length
                   43
% identity
NCBI Description
                   (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                   32999
                   311821 1.R1040
Contig ID
                   jC-qmf102220099e04a1
5'-most EST
                   33000
Seq. No.
                   311834 1.R1040
Contig ID
5'-most EST
                   q5676970
Method
                   BLASTX
NCBI GI
                   g2664212
BLAST score
                   462
E value
                   5.0e-46
Match length
                   134
% identity
NCBI Description
                   (AJ222645) asparaginyl-tRNA synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   33001
                   311844 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810090g12d1
Seq. No.
                   311856 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220099a06a1
Seq. No.
                   33003
                   311859 1.R1040
Contig ID
5'-most EST
                   q5753537
Seq. No.
                   33004
                   311869 1.R1040
Contig ID
                   jC-qmf102220099e01a1
5'-most EST
Seq. No.
                   33005
```

5008

311879 1.R1040

```
jC-qmf102220099b01d1
5'-most EST
Method
                   BLASTX
                   g3152577
NCBI GI
BLAST score
                   432
                   1.0e-42
E value .
Match length
                   149
% identity
                   61
NCBI Description
                   (AC002986) Contains similarity to Kinesin-like protein C
                   gb D21138 from A. thaliana. [Arabidopsis thaliana]
                   33006
Seq. No.
                   311880 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220099c07a1
                   33007
Seq. No.
                   311895 1.R1040
Contig ID
                   jC-gmf\overline{1}02220099d06d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4038030
BLAST score
                   448
E value
                   2.0e-44
Match length
                   167
% identity
                   23
NCBI Description
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
                   thaliana]
Seq. No.
                   33008
                   311928 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220099e06a1
Seq. No.
                   33009
                   311937 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220099f04d1
                   33010
Seq. No.
Contig ID
                   311945_1.R1040
                   jC-gmro02800024e03d1
5'-most EST
Method
                   BLASTX
                   q3434969
NCBI GI
BLAST score
                   150
                   2.0e-09
E value
Match length
                   57
% identity
                   56
                   (AB008104) ethylene responsive element binding factor 2
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   33011
Contig ID
                   311953 1.R1040
5'-most EST
                   jC-gmro02800042g05d1
Method
                   BLASTX
                   g4539006
NCBI GI
BLAST score
                   382
E value
                   9.0e-37
                   90
Match length
% identity
                   80
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
```

5'-most EST

```
33012
Seq. No.
                   311979 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220100c04a1
                   33013
Seq. No.
                   312053 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400045h12d1
                   33014
Seq. No.
                   312068 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220101d05d1
                   33015
Seq. No.
                   312076 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220101d09d1
Seq. No.
                   33016
                   312087 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220101e05a1
Method
                   BLASTX
NCBI GI
                   q1143445
BLAST score
                   404
E value
                   1.0e-39
Match length
                   114
                   68
% identity
NCBI Description
                   (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
                   33017
Seq. No.
                   312156 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220102b01a1
Method
                   BLASTX
NCBI GI
                   q2894600
BLAST score
                   259
E value
                   3.0e-22
Match length
                   82
% identity
                   57
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   33018
Seq. No.
                   312187 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810031b04d1
Method
                   BLASTX
NCBI GI
                   q2924784 .
BLAST score
                   482
E value
                   4.0e-48
Match length
                   173
% identity
                   51
NCBI Description
                   (AC002334) similar to jasmonate inducible protein
                   [Arabidopsis thaliana]
                   33019
Seq. No.
                   312263 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220103f07d1
                   33020
Seq. No.
                   312285 1.R1040
Contig ID
```

jC-gmf102220103c03a1

BLAST score

106

```
33021
Seq. No.
Contig ID
                   312296 1.R1040
5'-most EST
                   q4260293
Method
                   BLASTX
NCBI GI
                   g2245020
BLAST score
                   185
E value
                   1.0e-13
Match length
                   132
                   39
% identity
NCBI Description
                   (Z97341) growth regulator homolog [Arabidopsis thaliana]
                   33022
Seq. No.
                   312331 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy315f02b1
Method
                   BLASTX
NCBI GI
                   q3882273
BLAST score
                   260
E value
                   3.0e-22
Match length
                  _ 175
% identity
                   33
                   (AB018319) KIAA0776 protein [Homo sapiens]
NCBI Description
                   33023
Seq. No.
Contig ID
                   312354 1.R1040
5'-most EST
                   jC-gmfl02220103f12d1
Method
                   BLASTN
                   g3021356
NCBI GI
BLAST score
                   80
E value
                   6.0e-37
Match length
                   108
% identity
                   94
                   Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,
NCBI Description
                   clone GEPI48
                   33024
Seq. No.
Contig ID
                   312358 1.R1040
5'-most EST
                   uC-gmrominsoy308h09b1
Seq. No.
                   33025
                   312391 1.R1040
Contig ID
5'-most EST
                   jC-gmr002910068a04d1
Seq. No.
                   33026
                   312439 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220104c12a1
                   33027
Seq. No.
                   312446 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400004a04d1
Seq. No.
                   33028
                   312463 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220113h11d1
                  BLASTN
Method
                   g861·154
NCBI GI
```

```
2.0e-52
E value
Match length
                   214
                   87
% identity
                   V.faba VFCWINV1 mRNA for cell wall invertase I
NCBI Description
Seq. No.
                   33029
Contig ID
                   312497 1.R1040
                   jC-gmst02400053d10a1
5'-most EST
                   33030
Seq. No.
Contig ID
                   312513 1.R1040
5'-most EST
                   jC-qmle01810061b01d1
                   33031
Seq. No.
                   312519 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400056f08d1
                   33032
Seq. No.
Contig ID
                   312549 1.R1040
5'-most EST
                   jC-gmf\overline{1}02220106b09a1
Method
                   BLASTX
NCBI GI
                   g4559356
BLAST score
                   218
E value
                   2.0e-17
Match length
                   183
                   8
% identity
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33033
                   312555 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220106c01a1
Seq. No.
                   33034
                   312673 1.R1040
Contig ID
                   jC-qmf\(\bar{1}\)02220108d10a1
5'-most EST
                   33035
Seq. No.
                   312755 1.R1040
Contig ID
5'-most EST
                   jC-qmf\overline{1}02220112d06d1
                   33036
Seq. No.
                   312763 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220112e07d1
Seq. No.
                   33037
                   312771 1.R1040
Contig ID
5'-most EST
                   g5057800
Method
                   BLASTX
NCBI GI
                   g2129929
BLAST score
                   376
                   7.0e-36
E value
Match length
                   174
                   44
% identity
                   DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -
NCBI Description
                   tomato >gi_1049068 (U28403) RNA polymerase II subunit 2
```

[Solanum lycopersicum]

```
33038
Seq. No.
                   312788 1.R1040
Contig ID
5'-most EST
                  -jC-gmf102220143g10d1
Method
                   BLASTX
                   g2244732
NCBI GI
BLAST score
                   201
                   2.0e-15
E value
Match length
                   40
% identity
                   82
NCBI Description
                   (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                   33039
Seq. No.
                   312822 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220113c06d1
Method
                   BLASTX
                   q2506139
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
                   86
Match length
                   71
% identity
NCBI Description
                   COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                   archain/delta-COP [Oryza sativa]
                   33040
Seq. No.
                   312860 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810000c08d1
                   33041
Seq. No.
                   312876 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220113h08d1
                   33042
Seq. No.
                   312882 1.R1040
Contig ID
                   jC-gmf102220114a02a1
5'-most EST
                   33043
Seq. No.
Contig ID
                   312928 1.R1040
                   jC-gmf102220114c09a1
5'-most EST
                   33044
Seq. No.
                   312970 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220114f02a1
Method
                   BLASTX
NCBI GI
                   g3785994
BLAST score
                   331
                   1.0e-30
E value
Match length
                   122
% identity
                   53
NCBI Description
                   (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33045
                   313033 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810063g12a1
Method
                   BLASTX
                   q4519258
NCBI GI
```

154

BLAST score

BLAST score

274

```
5.0e-10
E value
Match length
                   168
                   29
% identity
                   (AB017914) L-zip+NBS+LRR [Oryza sativa]
NCBI Description
                   33046
Seq. No.
                   313182_1.R1040
Contig ID
                   jC-gmf102220125d11a1
5'-most EST
Method
                   BLASTX
                   g2832692
NCBI GI
BLAST score
                   196
                   6.0e-15
E value
                   129
Match length
% identity
                   36
                   (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
                   33047
Seq. No.
                   313183 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220135e12d1
Method
                   BLASTX
NCBI GI
                   g2760326
BLAST score
                   165
E value
                   3.0e-11
Match length
                   83
% identity
                   42
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33048
                   313189 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400037h07d2
Seq. No.
                   33049
                   313211 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy286d02b1
Seq. No.
                   33050
                   313232 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220125f05d1
                   33051
Seq. No.
Contig ID
                   313262 1.R1040
5'-most EST
                   jC-gmro02910031f01a1
Method
                   BLASTX
NCBI GI
                   g4263795
BLAST score
                   195
E value -
                   9.0e-15
Match length
                   69
% identity
                   (AC006068) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   33052
                   313266 1.R1040
Contig ID
                   jC-gmf\overline{1}02220125h04d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2959781 ·
```

BLAST score

412

```
4.0e-24
E value
Match length
                    75
% identity
                    75
                    (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    33053
                    313271 1.R1040
Contig ID
5'-most EST
                    jC-gmf\(\bar{1}\)02220125h08a1
Seq. No.
                    33054
                    313289 1.R1040
Contig ID
                    jC-qmf102220131a02a1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3249110
BLAST score
                    430
E value '
                    2.0e-42
Match length
                    153
% identity
                    58
NCBI Description
                    (AC003114) T12M4.6 [Arabidopsis thaliana]
Seq. No.
                    33055
                    313341 1.R1040
Contig ID
5'-most EST
                    jC-qmle01810002a07d1
                    33056
Seq. No.
                    313466 1.R1040
Contig ID
5'-most EST
                    jC-qmle01810047b10a1
                    33057
Seq. No.
                    313468 1.R1040
Contig ID
5'-most EST
                    jC-gmf102220128h09a1
                    33058
Seq. No.
                    313520 1.R1040
Contig ID
5'-most EST
                    jC-gmf102220130d03a1
Method
                    BLASTX
                    q2467272
NCBI GI
BLAST score
                    294
E value
                    2.0e-26
Match length
                    183
% identity
                    24
NCBI Description
                    (299759) hypothetical protein [Schizosaccharomyces pombe]
                    33059
Seq. No.
                    313560 1.R1040
Contig ID
5'-most EST
                    jC-gmf\overline{1}02220130f07d1
Seq. No.
                    33060
Contig ID
                    313626 1.R1040
5'-most EST
                    jC-gmf\overline{1}02220131a10d1
                    33061
Seq. No.
Contig ID
                    313663 1.R1040
5'-most EST
                    jC-gmf\overline{1}02220131f01d1
Method
                    BLASTX
                    g4530126
NCBI GI
```

```
4.0e-40
E value
Match length
                   140
                   56
% identity
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
                   33062
Seq. No.
Contig ID
                   313667 1.R1040
5'-most EST
                   uC-gmrominsoy0001h10a1
Seq. No.
                   33063
                   313704 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220132aa03d1
Seq. No.
                   33064
                   313778 1.R1040
Contig ID
                   jC-gmf\overline{1}02220132ae10a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g167227
BLAST score
                   212
                   1.0e-115
E value
Match length
                   460
% identity
                   87
NCBI Description
                   Canavalia ensiformis urease (ure) mRNA, complete cds
                   33065
Seq. No.
                   313847 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220133f09a1
                   33066
Seq. No.
Contig ID
                   313851 1.R1040
5'-most EST
                   uC-gmropic104d10b1
Method
                   BLASTX
NCBI GI
                   g1773014
BLAST score
                   670
E value
                   2.0e-70
Match length
                   217
% identity
                   62'
NCBI Description
                   (Y10338) chloride channel Stclc1 [Solanum tuberosum]
                   33067
Seq. No.
Contig ID
                   313964 1.R1040
5'-most EST
                   jC-gmf102220138a06d1
                   33068
Seq. No.
                   313966_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910008h03a1
Method
                   BLASTX
NCBI GI
                   q4558550
BLAST score
                   659
                   3.0e-69
E value
Match length
                   156
% identity
                   (AC007138) putative protein transport factor [Arabidopsis
NCBI Description
                   thaliana]
```

33069

Seq. No.

```
314024 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810048c01d1 .
                   33070
Seq. No.
                   314102 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220139d01d1
Seq. No.
                   33071
                   314128 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220139g07a1
                   33072
Seq. No.
                   314143 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220139h05d1
                   33073
Seq. No.
                   314172 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220140c03d1
Seq. No.
                   33074
                   314180 1.R1040
Contig ID
5'-most EST
                   q5510346
Method
                   BLASTX
NCBI GI
                   q509810
BLAST score
                   145
E value.
                   5.0e-09
                   38
Match length
                   71
% identity
                   (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33075
                   314242 1.R1040
Contig ID
                   jC-qmf102220141d01d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2104674
BLAST score
                   38
E value
                   5.0e-12
Match length
                   134
% identity
                   86
NCBI Description V.faba mRNA for transcription factor containing bZIP
Seq. No.
                   314259 1.R1040
Contig ID
5'-most EST
                   jC-gmf\overline{1}02220141d11d1
Seq. No.
                   33077
                   314362 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220142d05d1
                   33078
Seq. No.
                   314363 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220142c06a1
Method
                   BLASTN
                   g3641869
NCBI GI
BLAST score
                   133
                   1.0e-68
E value
                   277
Match length
```

Seq. No.

Contig ID

```
% identity
                   Cicer arietinum epicotyl EST, clone Can133
NCBI Description
                   33079
Seq. No.
                   314365 1.R1040
Contig ID
                   jC-gmf\overline{1}02220142c07d1
5'-most EST
                   33080
Seq. No.
                   314394 1.R1040
Contig ID
                   jC-gmf\overline{1}02220142e04a1
5'-most EST
                   33081
Seq. No.
                   314409 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220142f02a1
                   33082
Seq. No.
Contig ID
                   314467 1.R1040
5'-most EST
                   g5510140
Seq. No.
                   33083
                   314477 1.R1040
Contig ID
                   iC-qmf102220143b08a1
5'-most EST
Seq. No.
                   33084
                   314488 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220143c03d1
                   33085
Seq. No.
                   314518 1.R1040
Contig ID
                   jC-gmf\overline{1}02220143d12a1
5'-most EST
                   33086
Seq. No.
                   314546 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220143f06a1
Method
                   BLASTX
NCBI GI
                   q2147484
BLAST score
                   359
                   6.0e-34
E value
                   93
Match length
% identity
                   homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                   homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                   33087
Seq. No.
                   314584 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400055e10d1
Method
                   BLASTX
NCBI GI
                   q2811226
BLAST score
                   339
E value
                   1.0e-31
Match length
                   94
% identity
                   (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi 2811232
NCBI Description
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
                   33088 `
```

314665 1.R1040

```
5'-most EST
                   jC-gmf102220144g10a1
                   33089
Seq. No.
                   314716 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220145e07a1
                   33090
Seq. No.
                   314729 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220145g05a1
Seq. No.
                   33091
                   314822 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy010h04b1
Seq. No.
                   33092
                   314831 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220146h06a1
                   BLASTX
Method
                   g1351945
NCBI GI
BLAST score
                   230
                   5.0e-19
E value
                   69
Match length
                   68
% identity
NCBI Description
                   FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
                   APETALA2 protein [Arabidopsis thaliana]
                   >gi_2464888_emb_CAB16765_ (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
                   33093
Seq. No.
                   314910 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810016b08a1
Method
                   BLASTX
                   g556853
NCBI GI
BLAST score
                   189
E value
                   4.0e-14
Match length
                   154
% identity:
                   34
                 (Z37996) incomplete orf, len: 744, CAI: 0.14 [Saccharomyces
NCBI Description
                  cerevisiae]
                   33094
Seq. No.
                   314911 1.R1040
Contig ID
                   jC-gmle01810016b07d1
5'-most EST
                   33095
Seq. No.
                   314912_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810016b10a1
Method
                   BLASTX
NCBI GI
                   g4531442
BLAST score
                   277
E value
                   2.0e-24
Match length
                   162
                   43
% identity
NCBI Description
                   (AC006224) hypothetical protein [Arabidopsis thaliana]
                   33096
Seq. No.
```

314913 1.R1040

Contig ID

```
5'-most EST
                  jC-gmle01810016a09d1
                  33097
Seq. No.
                  314932 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810016d01a1
Seq. No.
                  33098
                  314938 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910052e01a1
Method
                  BLASTN
                  g310560
NCBI GI
BLAST score
                  57
                   6.0e-23
E value
Match length
                  57
                  100
% identity
NCBI Description
                  Soybean ascorbate peroxidase mRNA, complete cds
Seq. No.
                  33099
                  314979_1.R1040
Contig ID
5'-most EST
                  jC-gmle01810000f04a1
Method
                  BLASTX
NCBI GI
                  g133872
BLAST score
                  180
E value
                   4.0e-13 ↔
                  125
Match length
% identity
                  31
                  30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                  >gi 282838 pir S26494 ribosomal protein S1, chloroplast -
                  spinach >gi_322404_pir_A44121 small subunit ribosomal
                  protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                  >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                  33100
                  314985 1.R1040
Contig ID
                  jC-gmle01810000f08a1
5'-most EST
Method
                  BLASTX
                  q1477565
NCBI GI
BLAST score
                  191
                  2.0e-14
E value
Match length
                  143
% identity
NCBI Description
                   (U50078) p532 [Homo sapiens]
                  >gi 4557026 ref NP 003913.1 pHERC1 hect (homologous to the
                  E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                   (CHC1)-like domain (RLD)
                  33101
Seq. No.
                  314987 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810065b03a1
                  BLASTN
Method
                  g402243
NCBI GI
BLAST score
                  184
E value
                  7.0e-99
Match length
                  455
```

85

% identity

Contig ID 5'-most EST

```
NCBI Description Neurospora crassa 740R23 1A ubiquitin/ribosomal protein
                  S27a fusion protein (ubi/crp-6) mRNA, complete cds
Seq. No.
                  314990 1.R1040
Contig ID
                  jC-gmle01810016f12a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1168347
BLAST score
                  235
E value
                  1.0e-19
Match length
                  94
% identity
                  53
                  ALCOHOL DEHYDROGENASE (ADH-T) >gi_282375_pir__A42654
NCBI Description
                  alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus
                  stearothermophilus >gi_216230_dbj_BAA14411_ (D90421)
                  alcohol dehydrogenase [Bacillus stearothermophilus]
                  33103
Seq. No.
                  315019 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810000h12a1
Method
                  BLASTX
NCBI GI
                  q1723472
BLAST score
                  141
E value
                  1.0e-08
Match length
                  75
% identity
                  HYPOTHETICAL 25.9 KD PROTEIN C6C3.07 IN CHROMOSOME I
NCBI Description
                  >gi_1204247_emb_CAA93620_ (Z69731) unknown
                  [Schizosaccharomyces pombe]
Seq. No.
                  33104
                  315024 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810001a05a1
Method
                  BLASTX
NCBI GI
                  g3461817
BLAST score
                  318
E value
                  2.0e-29
Match length
                  141
% identity
                  46
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
                  33105
Seq. No.
                  315026 1.R1040
Contig ID
                  jC-gmle01810091c11a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4335745
BLAST score
                  303
E value
                  2.0e-27
Match length
                  134
% identity
                  (AC006284) putative hydrolase (contains an
NCBI Description
                  esterase/lipase/thioesterase active site serine domain
                  (prosite: PS50187) [Arabidopsis thaliana]
                  33106
Seq. No.
```

315033 1.R1040

jC-qmle01810017h02d2

Contig ID

```
Method
                   BLASTX
NCBI GI
                   q1813489
BLAST score
                   154
E value
                   4.0e-10
                   70
Match length
% identity
                   50
                   (U64312) amidase [Bacillus firmus]
NCBI Description
                   33107
Seq. No.
Contig ID
                   315060 1.R1040
5'-most EST
                   jC-qmle01810001c11d1
Seq. No.
                   33108
                   315071 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810001d10a1
Seq. No.
                   33109
                   315072 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810048c11a1
Seq. No.
                   33110
Contig ID
                   315081 1.R1040
5'-most EST
                   jC-gmle01810001e09d1
                   33111
Seq. No.
                   315083 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400004c11d1
                   33112
Seq. No.
Contig ID
                   315086 1.R1040
                   jC-gmle01810017c11a2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006910
BLAST score
                   196
E value
                   6.0e-15
Match length
                   72
% identity
                   54
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   33113
Contig ID
                   315087 1.R1040
5'-most EST
                   jC-gmle01810001f03a1
                   33114
Seq. No.
                   315098 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810001g01a1
Seq. No.
                   33115
                   315099 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810001h01a1
Seq. No.
                   33116
                   315123 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810001h10d1
Seq. No.
                   33117
```

315174 1.R1040

5'-most EST

```
jC-qmle01810018c11a2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2275204
BLAST score
                   240
E value
                   8.0e-20
Match length
                   53
% identity
                   79
NCBI Description
                   (AC002337) DNA binding protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   33118
                   315191 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810041h12d1
Seq. No.
                   33119
                   315221 1.R1040
Contig ID
5'-most EST
                   fC-gmro700763905d4
                   33120
Seq. No.
                   315245 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810002h07a1
Seq. No.
                   33121
                   315252 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810008f04d1
Method
                   BLASTX
NCBI GI
                   a4510389
BLAST score
                   618
                   3.0e-64
E value
Match length
                   172
% identity
                   (AC007017) putative solute carrier protein [Arabidopsis
NCBI Description
                   thaliana]
                   33122
Seq. No.
Contig ID
                   315259 1.R1040
                   jC-gmle01810019g05a2
5'-most EST
                   33123
Seq. No.
                   315277 1.R1040
Contig ID
                   jC-qmle01810083f02d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3822403
BLAST score
                   409
                   5.0e-40
E value
                   106
Match length
% identity
NCBI Description
                   (AF087932) hydroperoxide lyase [Arabidopsis thaliana]
Seq. No.
                   33124
                   315278 1.R1040
Contig ID
5'-most EST
                   uC-gmropic014b08b1
Seq. No.
                   33125
                   315293 1.R1040
Contig ID
```

--:-

jC-gmle01810019g12a2

5'-most EST

```
33126
Seq. No.
                   315297 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810003h03a1
Method
                   BLASTX
NCBI GI
                   g3063473
BLAST score
                   345
E value
                   2.0e-32
Match length
                   97
% identity
NCBI Description
                   (AC003981) F22013.35 [Arabidopsis thaliana]
Seq. No.
                   315313 1.R1040
Contig ID
5'-most EST
                   iC-gmle01810004a08d1
Method
                   BLASTX
NCBI GI
                   q1352934
BLAST score
                   194
                   8.0e-15
E value
Match length
                   61
% identity
                   59
                   HYPOTHETICAL 161.2 KD PROTEIN IN NMD5-HOM6 INTERGENIC
NCBI Description
                   REGION >gi_1078403_pir__S57160 sulfite reductase homolog
                   YJR137c - yeast (Saccharomyces cerevisiae)
                   >gi_1015876_emb_CAA89669_ (Z49637) ORF YJR137c
                   [Saccharomyces cerevisiae]
                   33128
Seq. No.
                   315315 1.R1040
Contig ID
                   jC-gmle01810004a10a1
5'-most EST
                   BLASTX
Method
                   g3426037
NCBI GI
BLAST score
                   256
                   3.0e-37
E value
Match length
                   169
% identity
                   35
NCBI Description
                   (AC005168) putative ABC transporter protein [Arabidopsis
                   thaliana]
                   33129
Seq. No.
                   315317 1.R1040
Contig ID
                   jC-gmle01810004a11d1
5'-most EST
Method
                   BLASTX
                   g1931652
NCBI GI
BLAST score
                   677
                   4.0e-71
E value
Match length
                   226
% identity
                   63
NCBI Description
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
                   [Arabidopsis thaliana]
                   33130
Seq. No.
                   315354 1.R1040
Contiq ID
5'-most EST
                   jC-qmle01810004c09d1
                   33131
Seq. No.
                   315383 1.R1040
Contig ID
```

jC-gmle01810094b07d1

```
Method
                   BLASTX
NCBI GI
                   q1399380
BLAST score
                   368
E value
                   3.0e-35
                   93
Match length
                   69
% identity
                   (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                   methyltransferase [Glycine max]
Seq. No.
                   33132
Contig ID
                   315395 1.R1040
5'-most EST
                   jC-gmle01810004f06d1
                   33133
Seq. No.
Contig ID
                   315467 1.R1040
5'-most EST
                   jC-gmle01810005b05d1
                   33134
Seq. No.
                   315509 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810005d07d1
                   33135
Seq. No.
                   315547 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810005f08d1
                   33136
Seq. No.
Contig ID
                   315604 1.R1040
5'-most EST
                   g4397395
                   BLASTX
Method
NCBI GI
                   g1621461
BLAST score
                   547
E value
                   6.0e-56
Match length
                   224
                   50
% identity
NCBI Description
                   (U73103) laccase [Liriodendron tulipifera]
                   33137
Seq. No.
Contig ID
                   315608 1.R1040
5'-most EST
                   g5677524
                   33138
Seq. No.
                   315630 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810006b11d1
                   33139
Seq. No.
                   315651 1.R1040
Contig ID
                   jC-gmle01810062d11d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2864618
BLAST score
                   156
E value
                   2.0e-10
Match length
                   44
% identity
                   61
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
                   33140
Seq. No.
```

315658 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   jC-qmle01810006d04a1
                  33141
Seq. No.
Contig ID
                   315670 1.R1040
5'-most EST
                   jC-gmle01810006d11d1
                   33142
Seq. No.
                   315704 1.R1040
Contig ID
5'-most EST
                   jC-gmr002910006b01a1
Method
                   BLASTX
NCBI GI
                   q4092534
BLAST score
                   317
                   6.0e-29
E value
Match length
                   221
% identity
                   35
                   (AF097830) suppressor of forked protein; Su(f) protein
NCBI Description
                   [Drosophila virilis]
Seq. No.
                   33143
Contig ID
                   315743 1.R1040
5'-most EST
                   jC-gmle01810007a04a1
                   33144
Seq. No.
                   315749 1.R1040
Contig ID
                   jC-gmle01810007f05a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1084643
BLAST score
                   347
E value
                   1.0e-32
                   98
Match length
                   62
% identity
NCBI Description
                  STE23 protein - yeast (Saccharomyces cerevisiae) >gi_625109
                   (U19729) Ste23p [Saccharomyces cerevisiae]
                   33145
Seq. No.
                   315765_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810007c04a1
Method
                  BLASTX
                   g3738306
NCBI GI
BLAST score
                   605
E value
                   7.0e-63
Match length
                  166
% identity
                   63
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33146
Contig ID
                   315822 1.R1040
5'-most EST
                   jC-gmle01810007h12d1
Seq. No.
                   33147
                   315834 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810008b02d1
Seq. No.
                   33148
Contig ID
                   315836 1.R1040
```

jC-gmle01810027b04d1

```
Seq. No.
                   33149
                   315911 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810009f03a1
Seq. No.
                   33150
                   315948 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy070h04b1
Seq. No.
                   33151
Contig ID
                   315949 1.R1040
5'-most EST
                   jC-gmle01810009c08d1
Method
                  BLASTX
NCBI GI
                  q3335367
BLAST score
                  256
E value
                   4.0e-22
Match length
                  59
% identity
NCBI Description
                   (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33152
                  315965 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810009d06d1
                  33153
Seq. No.
                  316063 2.R1040
Contig ID
5'-most EST
                  jC-gmle01810092d11d1
                  33154
Seq. No.
                  316063 3.R1040
Contig ID
5'-most EST
                   jC-gmle01810045f08d1
Seq. No.
                  33155
                  316074 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810010f10d1
                  33156
Seq. No.
Contig ID
                  316076 1.R1040
5'-most EST
                  jC-gmle01810010c09a1
                  33157
Seq. No.
                  316194 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810011c07a1
Method
                  BLASTX
NCBI GI
                  g3123100
BLAST score
                  197
E value
                  5.0e-15
Match length
                  65
% identity
                  58
NCBI Description
                  HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I
                  >gi 4490640_emb_CAB11472.1_ (Z98762) SPAC4A8.02c, unknown,
                  len:142aa, similar eg. to YJBQ _ECOLI, P32698, hypothetical
                  15.7 kd protein, (138aa), fast a scores, opt:403, E():
                  2.4e-32, (41.0% identity in 134 aa overlap)
                   [Schizosaccharomyces pombe]
```

33158

316212 1.R1040

Seq. No. Contig ID

Seq. No.

33167

<u>.</u> .

```
5'-most EST
                   jC-gmle01810011d06a1
                   33159
Seq. No.
                   316221 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400049c09a1
                   33160
Seq. No.
                   316282 1.R1040
Contig ID
5'-most EST >
                   g4260071
                   BLASTX
Method
NCBI GI
                   q3297815
BLAST score
                   187
E value
                   4.0e-17
Match length
                   72
% identity
                   65
                   (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   33161
Seq. No.
                   316305 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810012a07d1
                   33162
Seq. No.
Contig ID
                   316313_1.R1040
5'-most EST
                   jC-gmst02400031c03a1
                                                                     . . .
Seq. No.
                   33163
                   316313 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810012b02a1
                   33164
Seq. No.
Contig ID
                   316313 3.R1040
5'-most EST
                   uC-gmflminsoy019h04b1
                   33165
Seq. No.
                   316350_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810012d05a1
Method
                   BLASTX
NCBI GI
                  g2924521
BLAST score
                   269
E value
                   3.0e-23
Match length
                   134
                   45
% identity
NCBI Description
                   (AL022023) putative protein [Arabidopsis thaliana]
                   33166
Seq. No.
                   316422_1.R1040
Contig ID
5'-most EST
                   fC-gmst700839356d1
Method
                   BLASTX
NCBI GI
                   g3256035
BLAST score
                   470
E value
                   1.0e-46
Match length
                   199
                   47
% identity
NCBI Description
                   (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor]
```

```
316489 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810026f10d1
Seq. No.
                   316517 1.R1040
Contig ID
                   g4303947
5'-most EST
Seq. No.
                   33169
                   316537 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810014f11d1
Method
                   BLASTX
NCBI GI
                   q2289786
BLAST score
                   189
E value
                   5.0e-14
Match length
                   82
% identity
                   45
NCBI Description
                   (D88153) HYA22 [Homo sapiens]
                   33170
Seq. No.
Contig ID
                   316631 1.R1040
5'-most EST
                   jC-gmle01810036g02d1
Seq. No.
                   33171
                   316754 1.R1040-
Contig ID
5'-most EST
                   jC-qmle01810048g09a1
                   33172
Seq. No.
                   316847 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810017h04a2
Seq. No.
                   33173
                   317053 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810042h07d1
                   33174
Seq. No.
Contig ID
                   317065 1.R1040
5'-most EST
                   jC-qmle01810020b10a1
                   33175
Seq. No.
                   317070 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810020b12d1
Seq. No.
                   33176
                   317076 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810020c06a1
Seq. No.
                   33177
                   317092 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810020g06d1
Method
                   BLASTX
NCBI GI
                   q3608147
BLAST score
                   159
E value
                   1.0e-10
Match length
                   79
                   43
% identity
NCBI Description
                   (AC005314) putative chloroplast 31 kDa ribonucleoprotein
```

precursor [Arabidopsis thaliana]

NCBI Description

```
33178
Seq. No.
Contig ID
                   317141 1.R1040
5'-most EST
                   jC-gmst02400060a05d1
Method
                   BLASTX
NCBI GI
                   g2947062
BLAST score
                   208
E value
                   2.0e-16
Match length
                   .79
% identity
                   54
NCBI Description
                   (AC002521) unknown protein [Arabidopsis thaliana]
                   33179
Seq. No.
Contig ID
                   317164_1.R1040
5'-most EST
                   uC-gmrominsoy186g02b1
Method
                   BLASTX
NCBI GI
                   g2191175
BLAST score
                   189
E value
                   5.0e-14
Match length
                   123
                   37.
% identity
NCBI Description
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
                   thaliana]
Seq. No.
                   33180
Contig ID
                   317164 2.R1040
5'-most EST
                   jC-gmle01810020g12d1
Method
                   BLASTX
NCBI GI
                   q2335096
BLAST score
                   147
E value
                   5.0e-09
Match length
                   129
% identity
NCBI Description
                   (AC002339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33181
Contig ID
                   317227 1.R1040
5'-most EST
                   uC-gmropic056d09b1
Seq. No.
                   33182
Contig ID
                   317248 1.R1040
5'-most EST
                   jC-gmle01810021c12d1
Seq. No.
                   33183
Contig ID
                   317251 1.R1040
5'-most EST
                   jC-gmle01810021d02d1
Seq. No.
                   33184
Contig ID
                   317274 1.R1040
5'-most EST
                   jC-gmle01810021e07d1
Method
                   BLASTX
NCBI GI
                   g2213586
BLAST score
                   177
E value
                   1.0e-12
                   73
Match length
% identity
                   49
```

(AC000348) T7N9.6 [Arabidopsis thaliana]

BLAST score

303

```
Seq. No.
                   33185
Contig ID
                   317285 1.R1040
5'-most EST
                   jC-gmle01810073a09d1
Method
                   BLASTX
                   q3894197
NCBI GI
BLAST score
                   303
                   1.0e-27
E value
Match length
                   64
% identity
                   84
NCBI Description
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33186
                   317316 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810091e09d1
                   33187
Seq. No.
Contig ID
                   317348 1.R1040
5'-most EST
                   jC-gmro02910001a02d1
Seq. No.
                   33188
Contig ID
                   317350 1.R1040
5'-most EST
                   jC-gmle01810022b07a1
Seq. No.
                   33189
Contig ID
                   317379 1.R1040
5'-most EST
                   q5687996
Method
                   BLASTN
NCBI GI
                   q4115370
BLAST score
                   41
E value
                   1.0e-13
Match length
                   89
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F27D4 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   33190
Contig ID
                   317380 1.R1040
5'-most EST
                   jC-gmle01810022c05a1
                   33191
Seq. No.
Contig ID
                   317481 1.R1040
5'-most EST
                   jC-gmle01810055b02a1
Method
                   BLASTX
NCBI GI
                   q3355467
BLAST score
                   267
E value
                   4.0e-23
Match length
                   139
% identity
NCBI Description
                   (AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   317486 1.R1040
5'-most EST
                   jC-gmle01810023b05a1
Method
                   BLASTX
NCBI GI
                   g2501644
```

5'-most EST

```
2.0e-27
E value
Match length .
                  153
% identity
                   42
                  URICASE (URATE OXIDASE) >gi_2131155_pir_ JC5140 urate
NCBI Description
                  oxidase (EC 1.7.3.3) - yeast (Pichia jadinii)
                  >gi 1741860 dbj BAA06804 (D32043) uricase [Candida utilis]
Seq. No.
                  317512 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810023d07a1
Seq. No.
                   33194
                  317513 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810023d07d1
Seq. No.
                   317531 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810023e06a1
Seq. No.
                  33196
                   317597 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810093b04a1
Seq. No.
                   33197
                   317651 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810024f10a1
                   33198
Seq. No.
                   317682 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400068d08d1
Method
                  BLASTX
NCBI GI
                   g2262113
BLAST score
                   237
                   8.0e-20
E value
Match length
                   56
% identity
                   73
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   33199
Seq. No.
                   317728 1.R1040
Contig ID
                   jC-gmle01810025c04a1
5'-most EST
Method
                  BLASTN
                  g170073
NCBI GI
BLAST score
                   76
E value
                   1.0e-34
Match length
                  118
% identity
                   92
NCBI Description
                  Soybean calmodulin (SCaM-3) mRNA, complete cds
Seq. No.
                   33200
                   317748 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910007d04d1
Seq. No.
                  33201
                  317804 1.R1040
Contig ID
```

jC-gmle01810025g10d1

Seq. No.

33210

```
33202
Seq. No.
                  317832 1.R1040
Contig ID
                  jC-gmle01810026a08d1
5'-most EST
                  33203
Seq. No.
                  317833 1.R1040
Contig ID
                  g5126688
5'-most EST
                  33204
Seq. No.
                  317836 1.R1040
Contig ID
                  jC-gmle01810027d04a1
5'-most EST
                  BLASTN
Method
                  g3378649
NCBI GI
                  35
BLAST score
                  3.0e-10
E value
Match length
                  119
                  87
% identity
                  M.sativa mRNA translated from abscisic activated gene
NCBI Description
                  33205
Seq. No.
                  317849 1.R1040
Contig ID
                  jC-gmle01810026b06a1
5'-most EST
Method
                  BLASTX
                  g417674
NCBI GI
                  758
BLAST score
                  1.0e-80
E value
                  238
Match length
% identity
                   62
                  60S RIBOSOMAL PROTEIN L7 >gi 103356 pir S21500 ribosomal
NCBI Description
                  protein L7.e - fruit fly (Drosophila melanogaster)
                  >qi 8484 emb CAA33207 (X15109) ribosomal protein
                   [Drosophila melanogaster]
                   33206
Seq. No.
                   317884 1.R1040
Contig ID
                   jC-gmle01810026d06a1
5'-most EST
Seq. No.
                   33207
Contig ID
                   317935 1.R1040
5'-most EST
                   jC-gmle01810026h03a1
Method
                   BLASTX
NCBI GI
                   g2213611
BLAST score
                   283
                   2.0e-25
E value
Match length
                   73
% identity
                   (AC000103) F21J9.5 [Arabidopsis thaliana]
NCBI Description
                   33208
Seq. No.
Contig ID
                   317938 1.R1040
                   jC-gmle01810027a01a1
5'-most EST
Seq. No.
                   33209
                   317940 1.R1040
Contig ID
                   jC-gmle01810042h08d1
5'-most EST
```

```
317982 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400002e02d1
                   33211
Seq. No.
                   317997 1.R1040
Contig ID
                   jC-gmle01810035f12d1
5'-most EST
                   33212
Seq. No.
Contig ID
                   318029 1.R1040
                   jC-gmle01810027f09d1
5'-most EST
                   33213
Seq. No.
                   318075 1.R1040
Contig ID
                   jC-gmle01810028b02a1
5'-most EST
Seq. No.
                   33214
                   318100 1.R1040 ·
Contig ID
5'-most EST
                   jC-gmst02400076d09a1
Method
                   BLASTX
NCBI GI
                   g2444174
                   604
BLAST score
                   3.0e-78
E value
Match length
                   176
                   79
% identity
                   (U94781) unconventional myosin [Helianthus annuus]
NCBI Description
Seq. No.
                   33215
                   318109 1.R1040
Contig ID
                   jC-gmro02910061e02d1
5'-most EST
                   BLASTX
Method
                   g2832241
NCBI GI
BLAST score
                   186
E value
                   1.0e-13
                   87
Match length
                   28
% identity
                   (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
NCBI Description
                   thaliana]
                   33216
Seq. No.
                   318121 1.R1040
Contig ID
                   jC-gmle01810064b01a1
5'-most EST
                   33217
Seq. No.
                   318132 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810035f08d1
                   33218
Seq. No.
Contig ID
                   318144 1.R1040
5'-most EST
                   jC-gmle01810028f05d1
                   33219
Seq. No.
                   318146 1.R1040
Contig ID
                   uC-gmropic0001g04a1
5'-most EST
Method
                   BLASTX
                   g2088651
NCBI GI
BLAST score
                   201
```

3.0e-15 '

E value

Contig ID

```
Match length
                   65
                   55
% identity
NCBI Description
                   (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
                   33220
Seq. No.
                   318151 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810028f09d1
                   33221
Seq. No.
                   318185 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810028h08d1
                   BLASTX
Method
NCBI GI
                   g3935150
BLAST score
                   321
E value
                   1.0e-29
Match length
                   75
                   77
% identity
                   (AC005106) T25N20.14 [Arabidopsis thaliana]
NCBI Description
                   33222
Seq. No.
Contig ID
                   318209 1.R1040
                   jC-gmle01810029b01a1
5'-most EST
                   33223
Seq. No.
Contig ID
                   318210 1.R1040
                   jC-gmle01810029b01d1
5'-most EST
                   33224
Seq. No.
                   318223 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810029b10d1
                   33225
Seq. No.
                   318254 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810029d08d1
Seq. No.
                   33226
                   318279 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810029f05a1
                   33227
Seq. No.
Contig ID
                   318349 1.R1040
5'-most EST
                   jC-gmle01810030c02d1
                   33228
Seq. No.
                   318370 1.R1040
Contig ID
5'-most EST
                   fC-gmst700605413r1
Method
                   BLASTX
NCBI GI
                   q2746079
BLAST score
                   256
E value
                   5.0e-22
Match length
                   65
% identity
NCBI Description
                   (AF015310) BTH1 [Brassica napus]
                   33229
Seq. No.
```

318376 1.R1040

E value

```
5'-most EST
                   jC-gmle01810030d11a2
                   BLASTX
Method
                   q3413511
NCBI GI
BLAST score
                   441
                   1.0e-43
E value
                   129
Match length
% identity
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                   oleracea]
                   33230
Seq. No.
                   318377 1.R1040
Contig ID
                   jC-gmle01810030d11d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4220528
                   506
BLAST score
                   2.0e-51
E value
Match length
                   106
                   89
% identity
                   (AL035356) glucose-6-phosphate isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   33231
Seq. No.
                   318388 1.R1040
Contig ID ....
5'-most EST
                   jC-gmle01810078h03d1
Seq. No.
                   33232
                   318452 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810031a05a2
                   BLASTX
Method ·
NCBI GI
                   g2262157
BLAST score
                   311
                   2.0e-44
E value
Match length
                   173
                   60
% identity
                   (AC002329) putative ligand-gated ion channel protein
NCBI Description
                   [Arabidopsis thaliana]
                   33233
Seq. No.
                   318458 1.R1040
Contig ID
                   jC-gmle01810033e03d1
5'-most EST
Seq. No.
                   33234
                   318459 1.R1040
Contig ID
                   jC-gmle01810033e05d1
5'-most EST
                   33235
Seq. No.
Contig ID
                   318490 1.R1040
5'-most EST
                   jC-gmle01810033g05d1
                   33236
Seq. No.
                   318511_1.R1040
Contig ID
                   jC-gms\(\overline{t}\) 02400016c09d1
5'-most EST
Method
                   BLASTX
                   g4262162
NCBI GI
                   277
BLAST score
```

2.0e-24

```
Match length
                  69
                  72
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  33237
Seq. No.
                  318536 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810033e09d1
                  33238
Seq. No.
                  318552 1.R1040
Contig ID
                  jC-gmle01810033d03d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3941543
BLAST score
                  381
E value
                  1.0e-36
Match length
                  90
% identity
                   (AF069497) pelota [Arabidopsis thaliana]
NCBI Description
                  >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                  [Arabidopsis thaliana]
Seq. No.
                  33239
                  318560 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810031h03d1
                  33240
Seq. No.
                  318570 1.R1040
Contig ID
                  jC-gmle01810032a01d1
5'-most EST
Seq. No.
                  33241
                  318588 1.R1040
Contig ID
5'-most EST
                  q5752954
                  BLASTX
Method
NCBI GI
                  g2462839
BLAST score
                  156
E value
                  4.0e-10
Match length
                  63
% identity
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33242
                  318597 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810032c09d1
Seq. No.
                  33243
Contig ID
                  318597_2.R1040
5'-most EST
                  jC-qmro02910046h05d1
Seq. No.
                  33244
Contig ID
                  318603 1.R1040
5'-most EST
                  jC-qmle01810033g06d1
Seq. No.
                  33245
                  318605 1.R1040
Contig ID
```

jC-gmle01810033g10d1

NCBI Description

```
33246
Seq. No.
                   318654 1.R1040
Contig ID
                   jC-gmle01810094f09d1
5'-most EST
                   33247
Seq. No.
                   318680 1.R1040
Contig ID
                   jC-gmle01810033b01a2
5'-most EST
                   33248
Seq. No.
                   318697 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810033c01d1
Seq. No.
                   33249
                   318742 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810033e08a2
                   33250
Seq. No.
                   318748 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810033e12d1
                   33251
Seq. No.
                   318801_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810034a06d1
                   33252
Seq. No.
                   318809 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810034a11d1
                   33253
Seq. No.
                   318848 1.R1040
Contig ID
                   jC-gmle01810034e02d1
5'-most EST
                   BLASTX
Method
                   g4559327
NCBI GI
BLAST score
                   257
E value
                   4.0e-22
Match length
                   122
                   48
% identity
NCBI Description
                   (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33254
                   318891 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810034h09d1
Seq. No.
                   33255
                   318919 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810035b04a2
                   33256
Seq. No.
                   318923 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910075g03d1
Method
                   BLASTX
NCBI GI
                   g3935170
BLAST score
                   239
E value
                   4.0e-20
                   59
Match length
                   76
% identity
```

(AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No.

```
Seq. No.
                  33257
                  319060 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810036a12a2
                  33258
Seq. No.
Contig ID
                  319070 1.R1040
                  jC-gmle01810036b12a2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g945086
BLAST score
                  71
E value
                  2.0e-31
Match length
                  107
                  92
% identity
NCBI Description Glycine max transcription factor TFIIB mRNA, complete cds
Seq. No.
                  33259
                  319071 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810036d01d1
                                                                            . :
Method
                  BLASTX
NCBI GI
                  g3063710
BLAST score
                  196
                  5.0e-15
E value
                  59
Match length
% identity
                  53
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33260
                  319074 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810036h02d1
Seq. No.
                  33261
                  319155 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810037c10a2
Method
                  BLASTX
NCBI GI
                  g2262177
BLAST score
                  299
E value
                  5.0e-27
Match length
                  126
% identity
                  59
NCBI Description
                  (ACO02329) hypothetical protein similar to T18A10.3
                  [Arabidopsis thaliana]
Seq. No.
                  33262
                  319184 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810037f08a2
Method
                  BLASTX
NCBI GI
                  g2494301
BLAST score
                  672
                  8.0e-71
E value
Match length
                  161
% identity
                  80
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT
NCBI Description
                  (EIF-2-GAMMA) >gi 1049318 (U37354) initiation factor eIF-2
                  gamma subunit [Schizosaccharomyces pombe]
```

```
319211 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910013f08d1
                   33264
Seq. No.
                   319222 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810038b04d1
Seq. No.
                   33265
                   319231 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810038d07d1
Seq. No.
                   319294 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810040d07a1
Seq. No.
                   319352 1.R1040
Contig ID
                   jC-gmle01810040h10d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3335331
BLAST score
                   36
E value
                   1.0e-10
Match length
                   56
% identity
                   91
                   Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   33268
Seq. No.
                   319356 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810041a02a1
Method
                   BLASTX
NCBI GI
                   g2829870
BLAST score
                   249
                   3.0e-21
E value
Match length
                   89
% identity
                   25
NCBI Description
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
                   33269
Seq. No.
                   319360 1.R1040
Contiq ID
5'-most EST
                   jC-gmle01810041a06a1
                   33270
Seq. No.
                   319429 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810041f11a1
                   BLASTX
Method
NCBI GI
                   q2077896
BLAST score
                   393
E value
                   5.0e-38
Match length
                   153
                   49
% identity
NCBI Description
                   (AB003470) beta-D-glucosidase [Aspergillus kawachii]
Seq. No.
                   33271
                   319467 1.R1040
Contig ID
```

jC-gmle01810042d10a1

```
33272
Seq. No.
                   319482 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810042b06a1
                   33273
Seq. No.
                   319692 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810044c09a1
                   33274 : -
Seq. No.
                   319703 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810043e05d1
Seq. No.
                   33275
                   319706 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810043e07d1
                   33276
Seq. No.
                   319738 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810043g03d1
                   33277
Seq. No.
                   319770 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400073e09d1
Seq. No.
                   33278
                   319818 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810044b11d1
                   33279
Seq. No.
                   319840 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810044c11a1
                   BLASTX
Method
NCBI GI
                   g3560136
BLAST score
                   505
E value
                   3.0e-51
Match length
                   166
% identity
                   (AL031534) 2-isopropylmalate synthase. [Schizosaccharomyces
NCBI Description
                   pombe]
Seq. No.
                   33280
                   319841 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810044c11d1
Seq. No.
                   33281
Contig ID
                   320112 1.R1040
5'-most EST
                   jC-qmle01810046e06a1
Seq. No.
                   33282
                   320136 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810046d05a1
Method
                   BLASTX
NCBI GI
                   q3688186
BLAST score
                   557
                   2.0e-57
E value
Match length
                   139
```

73

% identity

NCBI Description

```
(AL031804) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                     33283
                     320192 1.R1040
 Contig ID
 5'-most EST
                     jC-gmle01810046f05d1
 Method
                     BLASTX
 NCBI GI
                     g4314371
 BLAST score
                     148
 E value
                     1.0e-09
 Match length
                     40
 % identity
                     65
                     (AC006340) putative G9a protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                     33284
                     320313 1.R1040
 Contig ID
 5'-most EST
                     uC-qmropic014b11b1
· Seq. No.
                     33285
 Contig ID
                     320315 1.R1040
                     jC-gms\overline{t}02400020da07d1
 5'-most EST
 Seq. No.
                     33286
 Contig ID
                     320407_1.R1040
 5'-most EST
                     jC-gmle01810048b12d1
 Seq. No.
                     33287
                     320438 1.R1040
 Contig ID
 5'-most EST
                     jC-gmle01810048d09d1
 Seq. No.
                     33288
 Contig ID
                     320446 1.R1040
 5'-most EST
                     jC-gmle01810048e03a1
 Seq. No.
                     33289
                     320447_1.R1040
 Contig ID
 5'-most EST
                     jC-gmle01810048e03d1
 Seq. No.
                     33290
 Contig ID
                     320552 1.R1040
                     jC-gmle01810049d06d1
 5'-most EST
 Seq. No.
                     33291
 Contig ID
                     320558 1.R1040
 5'-most EST
                     jC-gmle01810049e01d1
 Seq. No.
                     33292
 Contig ID
                     320642_1.R1040
                     jC-gmle01810050e10a1
 5'-most EST
 Method
                     BLASTN
 NCBI GI
                     g11576
 BLAST score
                     433
 E value
                     0.0e + 00
 Match length
                     465
 % identity
```

NADH dehydrogenase and ORF

Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,

```
33293
Seq. No.
                   320768 1.R1040
- Contig ID
5'-most EST
                   jC-gmle01810051f07a1
                   33294
Seq. No.
Contig ID
                   320770 1.R1040
5'-most EST
                   jC-gmle01810051f08a1
                   33295
Seq. No.
                   320810 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073b08a1
Seq. No.
                   33296
                   321044 1.R1040
Contig ID
5'-most EST
                   fC-gmro700565358r2
Method
                   BLASTX
NCBI GI
                   g642134
                   299
BLAST score
E value
                   4.0e-27
Match length
                   88
% identity
                   64
NCBI Description
                   (D45355) protein kinase [Arabidopsis thaliana]
                   >gi 3063704 emb CAA18595.1 (AL022537) protein kinase AME3
                   [Arabidopsis thaliana]
                                                                          14.7
                   33297
Seq. No.
                   321155 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy024c03b1
Seq. No.
                   33298
                   321256 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810056a07a1
Method
                   BLASTX
NCBI GI
                   g3445210
BLAST score
                   368
E value
                   4.0e-35
Match length
                   139
                   47
% identity
                   (AC004786) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   33299
Seq. No.
                   321264 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810056b03a1
Method
                   BLASTX
NCBI GI
                   g3892055
BLAST score
                   1195
                   1.0e-132
E value
Match length
                   243
% identity
                   (AC002330) putative transport protein [Arabidopsis
NCBI Description
                   thaliana]
                   33300
Seq. No.
                   321373 1.R1040
Contig ID
```

jC-gmst02400065b02d1

Contig ID

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33301
 Seq. No.
                    321416 1.R1040-
 Contig ID
                    jC-gmro02910067f02d1
5'-most EST
                    33302
 Seq. No.
                    321418 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810059d04d1
 Seq. No.
                    33303
                    321419 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810059d05a1
                    BLASTX
 Method
                    g4432821
 NCBI GI
                    296
 BLAST score
 E value
                    2.0e-26
                    207
 Match length
 % identity
                    40
                    (AC006593) putative transmembrane protein [Arabidopsis
 NCBI Description
                 thaliana]
                    33304
 Seq. No.
                    321438 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810059e03a1
 Seq. No.
                    33305
                    321512 1.R1040
 Contig ID
 5'-most EST
                    jC-qmle01810059h10d1
 Seq. No.
                    33306
                    321531 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810060b01d1
 Seq. No.
                    33307
 Contig ID
                    321560 1.R1040
 5'-most EST
                    jC-gmle01810060c09a1
 Seq. No.
                    33308
 Contig ID
                    321569 1.R1040
 5'-most EST
                    jC-gmle01810060d01d1
 Seq. No.
                    33309
                    321577 1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810087h11a1
 Seq. No.
                    33310
 Contig ID
                    321582 1.R1040
 5'-most EST
                    jC-qmle01810060d09d1
Method
                    BLASTX
 NCBI GI
                    q1871180
 BLAST score
                    280
 E value
                    8.0e-25
Match length
                    131
 % identity
NCBI Description
                    (U90439) unknown protein [Arabidopsis thaliana]
                    33311
Seq. No.
```

321604 1.R1040

```
5'-most EST
                   jC-gmle01810060e11d1
                   BLASTX
Method
                   g2191168
NCBI GI
                   273
BLAST score
                   5.0e-24
E value
Match length
                   70
% identity
                   80
NCBI Description
                   (AF007270) contains similarity to myosin heavy chain
                   [Arabidopsis thaliana]
                   33312
Seq. No.
                   321608 1.R1040
Contig ID
5'-most EST
                   iC-qmro02800027q09d1
Seq. No.
                   33313
                   321627 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810062h02d1
Seq. No.
                   33314
                   321632 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400028c02a1
                   33315
Seq. No.
                   321633 1.R1040
Contig ID
5'-most EST
                   g5752600
Method
                   BLASTX
                   q3702343
NCBI GI
BLAST score
                   555
E value
                   9.0e-57
Match length
                   223
                   53
% identity
                   (ACO05397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   33316
                   321729 1.R1040
Contiq ID
                   jC-gmle01810061h03a1
5'-most EST
Method
                   BLASTX
                   q3482941
NCBI GI
BLAST score
                   215
E value
                   3.0e-17
Match length
                   111
% identity
                   (AC005315) putative ligand-gated ionic channel [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   33317
                   321737 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810061g12a1
                   33318
Seq. No.
                   321798 1.R1040
Contig ID
5'-most EST
                   fC-qmle700685876b1
                   33319
Seq. No.
                   321964 1.R1040
Contig ID
5'-most EST
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jC-gmle01810063d05d1

Contig ID

```
BLASTX
Method
NCBI GI
                   g3786006
BLAST score
                   361
                   2.0e-34
E value
                   83
Match length
                   78
% identity
                   (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33320
                   322022 1.R1040
Contig ID
                   fC-gmro700646449r1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4468151
BLAST score
                   158
E value
                   2.0e-10
Match length
                   56
% identity
                   41
NCBI Description
                   (AJ131999) sucrose synthase [Craterostigma plantagineum]
Seq. No.
                   322035 1.R1040
Contig ID
5'-most EST
                   jC-qmro02800028b04d1
Seq. No.
                   322089 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810064b08d1
Seq. No.
                   322118 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810064c11a1
Seq. No.
                   322148 1.R1040
Contig ID
5'-most EST
                   fC-qmle7000786512d1
Seq. No.
                   33325
                   322182 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810064f11d1
                   33326
Seq. No.
Contig ID
                   322203 1.R1040
5'-most EST
                   q4396088
Method.
                   BLASTX
NCBI GI
                   q3249098
BLAST score
                   207
E value
                   3.0e-16
Match length
                   97
% identity
                   (AC003114) ESTs gb T04610, gb N38459, gb T45174, gb R30481
NCBI Description
                   and gb N64971 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   33327
                   322266 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810065d04d1
Seq. No.
                   33328.
```

322276 1.R1040

```
jC-gmle01810065d12d1
5'-most EST
                                                                   . .
Seq. No.
                  33329
                  322297 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810065f08d1
Method
                  BLASTX
NCBI GI
                  q1408460
BLAST score
                  252
                  1.0e-21
E value
                  124
Match length
                   44
% identity
                   (U40161) type 2A protein serine/threonine phosphatase 55
NCBI Description
                  kDa B regulatory subunit [Arabidopsis thaliana]
                  33330
Seq. No.
                  322310 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810065g11d1
Method
                  BLASTN
NCBI GI
                  g2764523
BLAST score
                  114
                   3.0e-57
E value
Match length
                  342
% identity
                  83
                  Pisum sativum mRNA for Rieske iron-sulfur protein Tic55
NCBI Description
Seq. No.
                  33331
                  322322 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400044q03d1
Seq. No.
                  322344 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810066c12d1
Seq. No.
                  322347 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810066d03d1
Seq. No.
                  322365 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910019a06d1
                  33335
Seq. No.
                  322382 1.R1040
Contig ID
                  jC-qmst02400032h02a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1350528
BLAST score
                  147
E value
                  3.0e-09
Match length
                  39
% identity
                   (L47602) ABA-responsive and embryogenesis-associated gene;
NCBI Description
                  LEA-like protein [Picea glauca]
                  33336
Seq. No.
                  322391 1.R1040
Contig ID
```

jC-gmle01810067a02d1

```
Seq. No.
                   33337
                   322395 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400074f02d1
                   33338
Seq. No.
                   322406 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810073a03d1
Seq. No.
                   .33339
                   322474 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810067g03a1
                   33340
Seq. No.
                   322488 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810067h01d1
Seq. No.
                   33341
                   322501 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400027a09d1
Seq. No.
                   33342
                   322524 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810068b08a1
Seq. No.
                   33343
                   322532 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810068c02a1
Method
                   BLASTX
NCBI GI
                   g1710055
BLAST score
                   328
E value
                   2.0e-30
Match length
                   118
% identity
                   54
NCBI Description
                   RDS1 PROTEIN >gi_1363621_pir__S58477 rds1 protein - fission
                   yeast (Schizosaccharomyces pombe) >gi 1184029 emb CAA54544
                   (X77328) rds1 [Schizosaccharomyces pombe]
Seq. No.
                   33344
                   322554 1.R1040
Contig ID
5'-most EST
                   iC-qmle01810071d01a1
Seq. No.
                   322578 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810068e10d1
Seq. No.
Contig ID
                   322583 1.R1040
5'-most EST
                   jC-qmle01810068f02d1
Seq. No.
                   33347
                   322609 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810068q10d1
Seq. No.
                   322615 1.R1040
Contig ID
```

- 4

jC-gmle01810068h05a1

```
Seq. No.
                   33349
                   322618 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810068h08a1
Seq. No.
                   33350
                   322650 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810069e03d1
Seq. No.
                   33351
                   322682 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810070a11a1
Seq. No.
                   33352
Contig ID
                   322705 1.R1040
5'-most EST
                   jC-qmle01810070c04d1
Method
                   BLASTX
NCBI GI
                   q3924606
BLAST score
                   324
                   1.0e-30
E value
Match length
                  89
                   75
% identity
                   (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   33353
Seq. No.
                   322740_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810070e12a1
Method
                  BLASTX
                  q2827534
NCBI GI
BLAST score
                   685
                   2.0e-72
E value
Match length
                  150
% identity
                  86
NCBI Description
                   (AL021633) predicted protein [Arabidopsis thaliana]
                  33354
Seq. No.
Contig ID
                   322741 1.R1040
5'-most EST
                   jC-gmle01810070f11d1
                   33355
Seq. No.
                   322763 1.R1040
Contig ID
                  jC-gmle01810070g02d1
5'-most EST
                  33356
Seq. No.
                  322775 1.R1040
Contig ID
                  jC-gmle01810070h09a1
5'-most EST
Seq. No.
                  33357
Contig ID
                  322776 1.R1040
                  jC-gmle01810070h09d1
5'-most EST
                  33358
Seq. No.
                  322850 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810071d12a1
                  33359
Seq. No.
                  322857 1.R1040
Contig ID
```

jC-gmle01810071e05d1

Seq. No.

```
33360
Seq. No.
                   322864 1.R1040
Contig ID
                   fC-gmro700565119r2
5'-most EST
                   33361
Seq. No.
                   322871 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810071f03d1
Method
                   BLASTX
NCBI GI
                   q3881976
BLAST score
                   497
                   2.0e-50
E value
Match length
                   118
% identity
                   76
NCBI Description
                   (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                   33362
                   322878 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810071f08d1.
Seq. No.
                   33363
                   322886 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810071g02d1
Seq. No.
                   33364
                   322908 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810071h06d1
Seq. No.
                   33365
                   322922 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810072b04d1
Seq. No.
                   33366
Contig ID
                   322953 1.R1040
5'-most EST
                   jC-qmle01810072d06d1
Method
                  BLASTX
NCBI ĞI
                   q1710055
BLAST score
                  188
E value
                   4.0e-14
Match length
                   100
% identity
                   39
                  RDS1 PROTEIN >gi 1363621 pir S58477 rds1 protein - fission
NCBI Description
                  yeast (Schizosaccharomyces pombe) >gi 1184029 emb CAA54544
                   (X77328) rds1 [Schizosaccharomyces pombe]
Seq. No.
                   33367 -
                   322972 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400006b09d1
Method
                  BLASTX
NCBI GI
                  g2739309
BLAST score
                  394
E value
                   4.0e-38
                  91
Match length
% identity
                   47
NCBI Description
                   (Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]
```

Seq. No.

33377 .

```
Contig ID
                   322994 1.R1040
5'-most EST
                   jC-gmle01810072h12d1
Seq. No.
                   33369
Contig ID
                   323119 1.R1040
5'-most EST
                   jC-gmle01810073h08a1
Method
                   BLASTX
NCBI GI
                   q3402751
BLAST .score
                   283
E value
                   6.0e-25
Match length
                   154
% identity
NCBI Description
                   (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                   33370
Contig ID
                   323132 1.R1040
5'-most EST
                   jC-gmle01810075a03a1
Seq. No.
                   33371
Contig ID
                   323213 1.R1040
5'-most EST
                   jC-gmst02400058b01d1
                   BLASTX
Method
NCBI GI
                   g2344887
BLAST score
                   676
E value
                   5.0e-71
Match length
                   174
                   79
% identity
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33372
Contig ID
                   323233 1.R1040
5'-most EST
                   jC-gmle01810093c06d1
Seq. No.
                   33373
                   323269 1.R1040
Contig ID
5'-most EST
                   fC-qmle700875686r1
                   33374
Seq. No.
Contig ID
                   323279 1.R1040
5'-most EST
                   jC-gmle01810077f11d1
Method
                   BLASTX
NCBI GI
                   g3335348
BLAST score
                   243
                   2.0e-20
E value
Match length
                   71
% identity
NCBI Description
                   (AC004512) T8F5.20 [Arabidopsis thaliana]
                   33375
Seq. No.
                   323283 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810078b07d1
Seq. No.
                   33376
                   323378 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400024e07d1
```

% identity

```
Contig ID
                   323461 1.R1040
5'-most EST
                   uC-gmflminsoy081d01b1
Method
                   BLASTX
NCBI GI
                   q4539389
BLAST score
                   653
E value
                   1.0e-68
Match length
                   136
% identity
                   94
NCBI Description
                   (AL035526) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   323507 1.R1040
5'-most EST
                   jC-gmle01810080d06d1
                   33379
Seq. No.
Contig ID
                   323512 1.R1040
5'-most EST
                   jC-gmle01810080d08d1
Method
                   BLASTX
NCBI GI
                   q4455328
BLAST score
                   239
                   7.0e-20
E value
Match length
                   55
% identity
                   (AL035525) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   33380
Seq. No.
Contig ID
                   323549_1.R1040
5'-most EST
                   jC-gmle01810080f09a1
Method
                   BLASTX
NCBI GI
                   g3511147
BLAST score
                   484
E value
                   1.0e-48
Match length
                   135
% identity
                   67
                   (AF061329) PR-4 type protein [Vitis vinifera]
NCBI Description
                   33381
Seq. No.
Contig ID
                   323558 1.R1040
5'-most EST
                   jC-gmle01810089d11d1
Method
                   BLASTX
NCBI GI
                   g4314384
BLAST score
                   344
E value
                   2.0e-32
Match length
                   101
% identity
                   (AC006232) putative cysteine proteinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   33382
                   323599 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810082a07a1
                   BLASTX
Method
NCBI GI
                   g119791
BLAST score
                   175
E value
                   2.0e-12
                                  Match length
                   101
```

% identity

```
NCBI Description
                   3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR
                   (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)
                   >gi 1084385 pir S22450 3-oxoacyl-[acyl-carrier-protein]
                   reductase (EC 1.1.1.100) precursor - Cuphea lanceolata
                   >gi 18046 emb CAA45866 (X64566) 3-oxoacyl-[acyl-carrier
                   protein] reductase [Cuphea lanceolata]
                   >gi 228929 prf 1814446A beta ketoacyl-ACP reductase
                   [Cuphea lanceolata]
                   33383
 Seq. No.
 Contig ID
                   323601 1.R1040
 5'-most EST
                   jC-gmle01810082a09a1
                   33384
 Seq. No.
                   323697 1.R1040
 Contig ID
 5'-most EST
                   jC-gmle01810082f10a1
 Method
                   BLASTX
 NCBI GI
                   q479413
 BLAST score
                   987
 E value
                   1.0e-107
 Match length
                   216
 % identity
                   91
 NCBI Description myosin-like protein - Arabidopsis thaliana
                   33385
 Seq. No.
 Contig ID
                   323815 1.R1040
 5'-most EST
                   jC-gmle01810083e02d1
                   33386
 Seq. No.
 Contig ID
                   323831 1.R1040
                   jC-gmle01810083e11a1
 5'-most EST
                   33387
 Seq. No.
 Contig ID
                   323850 1.R1040
                   jC-gmle01810083f10a1
-5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q731810
 BLAST score
                   404
 E value
                   3.0e-39
 Match length
                   109
                   67
 % identity
                   PROBABLE 60S RIBOSOMAL PROTEIN YIL052C
 NCBI Description
                   >gi 626886 pir S48427 ribosomal protein L34.e.B, cytosolic
                   - yeast (Saccharomyces cerevisiae) >gi_557816_emb_CAA86170_ .
                   (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77,
                   RL34 RAT P11250 60S RIBOSOMAL PROTEIN L34 [Saccharomyces
                   cerevisiae]
                   33388
 Seq. No.
                   323872 1.R1040
 Contig ID
 5'-most EST
                   jC-gmle01810083g11a1
                   BLASTX
 Method
 NCBI GI
                   g4006908
 BLAST score
                   217
 E value
                   4.0e-17
                   78
 Match length
```

NCBI Description

```
(Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33389
Contig ID
                   323923 1.R1040
5'-most EST
                  jC-gmle01810084c01d1
Seq. No.
                  33390
                  323996 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy109g10b1
Seq. No.
                  33391
                  324020 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810084h03a1
Seq. No.
                   33392
Contig ID
                   324042 1.R1040
5'-most EST
                  jC-gmle01810085a08d1
                  33393
Seq. No.
Contig ID
                   324063 1.R1040
5'-most EST
                  jC-qmle01810085c02a1
Method
                  BLASTX
NCBI GI
                  q2492509
BLAST score
                  159
E value
                  1.0e-10
Match length
                  114
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG >gi 2146083 pir S73497
NCBI Description
                  cell division protein ftsH - Mycoplasma pneumoniae (SGC3)
                   (ATCC 29342) >gi 1673833 (AE000018) Mycoplasma pneumoniae,
                  cell division protein FtsH; similar to Swiss-Prot Accession
                  Number P37476, from B. subtilis [Mycoplasma pneumoniae]
                  33394
Seq. No.
                  324112 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810085f06d1
Seq. No.
                  33395
                  324133 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810085g11a1
Seq. No.
                  33396
Contig. ID
                  324161 1.R1040
5'-most EST
                  jC-gmst02400063d12d1
Seq. No.
                  33397
                  324193 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400036d05d2
Method
                  BLASTX
                  g2191194
NCBI GI
BLAST score
                  132
                  6.0e-09
E value
                  83
Match length
% identity
```

[Arabidopsis thaliana]

(AF007271) contains weak to the SAPB protein (TR:E236624)

NCBI GI

...

```
33398.
Seq. No.
                  324231 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810086e02a1
Seq. No.
                  33399
Contig ID
                  324238 1.R1040
5'-most EST
                  jC-qmle01810086e06a1
                  BLASTX
Method
                  g2765817
NCBI GI
BLAST score
                  382
E value
                  1.0e-36
                  175
Match length
% identity
                  53
NCBI Description
                  (Z95352) AtMlo-hl [Arabidopsis thaliana]
                  >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                  33400
Seq. No.
                  324262 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810086f07a1
Method
                  BLASTX
NCBI GI
                  g3913996
BLAST score
                  305
                  3.0e - 31
E value
                  109
Match length
                  68
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR
NCBI Description
                  >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease
                  Lon [Spinacia oleracea]
                  33401
Seq. No.
                  324322 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810087a08d1
Seq. No.
                  33402
                  324382 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810087d11a1
Seq. No.
                  33403
                  324400 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810087e09a1
Method
                  BLASTX
NCBI GI
                  g1172441
BLAST score
                  167
E value
                  3.0e-11
Match length
                  53
% identity
                  POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883
NCBI Description
                  DNA-binding protein POSF21 - Arabidopsis thaliana
                  >gi_16429_emb_CAA43366 (X61031) posF21 [Arabidopsis
                  thaliana]
                  33404
Seq. No.
                  324501 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810088b11a1
Method
                  BLASTX
```

g3176709

NCBI GI

```
BLAST score
                   209
E value
                   1.0e-16
Match length
                   126
% identity
                   35
NCBI Description
                   (AC002392) putative anthranilate
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
                   33405
Seq. No.
Contig ID
                   324526 1.R1040
5'-most EST
                   jC-qmle01810088d03d1
Method
                   BLASTX
NCBI GI
                   q2765817
BLAST score
                   312
                   2.0e-28
E value
Match length
                   106
% identity
                   67
NCBI Description
                   (Z95352) AtMlo-h1 [Arabidopsis thaliana]
                   >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                   33406
Seq. No.
                   324639 1.R1040
Contig ID
5'-most EST
                  g5752874
Seq. No.
                   33407
Contig ID
                   324663 1.R1040
5'-most EST
                  g5677301
                   33408
Seq. No.
Contig ID
                   324676 1.R1040
5'-most EST
                   jC-gmle01810089c10a1
Seq. No.
                   33409
                   324686 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810089d03a1
Seq. No.
                   33,410
                   324742 1.R1040
Contig ID
                   jC-gmr002910009d08a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1272349
BLAST score
                  346
E value
                  2.0e-32
Match length
                  137
                  52
% identity
NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]
                  33411
Seq. No.
                  324826 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810090c04d1
                  33412
Seq. No.
Contig ID
                  324844 1.R1040
5'-most EST
                  jC-gmle01810090d03d1
Method
                  BLASTX
```

g2809246

Match length

```
276
BLAST score
                   9.0e-27
E value
                   107
Match length
% identity
                   52 -
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                   33413
                   324878 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810090e11a1
                   BLASTX
Method
NCBI GI
                   q4185136
BLAST score
                   411
E value
                   6.0e-40
Match length
                   216
% identity
                   40
                   (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
                   33414
Seq. No.
                   325006 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810091c12d1
Seq. No.
                   33415
                   325066 1.R1040
Contig ID
5'-most EST
                   uC-gmropic100f07b1
Method
                   BLASTX
NCBI GI
                   g2864618
BLAST score
                   413
E value
                   3.0e-40
Match length
                   131
% identity
                   57
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
                   33416
Seq. No.
                   325068 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810091f10d1
Seq. No.
                   33417
                   325075 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810094h06d1
Seq. No.
                   33418
                   325111 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810092a04d1
Seq. No.
                   33419
                   325157 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810092d11a1
Seq. No.
                   33420
                   325265 1.R1040
Contig ID
5'-most EST
                   jC-gmr002800032a06d1
Method
                   BLASTX
NCBI GI
                  g3924602
BLAST score
                  152
E value
                   8.0e-10
```

```
% identity
NCBI Description
                   (AF069442) predicted OR23 protein of unknown function
                   [Arabidopsis thaliana]
Seq. No.
                   33421
Contig ID
                   325314 1.R1040
5'-most EST
                   uC-gmflminsoy054h11b1
                   BLASTX
Method
NCBI GI
                   q4220477
BLAST score
                   284
E value
                   8.0e-38
Match length
                   133
% identity
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33422
                   325321 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810093d12a1
Seq. No.
                   33423
                   325372 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400036g05d2
                   33424
Seq. No.
                   325462 1.R1040
Contig ID
                   jC-gmle01810094h07d1
5'-most EST
Seq. No.
                   33425
                   325477 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810094d12a1
Method
                   BLASTN
NCBI GI
                   q1839634
BLAST score
                   292
E value
                   1.0e-163
Match length
                   502
                   91
% identity
                  heat shock protein 70=allergenic polypeptide {C-terminal,
NCBI Description
                   variable region} [Cladosporium herbarum, IMI 96220, mRNA
                   Partial, 1061 nt]
                   33426
Seq. No.
Contig ID
                   325484_1.R1040
5'-most EST
                   jC-gmle01810094e04a1
Method
                   BLASTX
NCBI GI
                  g2980784
BLAST score
                   651
E value
                   3.0e-68
Match length
                  201
% identity
                   (AL022198) puative protein [Arabidopsis thaliana]
NCBI Description
                   33427
Seq. No.
                   325675 1.R1040.
Contig ID
5'-most EST
                  jC-gmst02400064a11d1
```

5058

6 . . .

33428

325725 1.R1040

Seq. No.

Contig ID

```
5'-most EST
                   jC-qmro02800026c03a1
Method
                   BLASTX
NCBI GI
                   q2244866
BLAST score
                   323
E value
                   6.0e-30
Match length
                   134
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   33429
Seq. No.
Contig ID
                   325785 1.R1040
5'-most EST
                   jC-gmro02910071c01a1
Method
                   BLASTX
NCBI GI
                   q2459431
BLAST score
                   298
E value
                   7.0e-27
Match length
                   91
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33430
Contig ID
                   325792 1.R1040
5'-most EST
                   jC-gmro02800027d02d1
Seq. No.
                   33431
                   325805 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910022a11a1
Method
                   BLASTX
NCBI GI
                   g2832304
BLAST score
                   210
E value
                   2.0e-30
Match length
                   149
                   49
% identity
NCBI Description
                   (AF044489) receptor-like protein kinase [Oryza sativa]
                   33432
Seq. No.
                   325884 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800028e10a1
Method
                   BLASTX
NCBI GI
                   g3261631
BLAST score
                   177
E value
                   2.0e-12
Match length
                   105
% identity
                   42
NCBI Description
                  (Z79700) accA2 [Mycobacterium tuberculosis]
                   33433
Seq. No.
                   325981 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800029e04a1
Seq. No.
                   33434
                   326038 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800030a04d1
Method
                  BLASTX
NCBI GI
                   g2129623
BLAST score
                  204
E value
                   5.0e-16
```

::

```
Match length
                   73
% identity
                   53
NCBI Description
                   immunophilin FKBP15-2 - Arabidopsis thaliana >gi 1272408
                   (U52047) immunophilin [Arabidopsis thaliana]
Seq. No.
                   33435
Contig ID
                   326093 1.R1040
5'-most EST
                   jC-gmro02800042c08d1
Method
                   BLASTX
NCBI GI
                   g3785990
BLAST score
                   203
E value
                   8.0e-16
Match length
                   55
                   73
% identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4220487 (AC006069) hypothetical protein [Arabidopsis
                   thaliana]
                   33436
Seq. No.
                   326100 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800030e11d1
Seq. No.
                   33437
Contig ID
                  326152 1.R1040
                   jC-gmro02800031a04d1
5'-most EST
Seq. No.
                   33438
                   326177 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800031b07a1
Method
                   BLASTX
NCBI GI
                   g1762584
BLAST score
                   114
                   4.0e-09
E value
Match length
                   61
% identity
                   49
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   33439
                   326216 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800031d09d1
Seq. No.
                   33440
Contig ID
                   326292 1.R1040
5'-most EST
                   g4301729
Seq. No.
                   33441
                   326300 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800032a05d1
Seq. No.
                   33442
                   326318 1.R1040
Contig ID
5'-most EST
                   g42845\overline{2}6
Method
                   BLASTX
NCBI GI
                   q4335745
BLAST score
                   362
```

2.0e-34

E value

```
159
Match length
% identity
                   47
                   (AC006284) putative hydrolase (contains an
NCBI Description
                  esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                   33443
                   326500 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800033d09d1
                  33444
Seq. No.
                  326611 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800034f06a1
                  33445
Seq. No.
                  326612 1.R1040
Contig ID
5'-most EST
                   jC-gmr002800034f07a1
Method
                  BLASTX
NCBI GI
                  g1730576
BLAST score
                  246
E value
                   6.0e-21
Match length
                  82
                  56
% identity
NCBI Description
                  PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE)
                  >gi 1084134 pir JC4184 prolyl aminopeptidase (EC 3.4.11.5)
                  - Aeromonas sobria >gi 1236731 dbj BAA06380 (D30714)
                  prolyl aminopeptidase [Aeromonas sobria]
Seq. No.
                  33446
                  326622 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800035a04a1
Method
                  BLASTX
NCBI GI
                  g4510368
BLAST score
                  170
E value
                  5.0e-12
Match length
                  106
                   40
% identity
NCBI Description
                   (AC007017) putative transcription factor E2F5 [Arabidopsis
                  thaliana]
                  33447
Seq. No.
                  326711 1.R1040
Contig ID
5'-most EST
                  g4260415
Seq. No.
                  33448
                  326733 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy235e07b1
Method
                  BLASTX
NCBI GI
                  g2739381
BLAST score
                  350
E value
                  5.0e-33
Match length
                  126
% identity
NCBI Description
                   (AC002505) putative patatin [Arabidopsis thaliana]
```

33449

326800 1.R1040

Seq. No.

Contig ID

```
5'-most EST
                   jC-gmro02800038d09a1
Seq. No.
                   33450
Contig ID
                   326823 1.R1040
5'-most EST
                   uC-qmropic008h09b1
Method
                   BLASTX
NCBI GI
                   q2344900
BLAST score
                   277
E value
                   2.0e-24
Match length
                   112
% identity
                   47
NCBI Description
                   (AC002388) EREBP isolog [Arabidopsis thaliana]
                   33451
Seq. No.
Contig ID
                   326831 1.R1040
5'-most EST
                   jC-gmr002800038f08d1
Method
                   BLASTN
NCBI GI
                   q1432053
BLAST score
                   62
                   3.0e-26
E value
Match length
                   170
% identity
                   84
                   Oryza sativa asparagine synthetase mRNA, complete cds
NCBI Description
                   33452
Seq. No.
                   326949 1.R1040
Contig ID
5'-most EST
                   jC-qmr002800039e09a1
                   BLASTX
Method
NCBI GI
                   q100099
BLAST score
                   422
                   2.0e-41
E value
Match length
                   138
% identity
                   56
                   DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)
NCBI Description
                   CREB-like protein [Vicia faba]
Seq. No.
                   33453
Contig ID.
                   326950 1.R1040
5'-most EST
                   jC-gmro02910024g05d1
Method
                   BLASTX
NCBI GI
                   g2865394
BLAST score
                   141
E value
                   1.0e-08
Match length
                   49
% identity
                   (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
Seq. No.
Contig ID
                   327214 1.R1040
5'-most EST
                   jC-gmro02800042g07d1
Seq. No.
                   327251 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy048h09b1
                   33456
Seq. No.
                                                     12
```

327345 1.R1040

Contig ID

Contig ID

```
5'-most EST
                   jC-gmro02800044h04a1
                   BLASTX
Method
NCBI GI
                   g2344899
BLAST score
                   419
E value
                   6.0e-41
Match length
                   123
% identity
                   (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   327355 1.R1040
5'-most EST
                   jC-gmro02910011f07d1
Seq. No.
                   33458
                   327360 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910001b02d1
Method
                   BLASTX
NCBI GI
                   g3875246
BLAST score
                   172
                   3.0e-12
E value
Match length
                   59
% identity
                   51
                   (Z81490) similar to WD domain, G-beta repeats (2 domains);
NCBI Description
                   cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                   EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes
                   from this gene; cDNA EST yk449d4.5 comes from this gene;
Seq. No.
                   33459
                   327408 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910001f06d1
                   33460
Seq. No.
                   327416 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910001g01d1
                   33461
Seq. No.
                   327471 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910039a12d1
Seq. No.
                   33462
                   327490 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910002c11d1
                   33463
Seq. No.
Contig ID
                   327495_1.R1040
5'-most EST
                   jC-gmro02910007e03d1
Method
                  BLASTX
NCBI GI
                  g4490309
BLAST score
                  273
E value
                   4.0e-24
                  74
Match length
                  72
% identity
                   (AL035678) peroxidase ATP17a-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   33464
```

327498 1.R1040

```
5'-most EST
                   jC-gmro02910002d04d1
Seq. No.
                   33465
Contig ID
                   327512 1.R1040
5'-most EST
                   jC-gmro02910002d11d1
Seq. No.
                   33466
Contig ID
                   327580 1.R1040
5'-most EST
                   iC-qmro02910002h12d1
Method
                   BLASTX
NCBI GI
                   g4235430
BLAST score
                   216
E value
                   2.0e-17
Match length
                   56
% identity
NCBI Description
                   (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
Contig ID
                   327599 1.R1040
5'-most EST
                   jC-qmst02400069e02a1
Seq. No.
                   327716 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910004e12d1
Seq. No.
                   33469
Contig ID
                   327718 1.R1040
5'-most EST
                   jC-gmro02910016a08a1
Method
                   BLASTX
NCBI GI
                   g4510339
BLAST score
                   468
                   7.0e-47
E value
Match length
                   163
% identity
                   57
                   (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   33470
                   327719 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910004f03d1
                   BLASTX
Method
NCBI GI -
                   q4510339
BLAST score
                   223
                   3.0e-18
E value
Match length
                   62
% identity
                   (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   33471
Seq. No.
Contig ID
                   327729 1.R1040
5'-most EST
                   uC-gmflminsoy065c02b1
Seq. No.
                   33472
Contig ID
                   327751 1.R1040
5'-most EST
                   jC-qmst02400051d03d1
Method
                   BLASTX
```

```
NCBI GI
                  g3335169
BLAST score
                  160
                  8.0e-11
E value
                  70
Match length
                  47
% identity
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi 4455197_emb_CAB36520 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  33473
Seq. No.
                  327939_1.R1040
Contig ID
                  jC-gmr002910007f07a1
5'-most EST
Method
                  BLASTX
                  g2464865
NCBI GI
BLAST score
                  516
                  2.0e-52
E value
Match length
                  136
                  69
% identity
                  (Z99707) pectinesterase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33474
                  327940 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910007f07d1
Method
                  BLASTX
                  g3152618
NCBI GI
                  361
BLAST score
                  2.0e-34
E value
                  97
Match length
                  67
% identity
                   (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  >qi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                  thaliana]
                  33475
Seq. No.
                  327993 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910008h07a1
                  33476
Seq. No.
                  327999 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910006e11a1
                  BLASTX
Method
NCBI GI
                  g1669341
BLAST score
                  182
                  2.0e-13
E value
Match length
                  57
% identity
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
                  33477
Seq. No.
                  328018 1.R1040
Contig ID
5'-most EST
                  uC-gmropic070h10b1
                  33478
Seq. No.
                  328023 1.R1040
Contig ID
```

uC-gmronoir064f05b1

```
33479
Seq. No.
                   328063 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir042e08b1
                   BLASTX
Method
NCBI GI
                   g4539343
BLAST score
                   614
E value
                   7.0e-64
Match length
                   181
% identity
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   328076 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400027f03a1
                   33481
Seq. No.
                   328194 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910007h12a1
Seq. No.
                   33482
Contig ID
                   328339 2.R1040
5'-most EST
                   jC-gmro02910008g10d1
Method
                   BLASTX
NCBI GI
                   g4107480
BLAST score
                   155
                   3.0e-10
E value
Match length
                   59
                   35
% identity
NCBI Description
                   (AL035085) putative mitochondrial carrier protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   33483
                   328484_1.R1040
Contig ID
5'-most EST
                   uC-gmronoir060d02b1
Method
                   BLASTX
NCBI GI
                   g2462833
BLAST score
                   207
E value
                   5.0e-16
Match length
                   236
                   24
% identity
                   (AF000657) highly similar to froha and frohb, potential
NCBI Description
                   frohc [Arabidopsis thaliana]
                   33484
Seq. No.
Contig ID
                   328495_1.R1040
5'-most EST
                   uC-gmropic044c09b1
Method
                   BLASTX
NCBI GI
                   g3367574
BLAST score
                   181
                   3.0e-13
E value
Match length
                   109.
% identity
                   (AL031135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   33485
Seq. No.
Contig ID
                   328567 1.R1040
```

jC-gmro02910040e08d1

NCBI GI

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Seq. No. 🤼
                   33486
                   328593 1.R1040
Contig ID '
5'-most EST
                  jC-gmro02910011e10d1
Seq. No.
                   33487
                   328631 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910035g04d1
Seq. No.
                   33488
Contig ID
                   328661 1.R1040
5'-most EST
                   jC-qmro02910012b07a1
Method
                   BLASTX
                  g2832636
NCBI GI
BLAST score
                  186
E value
                   9.0e-14
Match length
                   61
                   54
% identity
NCBI Description
                   (AL021711) hypothetical protein [Arabidopsis thaliana]
                  >gi 4455157 emb CAA16697.1 (AL021687) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                  33489
                  328670 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910012b11d1
Seq. No.
                   33490
                   328757 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910012g09d1
Seq. No.
                   33491
                   328773 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910012h06d1
Method
                  BLASTX
                  g3337361
NCBI GI
BLAST score
                  168
E value
                   1.0e-11
Match length
                  54
% identity
NCBI Description
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                   33492
                   328804 1.R1040
Contig ID
5'-most EST
                   fC-gmro7000747276r1
Method
                  BLASTX
NCBI GI
                  q2459419
BLAST score
                  224
E value
                   4.0e-18
Match length
                  99
% identity
NCBI Description
                   (AC002332) hypothetical protein [Arabidopsis thaliana]
                  33493
Seq. No.
Contig ID
                  328817 1.R1040
5'-most EST
                  jC-gmro02910013b09d1
Method
                  BLASTX
```

g2708749

Match length

```
BLAST score
E value
                   3.0e-21
Match length
                   135
% identity
                   49
NCBI Description
                   (AC003952) putative senescence-assoc. rhodanese-like
                   protein [Arabidopsis thaliana]
                   33494
Seq. No.
Contig ID
                   328828 1.R1040
5'-most EST
                   jC-gmro02910013c04a1
Method
                   BLASTX
NCBI GI
                   g2245055
BLAST score
                   162
E value
                   6.0e-11
Match length
                   67
% identity
                   49
NCBI Description
                   (Z97342) resistance gene homolog (fragment) [Arabidopsis
                   thaliana]
                   33495
Seq. No.
                   328849 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400014c12d1
                   BLASTX
Method
                   g2117619
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
Match length
                   72
% identity
                  peroxidase (EC 1.11.1.7) 4 precursor - wheat
NCBI Description
                   >gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum
                   aestivum]
                   33496
Seq. No.
                   328849 2.R1040
Contig ID
                   jC-gmro02910074c05d1
5'-most EST
Seq. No.
                   33497
Contig ID
                   328879 1.R1040
                   jC-qmro02910013e08a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2851577
BLAST score
                   887
E value
                   8.0e-96
Match length
                   229
% identity
                   69
                   SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII)
NCBI Description
                   >gi 1877219 emb CAA70817 (Y09604) serine carboxypeptidase
                   III, CP-MIII [Hordeum vulgare]
Seq. No.
                   33498
                   328933 1.R1040
Contig ID
5'-most EST
                   uC-gmropic025h11b1
Method
                   BLASTX
NCBI GI
                  g2464901
BLAST score
                   263
                   9.0e-23
E value
```

```
% identity
NCBI Description (299708) putative protein [Arabidopsis thaliana]
                   33499
Seq. No.
Contig ID
                   328993 1.R1040
5'-most EST
                   jC-gmst02400020dc08d1
Method
                   BLASTX
NCBI GI
                  q3928097
BLAST score
                   216
E value
                   3.0e-17
Match length
                   88
% identity
                   49
NCBI Description
                   (AC005770) unknown protein, 5' partial [Arabidopsis
                  thaliana]
                   33500
Seq. No.
Contig ID
                   329011 1.R1040
5'-most EST
                  uC-gmronoir030d10b1
Method
                  BLASTX
NCBI GI
                   g1888357
BLAST score
                   359
                   5.0e-34
E value
Match length
                  83
                   77
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                   33501
                   329059 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910015a06d1
Seq. No.
                   33502
Contig ID
                   329077 1.R1040
5'-most EST
                   jC-qmro02910015c10d1
Method
                  BLASTX
NCBI GI
                   g3377507
BLAST score
                   525
E value
                   2.0e-53
Match length
                  119
% identity
                   (AF056026) auxin transport protein EIR1 [Arabidopsis
NCBI Description
                  thaliana] >gi_3661620 (AF093241) putative auxin efflux
                  carrier AGR [Arabidopsis thaliana] >gi 3746886 (AF087459)
                  polar-auxin-transport efflux component AGRAVITROPIC 1
                   [Arabidopsis thaliana] >gi_4206709 (AF086906) root
                  gravitropism control protein [Arabidopsis thaliana]
                   33503
Seq. No.
                   329171 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910016c04a1
Method
                  BLASTX
NCBI GI
                  g3334667
BLAST score
                  349
                  1.0e-38
E value
Match length
                  118
                  70
% identity
```

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NCBI Description
                  (Y10493) putative cytochrome P450 [Glycine max]
                  33504
Seq. No.
                   329194 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400065f11d1
                  33505
Seq. No.
                  329277 1.R1040
Contig ID
                  jC-gmro02910016h11d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3176684
BLAST score
                  422
                  3.0e-41
E value
Match length
                  128
% identity
                  62
NCBI Description
                   (AC003671) Contains similarity to equilibratiave nucleoside
                  transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317,
                  gb_T20785, gb_AA586285 and gb AA712578 come from this gene.
                   [Arabidopsis thaliana]
                  33506
Seq. No.
Contig ID
                  329290 1.R1040
5'-most EST
                  jC-gmro02910018b01a1
Method
                  BLASTX
                  g4165018
NCBI GI
BLAST score
                  226
E value
                  4.0e-33
Match length
                  155
                  53
% identity
NCBI Description
                  (D89053) Acyl-CoA synthetase 3 [Homo sapiens]
                  33507
Seq. No.
                  329291 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910017d03a1
                  33508
Seq. No.
Contig ID
                  329326 1.R1040
5'-most EST
                  jC-gmro02910024a12a1
                  33509
Seq. No.
Contig ID
                  329368_1.R1040
5'-most EST
                  jC-gmro02910019b01d1
Seq. No.
                  33510
                  329370 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910059g03d1
Method
                  BLASTX
NCBI GI
                  q3738298
BLAST score
                  399
E value
                  8.0e-39
Match length
                  150
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  >gi 4249394 (AC006072) unknown protein [Arabidopsis
                  thaliana]
```

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Contig ID
                   329460 1.R1040
5'-most EST
                   jC-gmro02910020e09d1
Seq. No.
                   33512
Contig ID
                   329587 1.R1040
5'-most EST
                   q4397439
Method
                   BLASTX
NCBI GI
                   q2244915
BLAST score
                   164
E value
                   2.0e-20
Match length
                   146
% identity
NCBI Description
                   (Z97339) strong homology to reverse transcriptase
                   [Arabidopsis thaliana]
Seq. No.
                   33513
                   329690 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910022f05d1
Seq. No.
                   329775 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910022f10a1
Seq. No.
                   33515
                   329828 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910023a08a1
Seq. No.
                   33516
                   329830 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910023b08a1
Seq. No.
                   33517
Contig ID
                   329919 1.R1040
5'-most EST
                   jC-gmro02910023f03d1
                   33518
Seq. No.
                   330002 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910024b08d1
                   33519
Seq. No.
                   330066_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024f10a1
Method
                   BLASTX
NCBI GI
                   q3395431
                   340
BLAST score
E value
                   7.0e-32
                   92
Match length
% identity
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33520
                   330120 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910051h03d1
Seq. No.
                   33521
                   330137 1.R1040
Contig ID
```

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jC-gmro02910025a04a1

BLAST score

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Seq. No.
                   33522
Contig ID
                   330191 1.R1040
5'-most EST
                   uC-gmrominsoy320a01b1
Method
                   BLASTX
NCBI GI
                   g4006908
BLAST score
                   226
E value
                   9.0e-19
Match length
                   107
% identity
                   (299708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33523
Contig ID
                   330216 1.R1040
5'-most EST
                   jC-gmst02400043a09d1
Seq. No.
                   33524
Contig ID
                   330330 1.R1040
5'-most EST
                   jC-gmro02910026e03a1
                   33525
Seq. No.
Contig ID
                   330409 1.R1040
5'-most EST
                   jC-gmr002910071a02d1
                   33526
Seq. No.
Contig ID
                   330421 1.R1040
5'-most EST
                   uC-gmrominsoy028h10b1
Method
                   BLASTX
NCBI GI
                   g3128185
BLAST score
                   332
                   6.0e-31
E value
Match length
                   171
% identity
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   330422 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400062b03d1
                                                                              . . .
Seq. No.
                   33528
                   330427 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910057f12a1
Method
                  BLASTN
NCBI GI
                  g2245682
BLAST score
                  192
                  1.0e-104
E value
Match length
                   411
% identity
NCBI Description
                  Glycine max peroxidase precursor (GMIPER1) mRNA, complete
                  33529
Seq. No.
                   330437 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910027b04d1
Method
                  BLASTX
                  g2702272
NCBI GI
```

Contig ID

```
2.0e-26
E value
Match length
                   135
% identity
                   13
                   (AC003033) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33530
                   330460 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy186f11b1
                   33531
Seq. No.
Contig ID
                   330468 1.R1040
                   jC-gmro02910027e04d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4567249
BLAST score
                   465
                   2.0e-46
E value
Match length
                   117
                   73
% identity
NCBI Description
                   (ACO07070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33532
                   330486_1.R1040
Contig ID
5'-most.EST
                   jC-gmro02910027g02d1
                   33533
Seq. No.
                   330518 1.R1040
Contig ID
5'-most EST
                   uC-gmropic040g03b1
Seq. No.
                   33534
                   330598 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910030b07d1
Seq. No.
                   33535
                   330616 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071f02d1
                   33536
Seq. No.
                   330631 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910030d08d1
Method
                   BLASTX
NCBI GI
                   g2346972
BLAST score
                   235
E value
                   1.0e-19
Match length
                   97
% identity
NCBI Description
                   (AB006598) ZPT2-11 [Petunia x hybrida]
                   33537
Seq. No.
                   330665 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910030g03a1
Seq. No.
                   33538
                   330711 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910031b04d1
Seq. No.
                   33539
```

330764 1.R1040

Method

NCBI GI

BLASTX

q4220541

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jC-gmro02910031f10d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3122572
BLAST score
                  209
E value
                  1.0e-16
Match length
                  93
% identity
                  53
                  NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                  (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                  SUBUNIT) >gi_1084434 pir_S52737 NADH dehydrogenase
                  (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                  >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial
                  complex I subunit [Solanum tuberosum]
Seq. No.
                  33540
Contig ID
                  330842 1.R1040
                  jC-gmro02910032e01d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4417296
BLAST score
                  219
E value
                  9.0e-18
Match length
                  55
% identity
NCBI Description
                  (AC007019) unknown protein [Arabidopsis thaliana]
                  33541
Seq. No.
Contig ID
                  330978 1.R1040
5'-most EST
                  jC-gmro02910034e02d1
Seq. No.
                  33542
                  330988 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910034e08d1
Method
                  BLASTN
                  q1370197
NCBI GI
BLAST score
                  55
                  4.0e-22
E value
                  235
Match length
% identity
                  87
                  L.japonicus mRNA for small GTP-binding protein, RAB8E
NCBI Description
Seq. No.
                  33543
Contig ID
                  330996 1.R1040
5'-most EST
                  jC-gmro02910034f02d1
                  33544
Seq. No.
                  331016 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910034g05d1
Seq. No.
                  33545
                  331041 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910071a10d1
                  33546
Seq. No.
Contig ID
                  331077 1.R1040
5'-most EST
                  q4260395
```

5'-most EST

```
BLAST score
                   315
E value
                   2.0e-39
Match length
                  237
% identity
                   47
NCBI Description
                   (AL035356) Rab geranylgeranyl transferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                  33547
Contig ID
                  331106 1.R1040
5'-most EST
                  jC-qmro02910036a10a1
Method
                  BLASTX
NCBI GI
                  g2130080
BLAST score
                  338
E value
                   4.0e-32
Match length
                  89
% identity
                  73
NCBI Description
                  Nrampl protein - rice >gi 1470320 bbs 177441 (S81897)
                  OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,
                  indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]
                   [Oryza sativa] >gi_2231132 (L41217) integral membrane
                  protein [Oryza sativa]
Seq. No.
                  33548
Contig ID
                  331114 1.R1040
5'-most EST
                  jC-qmro02910036h01d1
Method
                  BLASTX
NCBI GI
                  q4490736
BLAST score
                  149
E value
                  2.0e-09
Match length
                  50
% identity
NCBI Description
                  (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  33549
Contig ID
                  331153 1.R1040
5'-most EST
                  jC-gmro02910036f03a1
                  33550
Seq. No.
Contig ID
                  331191 1.R1040
5'-most EST
                  jC-gmro02910036g07a1
Seq. No.
                  33551
                  331310 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910037f11a1
Method
                  BLASTX
                  g3142295
NCBI GI
BLAST score
                  302
E value
                  3.0e-27
Match length
                  122
% identity
                  (AC002411) Strong similarity to phosphoribosylanthranilate
NCBI Description
                  transferase gb_D86180 from Pisum sativum. [Arabidopsis
                  thaliana]
Seq. No.
                  33552
Contig ID
                  331468 1.R1040
```

jC-gmr002910039b04d1

```
33553
Seq. No.
Contig ID
                   331526 1.R1040
5'-most EST
                   uC-gmropic057a04b1
Seq. No.
                   33554
Contig ID
                   331534 1.R1040
5'-most EST
                   jC-gmro02910039e10d1
Seq. No.
                   33555
Contig ID
                   331667 1.R1040
5'-most EST
                   fC-gmro700864430d3
Seq. No.
                   33556
Contig ID
                   331711 1.R1040
5'-most EST
                   jC-gmro02910040h10d1
Method
                   BLASTX
NCBI GI
                   g1771160
BLAST score
                   249
E value
                   3.0e-21
Match length
                   68
% identity
                   (X98929) SBT1 [Lycopersicon esculentum]
NCBI Description
                  >gi 3687305 emb CAA06999 (AJ006378) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   33557
Contig ID
                   331718 1.R1040
5'-most EST
                   g43966<del>6</del>9
Method
                   BLASTX
NCBI GI
                   q1354510
BLAST score
                   364
E value
                   1.0e-34
Match length
                   88
% identity
NCBI Description
                   (U55205) HAL2-like protein [Arabidopsis thaliana]
Seq. No.
                   33558
Contig ID
                   331728 1.R1040
5'-most EST
                   g5057699
Seq. No.
                   33559
Contig ID
                   331748 1.R1040
5'-most EST
                   jC-gmro02910041021a1
                   33560
Seq. No.
Contig ID
                   331900 1.R1040
5'-most EST
                   jC-gmro02910046b11d1
                   33561
Seq. No.
                   331913 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910046c07d1
Method
                   BLASTX
NCBI GI
                   g2961357
BLAST score
                   1217
                   1.0e-134
E value
Match length
                   322
```

141.

```
% identity
NCBI Description
                   (AL022140) putative protein [Arabidopsis thaliana]
                   33562
Seq. No.
                   332021_1.R1040
Contig ID
5'-most EST
                   jC-gmr002910047a02d1
                   33563
Seq. No.
                   332047 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910047g02d1
                   33564
Seq. No.
                   332068 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910068f04d1
                   33565
Seq. No.
                   332071 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910047e02a1
                   BLASTX
Method
NCBI GI
                   g1888357
BLAST score
                   742
                   7.0e-79
E value
                   200
Match length
                   69
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                   >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                   precursor [Arabidopsis thaliana]
                   33566
Seq. No.
                   332107_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910047h04a1
                   33567
Seq. No.
                   332126 1.R1040
Contig ID
5'-most EST
                   uC-gmropic074e11b1
                   33568
Seq. No.
                   332170 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910048e03d1
                   33569
Seq. No.
                   332193 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910048f09d1
Seq. No.
                   33570
                   332201 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910048g03d1
                   33571
Seq. No.
                   332231 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910049a07d1
                   33572
Seq. No.
                   332266_1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400031e03d1
```

33573

Seq. No.

```
332280 1.R1040
Contig ID
                  uC-gmrominsoy095b12b1
5'-most EST
Method .
                  BLASTX
NCBI GI
                  g3342798
BLAST score
                  268
E value
                  1.0e-23
Match length
                  70
                  73
% identity
                   (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                  33574
Seq. No.
Contig ID
                  332324 1.R1040
5'-most EST
                  jC-gmro02910050b07d1
Method
                  BLASTX
NCBI GI
                  q3202038
BLAST score
                  428
E value
                   4.0e-42
Match length
                  113
% identity
                   69
NCBI Description
                   (AF069322) permease 1 [Mesembryanthemum crystallinum]
                  33575
Seq. No.
Contig ID
                  332400 1.R1040
5'-most EST
                  jC-gmro02910051b10d1
Seq. No.
                  33576
Contig ID
                  332470 1.R1040
5'-most EST
                  jC-gmro02910051f05d1
                  33577
Seq. No.
Contig ID
                  332621 1.R1040
5'-most EST
                  fC-gmro700868519d3
                  33578
Seq. No.
Contig ID
                  332631 1.R1040
5'-most EST
                  fC-gmro7000764393r1
                  33579
Seq. No.
Contig ID
                  332686 1.R1040
5'-most EST
                  jC-gmr002910054g10a1
Seq. No.
                  33580
Contig ID
                  332720 1.R1040
5'-most EST
                  jC-gmro02910056e01a1
                  33581
Seq. No.
Contig ID
                  332814 1.R1040
5'-most EST
                  uC-gmronoir050e02b1
Method
                  BLASTX
NCBI GI
                  q1946371
BLAST score
                  358
E value
                  4.0e-34
Match length
                  101
% identity
NCBI Description
                  (U93215) regulatory protein Viviparous-1 isolog
```

[Arabidopsis thaliana]

```
33582
Seq. No.
                   332911 1.R1040
Contig ID
                   jC-gmro02910060a08d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1524177
BLAST score
                   94
                   2.0e-45
E value
                   186
Match length
% identity
                   88
NCBI Description
                   M.sativa mRNA for proteasome subunit
                   33583
Seq. No.
                   332916_1.R1040
Contig ID
5'-most EST
                   g42981\overline{2}4
Method
                   BLASTX
NCBI GI
                   g2344900
BLAST score
                   260
E value
                   2.0e-22
                   57
Match length
% identity
                   (AC002388) EREBP isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33584
                   333076 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910061c01d1
Method
                   BLASTX
NCBI GI
                   g2576363
BLAST score
                   396
                   2.0e-38
E value
Match length
                   133
                   57
% identity
NCBI Description
                   (U39783) amino acid transport protein [Arabidopsis
                   thaliana]
                   33585
Seq. No.
                   333129 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy197c12b1
Method
                   BLASTX
NCBI GI
                   g2224931
BLAST score
                   292
                   3.0e-26
E value
Match length
                   108
% identity
NCBI Description
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
                   thaliana]
                   33586
Seq. No.
                   333553 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400020d09a1
                   33587
Seq. No.
                   333630 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910065f08d1
Seq. No.
                   33588
```

333638_1.R1040

Contig ID

5'-most EST

```
5'-most EST
                  jC-gmro02910065g03a1
Seq. No.
                  33589
Contig ID
                  333639 1.R1040
5'-most EST
                  jC-gmro02910065g03d1
                  BLASTX
Method
                  g4512660
NCBI GI
BLAST score
                  142
                  2.0e-14
E value
Match length
                  87
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4544467 gb AAD22374.1 AC006580 6 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  33590
                  333749 1.R1040
Contig ID
5'-most EST
                  q5666807
Method
                  BLASTX
NCBI GI
                  q2262117
BLAST score
                  412
E value
                  7.0e-40
Match length
                  228
% identity
                   (AC002343) auxin inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  33591
Seq. No.
Contig ID
                  333788 1.R1040
5'-most EST
                  jC-gmro02910067b07d1
                  33592
Seq. No.
Contig ID
                  333841 1.R1040
5'-most EST
                  jC-gmst02400055g02a1
                  33593
Seq. No.
Contig ID
                  333841 2.R1040
5'-most EST
                  jC-gmro02910067d05d1
Seq. No.
                  333882 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910067f07a1
Seq. No.
                  33595
                  333965 1.R1040
Contig ID
5'-most EST
                  jC-qmro02910068c02a1
Method
                  BLASTX
NCBI GI
                  q2673916
BLAST score
                  188
E value
                  6.0e-14
Match length
                  51
% identity
NCBI Description
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  33596
                  334010 1.R1040
Contig ID
```

jC-qmro02910068f02a1

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   g4006856
BLAST score
                   442
E value
                   1.0e-43
Match length
                   163
% identity
                   30
NCBI Description
                   (Z99707) receptor kinase-like protein [Arabidopsis
                   thaliana]
                   33597
Seq. No.
Contig ID
                   334082 1.R1040
5'-most EST
                   fC-qmle700555604r2
                   33598
Seq. No.
                   334096_1.R1040
Contig ID
5'-most EST
                   jC-gmr002910069d07a1
Seq. No.
                   33599
                   334123 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910069f07a1
Method
                   BLASTN
NCBI GI
                   g3510347
BLAST score
                   52
E value
                   4.0e-20
Match length
                   92
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   33600
                   334151 1.R1040
Contig ID
5'-most EST
                   jC-gmr002910069h10d1
Method
                   BLASTX
NCBI GI
                   g1491617
                   270
BLAST score
                   1.0e-23
E value
Match length
                   82
% identity
                   (X99952) peroxidase [Arabidopsis thaliana]
NCBI Description
                   33601
Seq. No.
                   334213 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071h04a1
Seq. No.
                   33602
                   334269 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071a12d1
Method
                   BLASTX
NCBI GI
                   g2262111
BLAST score
                   194
E value
                   9.0e-15
Match length
                   76
% identity
                   (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                   thaliana]
```

```
334274 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071c04a1
                  BLASTX
Method
                  q3367587
NCBI GI
BLAST score
                   281
E value
                   6.0e-25
                   152
Match length
                   40
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33604
Contig ID
                   334327 1.R1040
5'-most EST
                   jC-gmro02910071d12d1
                  BLASTX
Method
                   g2827623
NCBI GI
BLAST score
                   667
                   6.0e-70
E value
Match length
                  142
% identity
                   (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33605
Contig ID
                   334376 1.R1040
5'-most EST
                  jC-gmro02910071g05a1
 :- .
Seq. No.
                   33606
Contig ID
                   334483 1.R1040
5'-most EST
                  jC-gmst02400009a04d1
Seq. No.
                  33607
                   334621 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910074c02d1
Method
                  BLASTX
NCBI GI
                  q4218113
BLAST score
                  144
                   7.0e-14
E value
                   56
Match length
% identity
NCBI Description
                   (AL035353) xyloglucan endotransglycosylase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   33608
Contig ID
                   334751 1.R1040
5'-most EST
                  jC-gmst02400063h10d1
                  33609
Seq. No.
                   334858 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400001a09d1
Method
                  BLASTX
NCBI GI
                  g2191135
BLAST score
                  234
E value
                  2.0e-19
Match length
                  117
% identity
                  39
NCBI Description
                   (AF007269) A IG002N01.14 gene product [Arabidopsis
```

thaliana]

```
Seq. No.
Contig ID
                   334879 1.R1040
5'-most EST
                   jC-gmst02400001b12a1
Seq. No.
Contig ID
                   334883 1.R1040
5'-most EST
                   jC-gmst02400001c02a1
                   33612
Seq. No.
Contig ID
                   334968 1.R1040
5'-most EST
                   jC-qmst02400001h10a1
Method
                   BLASTN
NCBI GI
                   q169048
BLAST score
                   147
                   9.0e-77
E value
Match length
                   387
% identity
                   85
NCBI Description
                   Pea farnesyltransferase beta-subunit mRNA, complete cds
                   33613
Seq. No.
                   335005 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy309a11b1
Seq. No.
                   335024 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400002d08d1
Seq. No.
                   33615
                   335055 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400002g02a1
Seq. No.
                   33616
Contig ID
                   335073 1.R1040
5'-most EST
                   jC-gmst02400002h10d1
Seq. No.
                   33617
                   335174 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400004b09d1
Seq. No.
                   33618
                   335284 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400005c07a1
Seq. No.
                   33619
                   335386 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400006c05a1
Seq. No.
                   33620
Contig ID
                   335403 1.R1040
5'-most EST
                   jC-gmst02400006d08d1
Method
                   BLASTX
NCBI GI
                   g2462781
BLAST score
                   217
E value
                   2.0e-17
Match length
                   51
% identity
                  (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
```



[Arabidopsis thaliana] Seq. No. 33621 335427 1.R1040 Contig ID 5'-most EST jC-gmst02400020db06d1 Seq. No. 33622 335428 1.R1040 Contig ID jC-gmst02400006g01a1 5'-most EST Seq. No. 33623 335429 1.R1040 Contig ID 5'-most EST jC-gmst02400006g01d1 Seq. No. 33624 Contig ID 335484 1.R1040 5'-most EST jC-gms\(\overline{t}\) 02400007b09d1 Method BLASTX NCBI GI g3256035 BLAST score 202

% identity 49 (Y14274) putative serine/threonine protein kinase [Sorghum NCBI Description

bicolor]

1.0e-15

77

33625 Seq. No.

E value

Match length

335487 1.R1040 Contig ID 5'-most EST fC-gmro700566572d3

Seq. No. 33626

335507 1.R1040 Contig ID

5'-most EST jC-gmst02400007d07d1

33627 Seq. No.

335541 1.R1040 Contig ID

5'-most EST jC-gmst02400007f07a1

Seq. No. 33628

335557 1.R1040 Contig ID

5'-most EST jC-gmst02400007g09d1

33629 Seq. No.

Contig ID 335564 1.R1040

5'-most EST jC-gmst02400007h05d1

BLASTX Method NCBI GI g2098575

BLAST score 185 E value 1.0e-13

Match length 44 % identity

NCBI Description (AC002115) F25451_2 [Homo sapiens]

33630 Seq. No.

Contig ID 335572 1.R1040

5'-most EST jC-gmst02400077e05d1

5'-most EST

```
Seq. No.
                   33631
                   335630 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400008d04d1
                   33632
Seq. No.
Contig ID
                   335732 1.R1040
5'-most EST
                   jC-gmst02400009b03d1
Method
                   BLASTX
NCBI GI
                   g3080433
BLAST score
                   290
                   5.0e-26
E value
Match length
                   140
% identity
                   46
                   (AL022605) putative gamma-glutamyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   33633
Seq. No.
                   335810 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400017c11a1
Seq. No.
                   33634
                   335885 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400011a08d1
Seq. No.
                   33635
                   336036 1.R1040
Contig ID
                   jC-gmst02400027h05d1
5'-most EST
Seq. No.
                   33636
                   336078 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400014b11a1
Seq. No.
                   33637
Contig ID
                   336162 1.R1040
5'-most EST
                   uC-gmrominsoy299f04b1
Method
                   BLASTX
NCBI GI
                   g2598575
BLAST score
                   354
                   8.0e-34
E value
Match length
                   98
% identity
NCBI Description
                   (Y15293) MtN21 [Medicago truncatula]
                   33638
Seq. No.
Contig ID
                   336172 1.R1040
5'-most EST
                   jC-gmst02400014g03a1
Method
                   BLASTX
NCBI GI
                   g3341687
BLAST score
                   170
E value
                   8.0e-12
Match length
                   66
% identity
NCBI Description
                   (AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.
                   33639
Contig ID
                   336203 1.R1040
```

jC-gmst02400014h07a1

BLAST score

```
Seq. No.
                   33640
Contig ID
                   336206 1.R1040
5'-most EST
                   jC-gmst02400014h09a1
                   BLASTX
Method
NCBI GI
                   g1621463
BLAST score
                   545
                   8.0e-56
E value
Match length
                   104
                   89
% identity
                   (U73104) laccase [Liriodendron tulipifera]
NCBI Description
Seq. No.
                   33641
                   336219 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400015a11a1
Method
                   BLASTX
NCBI GI
                   g3033391
BLAST score
                   265
                   4.0e-23
E value
Match length
                   138
% identity
                   38
                   (AC004238) putative amino acid transporter [Arabidopsis
NCBI Description
                   thaliana]
                   33642
Seq. No.
                   336220 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400015a11d1
Seq. No.
                   33643
                   336276 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400015e04a1
Seq. No.
                   33644
Contig ID
                   336476 1.R1040
5'-most EST
                   jC-gmst02400017b12a1
                   33645
Seq. No.
                   336483 1.R1040
Contig ID
5'-most EST
                   iC-cmst02400017c03d1
                   BLASTX
Method
                   g4099090
NCBI GI
BLAST score
                   379
E value
                   2.0e-36
Match length
                   101
% identity
                   70
NCBI Description
                   (U83178) unknown [Arabidopsis thaliana]
                   33646
Seq. No.
                   336508 1.R1040
Contig ID
5'-most EST
                   q5752853
Seq. No.
                   33647
                   336536 1.R1040
Contig ID
5'-most EST
                   fC-gmle7000786711d1
Method
                   BLASTX
NCBI GI
                   g3805845
```

NCBI GI

```
E value
                   5.0e-19
Match length
                   64
% identity
NCBI Description
                   (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   336562 1.R1040.
5'-most EST
                   jC-gmst02400068f05d1
Seq. No.
                   33649
Contig ID
                   336593 1.R1040
5'-most EST
                   jC-gmst02400033h01d1
                   33650
Seq. No.
Contig ID
                   336627 2.R1040
5'-most EST
                   jC-gmst02400018c09a1
Seq. No.
                   33651
                   336637 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir008c11b1
Seq. No.
                   33652
Contig ID
                   336699 1.R1040
                   jC-gms\overline{t}02400045e10a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2980790
BLAST score
                   156
E value
                   3.0e-10
                   101
Match length
                   44
% identity
NCBI Description
                   (AL022197) hypothetical protein [Arabidopsis thaliana]
                   33653
Seq. No.
Contig ID
                   336781 1.R1040
5'-most EST
                   jC-gmst02400020de04d1
                   33654
Seq. No.
                   336789 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400020f02a1
                   33655
Seq. No.
                   336855 1.R1040
Contig ID
5'-most EST
                   g5752695
Seq. No.
                   33656
                   336859 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400045g09d1
                   33657
Seq. No.
Contig ID
                   336900 1.R1040
5'-most EST
                   jC-gmst02400023d09d1
                   33658
Seq. No.
                   336944 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400023f03a1
Method
                   BLASTX
```

g4454056

Seq. No.

```
BLAST score
                   298
E value
                   5.0e-27
Match length
                   66
% identity
                   85
NCBI Description
                   (AJ000930) ClpP [Arabidopsis thaliana]
                   33659
Seq. No.
Contig ID
                   336970 1.R1040
5'-most EST
                   jC-gmst02400033d11d1
Method
                   BLASTX
                   g3451065
NCBI GI
BLAST score
                   175
E value
                   1.0e-12
Match length
                   32
% identity
NCBI Description
                   (AL031326) water channel - like protein [Arabidopsis
                   thaliana]
                                                .....
Seq. No.
                   33660
Contig ID
                   337003 1.R1040
5'-most EST
                   jC-gmst02400023h12d1
Seq. No.
                   33661
Contig ID
                   337171 1.R1040
5'-most EST
                   jC-qmst02400026b05a1
Method
                   BLASTX
NCBI GI
                   g3522938
BLAST score
                   188
E value
                   5.0e-23
Match length
                   132
% identity
NCBI Description
                   (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   337195 1.R1040
5'-most EST
                   jC-qmst02400026c06a1
Seq. No.
Contig ID
                   337251 1.R1040
5'-most EST
                   jC-gmst02400026f01a1
Seq. No.
                   33664
Contig ID
                   337289 1.R1040
5'-most EST
                   jC-gmst02400026h06a1
Method
                   BLASTX
NCBI GI
                   q2244878
BLAST score
                   489
E value
                   4.0e-49
Match length
                   193
% identity
NCBI Description
                   (Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33665
Contig ID
                   337337 1.R1040
5'-most EST
                   jC-gmst02400027b11a1
```

Contig ID

```
337441 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy093h12b1
Method
                   BLASTX
NCBI GI
                   g3298544
BLAST score
                   452
E value
                   8.0e-45
Match length
                   201
% identity
                   57
NCBI Description
                   (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   337446 1.R1040
5'-most EST
                   jC-gmst02400027h03a1
                   33668
Seq. No.
Contig ID
                   337465 1.R1040
5'-most EST
                   jC-qmst02400028b05a1
                   33669
Seq. No.
Contig ID
                   337503 1.R1040
5'-most EST
                   jC-gmst02400028d10a1
Method
                   BLASTX
NCBI GI
                   g3702340
BLAST score
                   375
E value
                   9.0e-36
Match length
                   215
% identity
NCBI Description
                   (AC005397) hypothetical protein [Arabidopsis thaliana]
                   33670
Seq. No.
Contig ID
                   337613 1.R1040
                   jC-gms\overline{t}02400029e01a1
5'-most EST
Method
                   BLASTX
                   g3776559
NCBI GI
BLAST score
                   699
E value
                   6.0e-74
Match length
                   165
                   77
% identity
NCBI Description
                   (AC005388) Strong similarity to gene F14J9.26 gi 3482933
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   33671
Contig ID
                   337662 1.R1040
5'-most EST
                   g5677286
Seq. No.
                   33672
Contiq ID
                   337706 1.R1040
5'-most EST
                   jC-gmst02400030a12a1
Seq. No.
                   33673
                   337708 1.R1040
Contig ID
5'-most EST
                   jC-gmsT02400030b01a1
Seq. No.
                   33674
```

337710 1.R1040

```
5'-most EST
                   jC-gmst02400030b02a1
Seq. No.
                   33675
Contig ID
                   337737 1.R1040
5'-most EST
                   jC-gmst02400030f06a1
                   33676
Seq. No.
                   337763 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400030g04d1
                   33677
Seq. No.
                   337777 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400030h04d1
                   BLASTN
Method
NCBI GI
                   g747979
BLAST score
                   35
                   5.0e-10
E value
Match length
                   47
% identity
                  Nicotiana tabacum UMP synthase (pyr5-6) mRNA, partial cds
NCBI Description
Seq. No.
                   33678
Contig ID
                   337788 1.R1040
5'-most EST
                   jC-gmst02400031a02d1
Seq. No.
                   33679
Contig ID
                   337951 1.R1040
5'-most EST
                   jC-qmst02400032b03d1
Method
                   BLASTX
NCBI GI
                   q3047089
BLAST score
                   207
E value
                   3.0e-16
Match length
                   97
                   47
% identity
NCBI Description
                   (AF058826) contains similarity to pseudouridylate
                   synthases [Arabidopsis thaliana]
Seq. No.
Contig ID
                   338030 1.R1040
5'-most EST
                   jC-gmst02400032f08d1
Seq. No.
Contig ID
                   338060 1.R1040
5'-most EST
                   jC-qmst02400032h07d1
Seq. No.
Contig ID
                   338065 1.R1040
5'-most EST
                   jC-qmst02400032h12d1
Seq. No.
Contig ID
                   338082 1.R1040
5'-most EST
                  jC-gmst02400033a08d1
Seq. No.
                   33684
Contig ID
                   338091 1.R1040
5'-most EST
                  jC-gmst02400033b03d1
```

33685 Seq. No. 338112_1.R1040 Contig ID 5'-most EST jC-gmst02400033c05d1 Seq. No. 33686 338180 1.R1040 Contig ID 5'-most EST jC-gmst02400033g03d1 33687 Seq. No. 338188 1.R1040 Contig ID 5'-most EST jC-gmst02400033g08d1 Seq. No. 33688 Contig ID 338192 1.R1040 5'-most EST jC-gmst02400033g12d1 Method BLASTN NCBI GI g499067 BLAST score 265 E value 1.0e-147 Match length 301 % identity 97 NCBI Description G.max gmr2 gene 33689 Seq. No. Contig ID 338204 1.R1040 5'-most EST jC-gmst02400033h08a1 Seq. No. Contig ID 338269 1.R1040 5'-most EST jC-gmst02400036a11d2 Seq. No. 33691 Contig ID 338281 1.R1040 5'-most EST jC-qmst02400036b11d2 Seq. No. Contig ID 338526 1.R1040 5'-most EST jC-gmst02400040b12a1 Seq. No. 338748 1.R1040 Contig ID 5'-most EST jC-gmst02400049e08d1 Seq. No. 33694 338812 1.R1040 Contig ID 5'-most EST jC-gmst02400043h05d1 33695 Seq. No. Contig ID 338830 1.R1040 5'-most EST jC-gmst02400044a06a1 33696 Seq. No. 338831 1.R1040 Contig ID 5'-most EST jC-gmst02400044a06d1 33697 Seq. No.

338843 1.R1040

Contig ID

% identity

```
5'-most EST
                   jC-gmst02400044b04d1
Seq. No.
                   33698
Contig ID
                   338896 1.R1040
5'-most EST
                   jC-gmst02400044f01d1
                   BLASTX
Method
                   q3063445
NCBI GI
BLAST score
                   118
                   2.0e-14
E value
Match length
                   104
% identity
                   37
NCBI Description
                   (AC003981) F22013.7 [Arabidopsis thaliana]
                   33699
Seq. No.
Contig ID
                   338929 1.R1040
5'-most EST
                   jC-qmst02400044h02d1
Seq. No.
                   33700
Contig ID
                   339048 1.R1040
5'-most EST
                   jC-gmst02400046a03d1
Seq. No.
                   33701
Contig ID
                   339074 1.R1040
5'-most EST
                   q4305020
Method
                   BLASTX
NCBI GI
                   g3169178
BLAST score
                   523
E value
                   5.0e-53
Match length
                   259
% identity
                   41
NCBI Description
                   (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   33702
Contig ID
                   339079 1.R1040
5'-most EST
                   jC-gmst02400046c08d1
                   33703
Seq. No.
Contig ID
                   339257 1.R1040
5'-most EST
                   jC-gmst02400047g03d1
                   33704
Seq. No.
                   339262 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400047h05a1
                   33705
Seq. No.
Contig ID
                   339265 1.R1040
5'-most EST
                   jC-gmst02400047h07a1
Seq. No.
                   33706
Contig ID
                   339302 1.R1040
5.'-most EST
                   jC-gmst02400048b10a1
                  BLASTX
Method
NCBI GI
                  g3582340
BLAST score
                   146
E value
                   2.0e-09
Match length
                   90
```

Method

BLASTX

```
NCBI Description
                   (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                   33707
Contig ID
                   339552 1.R1040
5'-most EST
                  uC-qmronoir046q03b1
Method
                  BLASTX
NCBI GI
                   q4512705
BLAST score
                   820
E value
                   2.0e-93
Match length
                   203
% identity
NCBI Description
                   (AC006569) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   33708
Contig ID
                   339613 1.R1040
                   jC-gmst02400050g11a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4455275
BLAST score
                  266
E value
                   3.0e-23
Match length
                  121
% identity
NCBI Description
                  (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  339617 1.R1040
5'-most EST
                  jC-gmst02400071f06d1
Seq. No.
                  33710
Contig ID
                  339656 1.R1040
5'-most EST
                  jC-gmst02400051b09d1
Seq. No.
                  33711
                  339670 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy008g11b1
Method
                  BLASTX
NCBI GI
                  g4457221
BLAST score
                  237
                  2.0e-19
E value
Match length
                  .88
% identity
NCBI Description
                  (AF127797) putative bZIP DNA-binding protein [Capsicum
                  chinense]
Seq. No.
                  33712
                  339684 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400051c12a1
Seq. No.
                  33713
                  339986 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400053f06a1
Seq. No.
                  33714
Contig ID
                  340111 1.R1040
5'-most EST
                  jC-gmst02400054e06d1
```

```
NCBI GI
                   g3335339
BLAST score
                   161
E value
                   8.0e-11
Match length
                   106
% identity
                   (AC004512) Contains similarity to MADS-box protein AGL3
NCBI Description
                   gb U81369 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   33715
Contig ID
                   340137 1.R1040
5'-most EST
                   uC-gmropic008e06b1
Method
                   BLASTN
NCBI GI
                   g2598656
BLAST score
                   52
E value
                   3.0e-20
Match length
                   100
% identity
                   93
NCBI Description
                   Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
Seq. No.
Contig ID
                   340162 1.R1040
5'-most EST
                   q4396083
Seq. No.
                   33717
Contig ID
                   340366 1.R1040
5'-most EST
                   q55090\overline{5}5
Seq. No.
                   33718
Contig ID
                   340398 1.R1040
5'-most EST
                   jC-qmst02400056f04a1
Method
                   BLASTX
NCBI GI
                   q818849
BLAST score
                   599
E value
                   4.0e-62
Match length
                   161
% identity
                   67
NCBI Description
                   (U25430) nucleotide pyrophosphatase precursor [Oryza
                   sativa]
Seq. No.
                   33719
Contig ID
                   340450 1.R1040
5'-most EST
                   jC-gmst02400057a05d1
Seq. No.
                   33720
Contig ID
                   340520 1.R1040
5'-most EST
                   jC-gmst02400057d11d1
Seq. No.
                   33721
Contig ID
                   340629 1.R1040
5'-most EST
                   jC-gmst02400058b05a1
Method
                   BLASTN
NCBI GI
                   g4567193
BLAST score
                   39
E value
                   1.0e-12
Match length
                   202
% identity
                   85
```

NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic

```
sequence, complete sequence
Seq. No.
                  33722
Contig ID
                  340648 1.R1040
5'-most EST
                  fC-qmse700754614d2
Seq. No.
                  33723
Contig ID
                  340682 1.R1040
5'-most EST
                  jC-qmst02400058e06d1
Method
                  BLASTX
NCBI GI
                  g3023721
BLAST score
                  196
E value
                  8.0e-15
Match length
                  114
% identity
NCBI Description
                  FLOWERING TIME CONTROL PROTEIN FCA
                  >gi 2204095 emb CAB05391 (Z82992) FCA gamma [Arabidopsis
                  thaliana]
                  33724
Seq. No.
                  340719 1.R1040
Contig ID
                  jC-gmst02400058h01a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g112717
BLAST score
                  155
E value
                  4.0e-10
Match length
                  53
% identity
                  62
NCBI Description
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911
                  hypothetical protein precursor - carrot
                  >gi 18312 emb CAA36642 (X52395) precursor polypeptide (AA
                  -22 to 171) [Daucus carota]
Seq. No.
                  33725
                  340790 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400060b05d1
Seq. No.
                  33726
                  340944 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400061c10d1
                  33727
Seq. No.
                  341021_1.R1040
Contig ID
5'-most EST
                  fC-gmst700892334r4
                  33728
Seq. No.
                  341035 1.R1040
Contig ID
```

Seq. No. 33729

5'-most EST

Contig ID 341095_1.R1040

5'-most EST jC-gmst02400062e10d1

jC-qmst02400062a10d1

Seq. No. 33730

Contig ID 341111_1.R1040

5'-most EST jC-gmst02400062f10a1

```
Seq. No.
                   33731
                   341174 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063b01d1
Seq. No.
                   33732
                   341201 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400063c06a1
Seq. No.
                   33733
Contig ID
                   341299 1.R1040
5'-most EST
                   jC-gmst02400063h08a1
Method
                   BLASTN
                   g4567259
NCBI GI
BLAST score
                   40
E value
                   5.0e-13
Match length
                   68
% identity
                   90
                   Arabidopsis thaliana chromosome II BAC F3K23 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   33734
Contig ID
                   341349 1.R1040
5'-most EST
                   jC-qmst02400064d10d1
Method
                   BLASTX
NCBI GI
                   q4049344
BLAST score
                   172
E value
                   3.0e-12
Match length
                   56
% identity
NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   341396 1.R1040
5'-most EST
                   jC-qmst02400065a07a2
Seq. No.
Contig ID
                   341417 1.R1040
5'-most EST
                   jC-qmst02400065b09a2
Method
                   BLASTX
NCBI GI
                   q2062174
BLAST score
                   253
E value
                   1.0e-21
Match length
                   53
% identity
                   87
NCBI Description
                   (AC001645) transcription factor (TINY) isolog [Arabidopsis
                   thaliana]
                   33737
Seq. No.
Contig ID
                   341444 1.R1040
5'-most EST
                   jC-gmst02400065d01d1
Method
                   BLASTX
NCBI GI
                   g1076531
BLAST score
                   325
E value
                   6.0e-30
Match length
                   64
                   89
% identity
NCBI Description hypothetical protein, pollen allergen homolog - garden pea
```

```
>gi_2129891_pir__S65056 pollen allergen homolog precursor
(clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
homology with pollen allergens [Pisum sativum]
```

```
Seq. No.
                   33738
Contig ID
                   341479 1.R1040
5'-most EST
                   jC-qmst02400078a08a1
Seq. No.
                   33739
Contig ID
                   341662 1.R1040
5'-most EST
                   jC-gmst02400066g09a2
Seq. No.
                   33740
Contig ID
                   341694 1.R1040
5'-most EST
                   jC-gmst02400067a03d1
Method
                   BLASTX
NCBI GI
                   q3668088
BLAST score
                   409
E value
                   5.0e-40
Match length
                   93
% identity
NCBI Description
                   (AC004667) G9a-like protein [Arabidopsis thaliana]
Seq. No.
                   341752 1.R1040
Contig ID
5'-most EST
                   jC-gms\overline{t}02400067e03a1
Seq. No.
Contig ID
                   341893 1.R1040
5'-most EST
                   jC-gmst02400069a03a1
Seq. No.
Contig ID
                   341918 1.R1040
5'-most EST
                   jC-gmst02400069c10a1
Seq. No.
                   341962 1.R1040
Contig ID
5'-most EST
                   jC-gms\(\tau_02400069g07a1\)
Method
                   BLASTX
NCBI GI
                   q2191152
BLAST score
                   745
E value
                   5.0e-79
Match length
                   223
% identity
NCBI Description
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
                   thaliana]
                   33745
Seq. No.
Contig ID
                   341981 1.R1040
5'-most EST
                   jC-gmst02400070a07d1
Seq. No.
                   341983 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400070b09a1
```

33,747

341996 1.R1040

Seq. No.

Contig ID

```
jC-gmst02400070b09d1
  5'-most EST
                                                                . S
  Seq. No.
                     33748
  Contig ID
                     342045 1.R1040
  5'-most EST
                     jC-gmst02400070e11d1
  Seq. No.
                     33749
Contig ID
                     342118 1.R1040
  5'-most EST
                     uC-gmropic061h07b1
  Method
                     BLASTX
  NCBI GI
                     g3176726
  BLAST score
                     864
  E value
                     4.0e-93
  Match length
                     220
  % identity
  NCBI Description
                     (AC002392) putative serine proteinase [Arabidopsis
                     thalianal
                     33750
  Seq. No.
  Contig ID
                     342120 1.R1040
  5'-most EST
                     g56771<del>6</del>3
  Method
                     BLASTX
                     q3004564
  NCBI GI
  BLAST score
                     153
                     6.0e-10
  E value
                     89
  Match length
  % identity
                     (AC003673) putative receptor Ser/Thr protein kinase
  NCBI Description
                     [Arabidopsis thaliana]
                     33751
  Seq. No.
                     342159 1.R1040
  Contig ID
  5'-most EST
                     jC-gmst02400071e01a1
  Seq. No.
                     33752
                     342173 1.R1040
  Contig ID
  5'-most EST
                     jC-gmst02400071e11d1
  Method
                     BLASTX
  NCBI GI
                     g3860273
  BLAST score
                     451
                     6.0e-45
  E value
  Match length
                     108
  % identity
                     71
                     (AC005824) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     >gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein
                     [Arabidopsis thaliana]
                     33753
  Seq. No.
  Contig ID
                     342224 1.R1040
  5'-most EST
                     jC-qmst02400071h08d1
  Seq. No.
                     33754
                     342557 1.R1040
  Contig ID
  5'-most EST
                     jC-gmst02400074b08d1
  Method
                     BLASTX
                     g3201656
  NCBI GI .
```

181

BLAST score

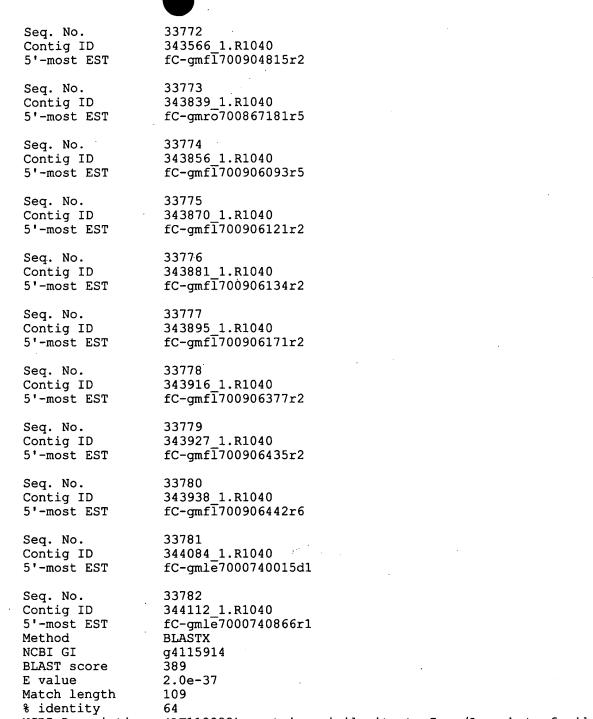
NCBI Description

```
6.0e-13
E value
Match length
                   131
% identity
                   (AF005933) galactokinase [Lactobacillus casei]
NCBI Description
Seq. No.
                   33755
                   342668 1.R1040
Contig ID
                   jC-gmst02400074h03a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3445238
BLAST score
                   437
E value
                   4.0e-43
Match length
                   193
                   48
% identity
                   (AL022347) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3451059_emb_CAA20455.1_ (AL031326) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   33756
Contig ID
                   342679 1.R1040
5'-most EST
                   jC-gmst02400074h09a1
                   BLASTX
Method
NCBI GI
                   g4206197
BLAST score
                   534
                   1.0e-54
E value
Match length
                   130
                   43
% identity
NCBI Description
                   (AF071527) putative pre-mRNA splicing factor [Arabidopsis
                   thaliana]
                   33757
Seq. No.
                   342775 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy116b09b1
                   33758
Seq. No.
                   342824 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400076f02a1
Seq. No.
                   33759
                   342843 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400076g03d1
Seq. No.
                   33760
Contig ID
                   342956 1.R1040
5'-most EST
                   jC-gmst02400077e06d1
Seq. No.
                   33761
Contig ID
                   343146 1.R1040
5'-most EST
                   fC-gmst700652684a1
Method
                   BLASTX
NCBI GI
                   g520582
BLAST score
                   237
E value
                   7.0e-20
                   67
Match length
% identity
```

(D37796) Ids3 [Hordeum vulgare]

```
33762
Seq. No.
Contig ID
                   343160 1.R1040
5'-most EST
                   fC-gmf1700862926r4
Seq. No.
                   33763
Contig ID
                   343179 1.R1040
5'-most EST
                   fC-gmse700862729r4
                   33764
Seq. No.
Contig ID
                   343192 1.R1040
5'-most EST
                   fC-qmf1700863558r3
                   33765
Seq. No.
Contig ID
                   343228 1.R1040
5'-most EST
                   fC-gmle700874601r1
Method
                   BLASTX
NCBI GI
                   g282881
BLAST score
                   385
E value
                   4.0e-37
Match length
                   130
% identity
                   55
NCBI Description
                   receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi 166846 (M84658) receptor-like protein kinase
                   [Arabidopsis thaliana]
                   33766
Seq. No.
                   343337 1.R1040
Contig ID
                   fC-gmf\overline{1}700902285r4
5'-most EST
                   33767
Seq. No.
                   343351_1.R1040
Contig ID
                   fC-gmf1700906289r2
5'-most EST
Seq. No.
                   33768
                   343351 4.R1040
Contig ID
5'-most EST
                   fC-gmro700744539r3
                   33769
Seq. No.
                   343439 1.R1040
Contig ID
                   fC-gmf1700904235d2
5'-most EST
                   33770
Seq. No.
Contig ID
                   343537 1.R1040
5'-most EST
                   fC-gmse700669533r3
                   33771
Seq. No.
                   343562_1.R1040
Contig ID
                   g4260372
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3510340
BLAST score
                   33
                   7.0e-09
E value
Match length
                   141
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MDN11, complete sequence [Arabidopsis thaliana]



NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1

(AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis

thaliana]

Seq. No. 33783

Contig ID 344116_1.R1040

```
fC-gmle7000740910r1
5'-most EST
                  33784
Seq. No.
                   344144 1.R1040
Contig ID
5'-most EST
                  fC-gmle7000741294r1
Seq. No.
                  33785
                   344207 1.R1040
Contig ID
5'-most EST
                   fC-gmse700758907a2
                  BLASTX
Method
                  g2569940
NCBI GI
BLAST score
                  302
                  2.0e-27
E value
                  132
Match length
                   49
% identity
                   (Y15194) GRS protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  33786
                  344281 1.R1040
Contig ID
                  fC-gmle700763807d4
5'-most EST
                  33787
Seq. No.
Contig ID
                  344285 1.R1040
5'-most EST
                  fC-qmle7000763827r1
Method
                  BLASTX
NCBI GI
                  g3192042
BLAST score
                  283
                  3.0e-25
E value
Match length
                  111
                   55
% identity
                   (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  33788
                  344313 1.R1040
Contig ID
                   fC-gmle700786228d4
5'-most EST
Method
                  BLASTX
                  g1076269
NCBI GI
BLAST score
                  182
                  3.0e-13
E value
Match length
                  56
                  57
% identity
                  pullulanase - spinach >gi 634093_emb CAA58803 (X83969)
NCBI Description
                  pullulanase [Spinacia oleracea]
Seq. No.
                  33789
                  344347 1.R1040
Contig ID
                  fC-gmro700567008r2
5'-most EST
Method
                  BLASTX
                  g1155255
NCBI GI
BLAST score
                  340
E value
                  8.0e-32
                  119
Match length
% identity
                  57
NCBI Description
                  (U39228) beta-glucosidase [Prunus avium]
                  33790
Seq. No.
                  344362 1.R1040
Contig ID
```

E value

```
5'-most EST
                   fC-gmle700553715d4
Method
                   BLASTX
NCBI GI
                   g3885336
BLAST score
                   219
                   1.0e-17
E value
Match length
                   97
% identity
                   (ACO05623) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   33791
Seq. No.
                   344373 1.R1040
Contig ID
5'-most EST
                   fC-gmle700553863r4
Seq. No.
                   33792
                   344466 1.R1040
Contig ID
5'-most EST
                   fC-gmle700555826d3
                   33793
Seq. No.
                   344470 1.R1040
Contig ID
5'-most EST
                   fC-gmle700555866r2
Seq. No.
                   33794
                   344517 1.R1040
Contig ID
5'-most EST
                   fC-gmle700557003d3
Seq. No.
                   33795
                   344577 1.R1040
Contig ID
5'-most EST
                   fC-gmle700557575d3
Seq. No.
                   33796
                   344599 1.R1040
Contig ID
5'-most EST
                   fC-gmle700557833d3
Seq. No.
                   33797
                   344756 1.R1040
Contig ID
5'-most EST
                   fC-gmle700560105b1
                   33798
Seq. No.
                   344759 1.R1040
Contig ID
5'-most EST
                   fC-gmle700560163r2
Seq. No.
                   33799
                   344799 1.R1040
Contig ID
5'-most EST
                   fC-gmle700742959r4
                   33800
Seq. No.
                   344808 1.R1040
Contig ID
5'-most EST
                   fC-gmle700681442r4
Seq. No.
                   33801
                   344836 1.R1040
Contig ID
5'-most EST
                   fC-gmle700684006f1
Method
                   BLASTX
NCBI GI
                   g2129541
BLAST score
                   623 .
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5.0e-65

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Contig ID

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33861

346248_1.R1040 fC-qmro700744202r4

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                   (SW:BGAL HUMAN) [Caenorhabditis elegans]
Seq. No.
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Contig ID
5'-most EST
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Seq. No.
Contig ID
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Contig ID
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NCBI GI
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BLAST score
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E value
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Match length
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% identity
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NCBI Description
                  Pisum sativum Wando ornithine carbamoyltransferase mRNA,
                  complete cds
Seq. No.
                  33860
Contig ID
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Method
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Contig ID 346618_1.R1040 5'-most EST fC-gmro700749247r4 Seq. No. 33914 Contig ID 346627_1.R1040 5'-most EST fC-gmro700749265r4 Seq. No. 33915 Contig ID 346632_1.R1040 5'-most EST fC-gmro700749283r4 Seq. No. 33916 Contig ID 346637_1.R1040 5'-most EST fC-gmro700749341r3 Seq. No. 33917 Contig ID 346643_1.R1040 5'-most EST fC-gmro700749381r3 Seq. No. 33918 Contig ID 346648_1.R1040	Contig ID	346612_1.R1040
Contig ID 346627_1.R1040 5'-most EST fC-gmro700749265r4 Seq. No. 33915 Contig ID 346632_1.R1040 5'-most EST fC-gmro700749283r4 Seq. No. 33916 Contig ID 346637_1.R1040 5'-most EST fC-gmro700749341r3 Seq. No. 33917 Contig ID 346643_1.R1040 5'-most EST fC-gmro700749381r3 Seq. No. 33918 Contig ID 346648_1.R1040	Contig ID	346618_1.R1040
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33931

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                  33930
Seq. No.
                  346742_2.R1040
Contig ID
5'-most EST
                  fC-gmro700794491r6
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33941

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346756 1.R1040
Contig ID
5'-most EST
                   fC-gmro700792724r8
Seq. No.
                   33932
Contig ID
                   346787 1.R1040
5'-most EST
                   fC-gmro700795004f1
Seq. No.
                   33933
Contig ID
                   346806 1.R1040
5'-most EST
                   fC-gmro700795654r6
Seq. No.
                   33934
Contig ID
                   346878 1.R1040
5'-most EST
                   fC-gmro700834955g1
Method
                   BLASTX
NCBI GI
                   q3335351
BLAST score
                   579
E value
                   1.0e-59
Match length
                   179
% identity
                   (AC004512) Similar to ERECTA receptor protein kinase
NCBI Description
                   qb D83257 from A. thaliana. ESTs qb T41629 and qb AA586072
                   come from this gene. [Arabidopsis thaliana]
                   33935
Seq. No.
Contig ID
                   346885 1.R1040 -
5'-most EST
                   fC-gmro700835567e1
                   33936
Seq. No.
Contig ID
                   347090 1.R1040
5'-most EST
                   fC-gmro700844704d4
                   BLASTX
Method
NCBI GI
                   q3096919
BLAST score
                   721
E value
                   3.0e-76
Match length
                   206
% identity
NCBI Description
                   (AL023094) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   33937
Seq. No.
Contig ID
                   347220 1.R1040
5'-most EST
                   fC-gmro700865409d3
                   33938
Seq. No.
Contig ID
                   347240 1.R1040
                   fC-gmro700847173f2
5'-most EST
Seq. No.
                   33939
Contig ID
                   347283 1.R1040
5'-most EST
                   fC-gmro700846785r4
                   33940
Seq. No.
Contig ID
                   347315 1.R1040
5'-most EST
                   fC-gmro700847042r7
```

. . .

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Contig ID
                   347422 1.R1040
5'-most EST
                   fC-gmro700848272r5
Seq. No.
                   33942
Contig ID
                   347579 1.R1040
5'-most EST
                   fC-gmro700864412r5
                   33943
Seq. No.
Contig ID
                   347591 1.R1040
5'-most EST
                   fC-gmst700791918r2
Seq. No.
                   33944
Contig ID
                   347611 1.R1040
5'-most EST
                   fC-gmro700864858r5
Seq. No.
                   33945
Contig ID
                   347732 1.R1040
5'-most EST
                   fC-gmro700865758r3
Seq. No.
                   33946
                   347908 1.R1040
Contig ID
5'-most EST
                   fC-gmro700868363r3
Seq. No.
                   33947
                   348010 1.R1040
Contig ID-
                   fC-gmst700890071d3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g886116
BLAST score
                   180
E value
                   3.0e-13
Match length
                   43
% identity
                   72
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
                   33948
Seq. No.
Contig ID
                   348076 1.R1040
5'-most EST
                   fC-gmro700873716d1
                   33949
Seq. No.
Contig ID
                   348077 1.R1040
5'-most EST
                   fC-gmro700873747d1
Seq. No.
                   33950
                   348081 1.R1040
Contig ID
5'-most EST
                   fC-gmst700891472r1
                   33951
Seq. No.
Contig ID
                   348300 1.R1040
5'-most EST
                   fC-gmse7000752657r1
Method
                   BLASTX
NCBI GI
                   g2245131
BLAST score
                   209
E value
                   2.0e-16
Match length
                   89
% identity
                   51
```

E value

3.0e-65

```
NCBI Description
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
                   33952
Seq. No.
Contig ID
                   348319 1.R1040
5'-most EST
                   fC-qmse7000753191f1
Method
                  BLASTX
NCBI GI
                  q232161
BLAST score
                   284
E value
                   2.0e-25
Match length
                  83
% identity
                   69
NCBI Description
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
                  >gi 68857 pir WMRZ19 19K globulin precursor - rice
                  >gi 20159 emb CAA45400 (X63990) 19 kDa globulin precursor
                   [Oryza sativa]
Seq. No.
                  33953
Contig ID
                   348339 1.R1040
                   fC-gmse700753764a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3608134
BLAST score
                  388
E value
                   3.0e-37
Match length
                  253
                  36
% identity
NCBI Description
                   (AC005314) dnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                   348349_1.R1040
Contig ID
5'-most EST
                   fC-gmse700754105d2
Seq. No.
                   33955
Contig ID
                   348371 1.R1040
5'-most EST
                   fC-gmse700754553d1
                  33956
Seq. No.
Contig ID
                  348455 1.R1040
5'-most EST
                   fC-gmse700762414d3
Method
                  BLASTX
NCBI GI
                  g4469013
BLAST score
                  347
E value
                  1.0e-32
Match length
                  122
% identity
                   61
NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
                  33957
Seq. No.
                  348562 1.R1040
Contig ID
5'-most EST
                  fC-gmse700758907d4
                  33958
Seq. No.
                  348674_1.R1040
Contig ID
5'-most EST
                  fC-gmst700649675a3
                  BLASTN
Method
NCBI GI
                  g169752
BLAST score
                  127
                             4
```

NCBI GI

```
Match length
                   223
% identity
                   89
NCBI Description
                   Rice alpha-amylase mRNA, complete cds, clone pOS103
                   33959
Seq. No.
Contig ID
                   348690 1.R1040
5'-most EST
                   fC-gmse700651322r1
                   33960
Seq. No.
                   348696 1.R1040
.Contig ID
5'-most EST
                   fC-gmst700654319g1
                   33961
Seq. No.
                   348858 1.R1040
Contig ID
5'-most EST
                   fC-gmse700655090d4
Method
                   BLASTX
NCBI GI
                   g1477480
BLAST score
                   234
E value
                   2.0e-19
                   70
Match length
% identity
                   67
                   (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                   [Arabidopsis thaliana]
                   33962
Seq. No.
                   349146 1.R1040
Contig ID
5'-most EST
                   fC-gmst700663510r4
Method
                   BLASTX
NCBI GI
                   g2499613
BLAST score
                   540
E value
                   3.0e-55
Match length
                   130
                   77
% identity
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
NCBI Description
                   >gi 1204129 emb CAA57719 (X82268) protein kinase [Medicago
                   sativa]
Seq. No.
                   33963
                   349151 1.R1040
Contig ID
5'-most EST
                   fC-gmst700662560y1
Method
                   BLASTX
NCBI GI
                   g1352980
BLAST score
                   207
E value
                   4.0e-16
Match length
                   64
% identity
                  ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR
NCBI Description
                   MTR4) >gi 1078374 pir S56822 SKI2 protein homolog YJL050w
                   - yeast (Saccharomyces cerevisiae)
                   >gi 1008185 emb CAA89341 (Z49325) ORF YJL050w
                   [Saccharomyces cerevisiae]
                   33964
Seq. No.
                   349170 1.R1040
Contig ID
5'-most EST
                   fC-gmse700658520r5
Method
                   BLASTN
```

g2636696

BLAST score

635 .

```
BLAST score
                    143
E value
                    1.0e-74
Match length
                    392
                    93
% identity
NCBI Description Mus musculus lysyl oxidase-2 (Lox2) mRNA, partial cds
Seq. No.
                    33965
                    349207 1.R1040
Contig ID
5'-most EST
                    fC-gmse700658863r5
                    33966
Seq. No.
                    349468 1.R1040
Contig ID
5'-most EST
                    fC-gmst700666737r3
                    33967
Seq. No.
                    349483 1.R1040
Contig ID
5'-most EST
                    fC-gmse700668119i2
Method
                    BLASTX
NCBI GI
                    g1651934
BLAST score
                    260
                    4.0e-22
E value
Match length
                    175
% identity
                    (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
                    33968
Seq. No.
                    349747 1.R1040
Contig ID
5'-most EST
                    fC-gmst700663367r1
                    33969
Seq. No.
                    349855 1.R1040
Contig ID
5'-most EST
                    fC-gmse700672209d4
Method
                    BLASTX
NCBI GI
                    g1708971
BLAST score
                    311
E value
                    4.0e-28
Match length
                    161
% identity
                    43
NCBI Description
                    (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                    (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                    >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                    (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi_1090776_prf__2019441A mandelonitrile lyase
                    [Prunus serotina]
                    33970
Seq. No.
                    349926 1.R1040
Contig ID
5'-most EST
                    fC-gmse700670512r3
                    33971
Seq. No.
                    349953 1.R1040
Contig ID
5'-most EST
                    fC-gmse700671032g1
Method
                    BLASTN
NCBI GI
                    g575730
```

Contig ID

```
E value
                  0.0e+00
Match length
                   753
                   97
% identity
                   Z.mays mRNA for transmembrane protein
NCBI Description
                   33972
Seq. No.
Contig ID
                   349985 1.R1040
5'-most EST
                   fC-gmse700671225d3
                   BLASTX
Method
NCBI GI
                   g3641836
BLAST score
                   158
E value
                   1.0e-10
                   70
Match length
                   56
% identity
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   33973
                   349988_1.R1040
Contig ID
5'-most EST
                   fC-gmse700671225z1
Method
                   BLASTX
NCBI GI
                   g3068705
BLAST score
                   264
E value
                   1.0e-22
                   176
Match length
                   35
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   33974
                   349995 1.R1040
Contig ID
5'-most EST
                   fC-gmst700664692r1
Seq. No.
                   33975
                   350026 1.R1040
Contig ID
5'-most EST
                   fC-gmse700671753g1
Method
                   BLASTX
NCBI GI
                   g1773287
BLAST score
                   1386
E value
                   1.0e-154
Match length
                   342
% identity
                   (U71080) cinnamate-4-hydroxylase [Arabidopsis thaliana]
NCBI Description
                   33976
Seq. No.
Contig ID
                   350084 1.R1040
5'-most EST
                   fC-gmse700672216f2
Method
                   BLASTX
NCBI GI
                   g3643604
BLAST score
                   407
E value
                   2.0e-39
                   228
Match length
% identity
                   (AC005395) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   33977
```

350085 1.R1040

33988

```
5'-most EST
                   fC-gmse700672216d3
Seq. No.
                   33978
Contig ID
                   350103 1.R1040
5'-most EST
                   fC-qmse700672249z1
Seq. No.
                   33979
Contig ID
                   350110 1.R1040
5'-most EST
                   fC-gmst700665136r1
Method
                   BLASTX
NCBI GI
                   g4234955
BLAST score
                   210
E value
                   1.0e-16
Match length
                   80
% identity
NCBI Description
                   (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                   33980
Contig ID
                   350113 1.R1040
5'-most EST
                   fC-gmse700672271z1
Method
                   BLASTN
NCBI GI
                   q168419
BLAST score
                   670
E value
                   0.0e+00
Match length
                   918
                   93
% identity
NCBI Description
                  Maize (Z.mays) aldolase mRNA, complete cds
                   33981
Seq. No.
Contig ID
                   350190 1.R1040
5'-most EST
                   fC-gmse700672612z1
Seq. No.
                   33982
Contig ID
                   350213 1.R1040
5'-most EST
                   fC-gmse700672781r5
Seq. No.
                   33983
Contig ID
                   350257 1.R1040
                   fC-gmse700673112r3
5'-most EST
Seq. No.
                   33984
Contig ID
                   350544 1.R1040
5'-most EST
                   fC-gmse700675307r3
Seq. No.
                   33985
Contig ID
                   350661 1.R1040
5'-most EST
                   g5605669
Seq. No.
                   33986
Contig ID
                   350744 1.R1040
5'-most EST
                   fC-gmse700752365d4
Seq. No.
                   33987
Contig ID
                   350780 1.R1040
5'-most EST
                   fC-gmse700753037d4
```

Contig ID 5'-most EST

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350803_1.R1040
Contig ID
                   fC-gmse700753340d4
5'-most EST
                                                                                - : · · +
Method
                   BLASTN
NCBI GI
                   g1770523
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
                   H.sapiens U32 small nucleolar RNA gene
NCBI Description
                   33989
Seq. No.
                   350818 1.R1040
Contig ID
5'-most EST
                   fC-gmse700753716d5
                   BLASTX
Method
NCBI GI
                   g4406761
BLAST score
                   323
E value
                   6.0e-30
Match length
                   78
                   76
% identity
                   (AC006836) putative ubiquinone biosynthesis protein
NCBI Description
                   [Arabidopsis thaliana]
                   33990
Seq. No.
                   350829 1.R1040 ·
Contig ID
                   fC-gmse700753825d1
5'-most EST
                   33991
Seq. No.
                   350849 1.R1040
Contig ID
5'-most EST
                   fC-gmse700754216d2
                   33992
Seq. No.
                   350881 1.R1040
Contig ID
5'-most EST
                   fC-gmse700754725d2
Method
                   BLASTN
NCBI GI
                   g2598586
BLAST score
                   221
E value
                   1.0e-121
Match length
                   473
                   88
% identity
NCBI Description
                   Medicago truncatula mRNA for cycloartenol synthase, partial
                   33993
Seq. No.
                   350902 1.R1040
Contig ID
5'-most EST
                   fC-gmse700755168d4
Seq. No.
                   33994
                   350991 1.R1040
Contig ID
5'-most EST
                   fC-gmse700757667d6
                   33995
Seq. No.
                   351263 1.R1040
Contig ID
5'-most EST
                   fC-gmst700665357r5
                   33996
Seq. No.
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351520_1.R1040

fC-gmse700856529r4

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33997
Seq. No.
                   351579 1.R1040
Contig ID
5'-most EST
                   fC-gmst700605402f4
Method
                   BLASTX
NCBI GI
                   g1076579
BLAST score
                   245
E value
                   6.0e-21
Match length
                   61
% identity
NCBI Description
                  alcohol dehydrogenase homolog ADH3a - tomato
                   33998
Seq. No.
Contig ID
                   351581 1.R1040
5'-most EST
                   fC-gmst700605413f4
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   547
E value
                   4.0e-56
Match length
                   170
                   59
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                   33999
Seq. No.
                   351584 1.R1040
Contig ID
5'-most EST
                   fC-gmst700605438a2
Method
                   BLASTX
NCBI GI
                  g3367596
BLAST score
                   458
E value
                   9.0e-46
                   149
Match length
% identity
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
                   34000
Seq. No.
                   351711 1.R1040
Contig ID
5'-most EST
                   fC-gmst700650943r1
                   34001
Seq. No.
                   351723 1.R1040
Contig ID
5'-most EST
                   fC-gmst700650945r6
Method
                  BLASTX
NCBI GI
                  g1514597
BLAST score
                   226
E value
                   3.0e-18
Match length
                  116
% identity
                   41
NCBI Description
                   (Y07595) transcription factor TFIIH [Homo sapiens]
                  >gi_4504201 ref NP 001508.1 pGTF2H4 general transcription
                  factor IIH, polypeptide 4 (52kD subunit)
                  34002
Seq. No.
                   351878 1.R1040
Contig ID
5'-most EST
                  fC-gmst700652684d1
                  34003
Seq. No.
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351906_1.R1040

Contig ID

5'-most EST

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5'-most EST
                   fC-gmst700651965d7
                   34004
Seq. No.
Contig ID
                   352072 1.R1040
5'-most EST
                   fC-gmst700653543r6
Method
                   BLASTX
NCBI GI
                   g861157
BLAST score
                   968
E value
                   1.0e-105
Match length
                   247
% identity
                   76
                   (Z35163) cell wall invertase II; beta-furanofructosidase
NCBI Description
                   [Vicia faba]
Seq. No.
                   34005
Contig ID
                   352186 1.R1040
5'-most EST
                   fC-gmst700653794r7
Seq. No.
                   34006
Contig ID
                   352317 1.R1040
5'-most EST
                   fC-gmst700660827r5
Seq. No.
                   34007
                   352327 1.R1040
Contig ID
5'-most EST
                   fC-gmst700660854r5
                   34008
Seq. No.
Contig ID
                   352407 1.R1040
5'-most EST
                   fC-gmst700661765r3
Seq. No.
                   34009
Contig ID
                   352411 1.R1040
5'-most EST
                   fC-gmst700661785d4
Seq. No.
                   34010
                   352454 1.R1040
Contig ID
5'-most EST
                   fC-qmst700662075r5
Seq. No.
                   34011
                   352478 1.R1040
Contig ID
                   fC-gmst700662785b1
5'-most EST
                   34012
Seq. No.
Contig ID
                   352518_1.R1040
                   fC-gmst700662684d3
5'-most EST
                   34013
Seq. No.
Contig ID
                   352596 1.R1040
5'-most EST
                   fC-gmst700663510r3
                   34014
Seq. No.
                   352799 1.R1040
Contig ID
                   fC-gms\(\overline{t}\)700664577r3
5'-most EST
Seq. No.
                   34015
Contig ID
                   353012 1.R1040
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fC-gmst700665233r6

Seq. No. Contig ID 5'-most EST

	Seq. No. Contig ID 5'-most EST	34016 353023_1.R1040 fC-gmst700665327r5
	Seq. No. Contig ID 5'-most EST	34017 353059_1.R1040 fC-gmst700665435r5
	Seq. No. Contig ID 5'-most EST	34018 353076_1.R1040 fC-gmst700665646r5
	Seq. No. Contig ID 5'-most EST	34019 353119_1.R1040 fC-gmst700665913r5
	Seq. No. Contig ID 5'-most EST	34020 353141_1.R1040 fC-gmst700665984r5
	Seq. No. Contig ID 5'-most EST	34021 353182_1.R1040 fC-gmst700666090r5
	Seq. No. Contig ID 5'-most EST	34022 353196_1.R1040 fC-gmst700666104r5
	Seq. No. Contig ID 5'-most EST	34023 353211_1.R1040 fC-gmst700666279r5
	Seq. No. Contig ID 5'-most EST	34024 353258_1.R1040 fC-gmst700666508r5
	Seq. No. Contig ID 5'-most EST	34025 353319_1.R1040 fC-gmst700667018r5
	Seq. No. Contig ID 5'-most EST	34026 353440_1.R1040 fC-gmst700892053r2
	Seq. No. Contig ID 5'-most EST	34027 353656_1.R1040 fC-gmst700890147y1
•	Seq. No. Contig ID 5'-most EST	34028 353906_1.R1040 uC-gmflminsoy001b10b1

34029 354050_1.R1040 uC-gmflminsoy082d09b1

NCBI Description

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34030
Seq. No.
Contig ID
                   354245 1.R1040
5'-most EST
                   uC-gmflminsoy008b08b1
Seq. No.
                   34031
Contig ID
                   354262 1.R1040
5'-most EST
                   uC-gmflminsoy008d08b1
                   34032
Seq. No.
Contig ID
                   354264 1.R1040
5'-most EST
                   uC-gmropic025a05b1
Method
                   BLASTX
NCBI GI
                   g4220462
BLAST score
                   561
E value
                   2.0e-57
Match length
                   121
% identity
NCBI Description
                   (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                   and bZIP PF 00170 domains. [Arabidopsis thaliana]
Seq. No.
                   34033
                   354297 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy010a08b1
Seq. No.
                   34034
Contig ID
                   354314 1.R1040
5'-most EST
                   uC-gmflminsoy010c06b1
Seq. No.
                   34035
                   354316 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy041c10b1
Method
                   BLASTX
                   g3367520
NCBI GI
BLAST score
                   141
E value
                   1.0e-08
Match length
                   70
% identity
NCBI Description
                   (AC004392) Similar to protein kinase APK1A,
                   tyrosine-serine-threonine kinase gb_D12522 from A.
                   thaliana. [Arabidopsis thaliana]
                   34036
Seq. No.
Contig ID
                   354362 1.R1040
5'-most EST
                   uC-gmflminsoy010h02b1
                   34037
Seq. No.
                   354384 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy011b03b1
Method
                   BLASTX
NCBI GI
                   g1786136
BLAST score
                   316
                   7.0e-29
E value
Match length
                   210
% identity
```

(AB000452) PEThy; ZPT2-6 [Petunia x hybrida]

NCBI Description

```
34038
Seq. No.
Contig ID
                   354418 1.R1040
5'-most EST
                   g4302953
Seq. No.
                   34039
Contig ID
                   354536 1.R1040
5'-most EST
                   uC-gmflminsoy014b10b1
Seq. No.
                   34040 -
Contig ID
                   354555 1.R1040
5'-most EST
                   uC-gmrominsoy250c10b1
Method
                   BLASTX
NCBI GI
                   g2244971
BLAST score
                   625
E value
                   3.0e-65
Match length
                   143
% identity
NCBI Description
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34041
                   354595 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy0001h10b1
Method
                   BLASTX
                   g4406820
NCBI GI
BLAST score
                   572
                   4.0e-59
E value
Match length
                   136
% identity
                   77
                   (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                   thaliana]
                   34042
Seq. No.
Contig ID
                   354599 1.R1040
5'-most EST
                   uC-gmflminsoy015c06b1
Method
                   BLASTX
NCBI GI
                   g3522943
BLAST score
                   717
                   5.0e-76
E value
                   177
Match length
% identity
NCBI Description
                   (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.
                   34043
Contig ID
                   354617 1.R1040
5'-most EST
                   uC-gmflminsoy016d06b1
Seq. No.
                   34044
                   354659 1.R1040
Contig ID
5'-most EST
                   uC-gmropic096e06b1
Method
                   BLASTX
NCBI GI
                   g3947735
BLAST score
                   313
E value
                   1.0e-28
Match length
                   139
% identity
                   48
```

(AJ009720) NL27 [Solanum tuberosum]

```
Seq. No.
                   34045
                   354744 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy018g10b1
Method
                BLASTN
NCBI GI
                   g4220645
BLAST score
                   36
E value
                   1.0e-10
Match length
                   171
% identity
                 . 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MYA6, complete sequence [Arabidopsis thaliana]
                   34046
Seq. No.
Contig ID
                   354833 1.R1040
5'-most EST
                   q4396975
Method
                   BLASTX
NCBI GI
                   g1673366
BLAST score
                   739
E value
                   1.0e-78
Match length
                   149
                   89
% identity
NCBI Description
                   (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis
                   thaliana]
                   34047 -
Seq. No.
Contig ID
                   354847 1.R1040
5'-most EST
                   uC-gmflminsoy020e04b1
                   BLASTX
Method
NCBI GI
                   g2853073
BLAST score
                   198
                   1.0e-26
E value
                   153
Match length
% identity
NCBI Description
                   (AL021768) putative protein [Arabidopsis thaliana]
                   34048
Seq. No.
Contig ID
                   355313 1.R1040
5'-most EST
                   uC-gmflminsoy026d04b1
Method
                   BLASTX
NCBI GI
                   g2224663
BLAST score
                   764
                   3.0e-81
E value
Match length
                   294
% identity
NCBI Description
                  (AB002359) KIAA0361 [Homo sapiens]
                   34049
Seq. No.
Contig ID
                   355483 1.R1040
5'-most EST
                   q5606799
Method
                  BLASTN
NCBI GI
                   q471307
BLAST score
                   34
E value
                   2.0e-09
Match length
                  52
% identity
                   94
```

NCBI Description G.max gene for cyclin

5'-most EST

Method -

```
Seq. No.
                   34050
                   355602 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy029h03b1
Method
                   BLASTX
                   g4559333
NCBI GI
BLAST score
                   148
E value
                   2.0e-09
Match length
                   79
% identity
                   44
NCBI Description
                   (AC007087) unknown protein [Arabidopsis thaliana]
                   34051
Seq. No.
Contig ID
                   355684 1.R1040
5'-most EST
                   uC-gmflminsoy030g12b1
Method
                   BLASTX
NCBI GI
                   q3935179
BLAST score
                   139
E value
                   2.0e-11
Match length
                   113
% identity
                   38
NCBI Description
                   (AC004557) F17L21.22 [Arabidopsis thaliana]
Seq. No.
                   34052
                   355704 1.R1040
Contig ID
5'-most EST
                   g5666621
Method
                   BLASTX
NCBI GI
                   g1653953
BLAST score
                   171
E value
                   5.0e-12
Match length
                   110
% identity
NCBI Description
                   (D90917) hypothetical protein [Synechocystis sp.]
Seq. No.
                   34053
Contig ID
                   355735 1.R1040
5'-most EST
                   uC-gmflminsoy036d05b1
Seq. No.
                   34054
Contig ID
                   355786 1.R1040
5'-most EST
                   uC-gmflminsoy062f06b1
                   34055
Seq. No.
Contig. ID
                   355814 1.R1040
5'-most EST
                   uC-qmflminsoy032f09b1
Method
                   BLASTN
NCBI GI
                   q1419035
BLAST score
                   244
E value
                   1.0e-135
Match length
                   388
% identity
                   91
NCBI Description
                  M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase,
                   P5CS-1
Seq. No.
                   34056
Contig ID
                   355869 1.R1040
```

uC-qmflminsoy078q06b1

BLASTX

34062

```
NCBI GI
                   q3176707
BLAST score
                   146 -
E value
                   2.0e-09
Match length
                   44
% identity
NCBI Description
                   (AC002392) putative proline-rich protein APG [Arabidopsis
                  thaliana]
                   34057
Seq. No.
Contig ID
                   355923 1.R1040
5'-most EST
                  uC-gmflminsoy035e10b1
Method
                  BLASTX
NCBI GI
                  g126722
BLAST score
                   154
E value
                   3.0e-10
Match length
                   85
% identity
                   35
NCBI Description
                  ALPHA-MANNOSIDASE II (MANNOSYL-OLIGOSACCHARIDE
                  1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI
                  ALPHA-MANNOSIDASE II) >gi_110673_pir__A41641
                  mannosyl-oligosaccharide \overline{1}, 3-1, 6-alpha-mannosidase (EC
                  3.2.1.114) - mouse >gi_49944 emb_CAA43480_ (X61172)
                  mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase [Mus
                  musculus]
                  34058
Seq. No.
Contig ID
                  355995 1.R1040
5'-most EST
                  uC-gmrominsoy194g07b1
                  34059
Seq. No.
Contig ID
                  355999 1.R1040
5'-most EST
                  g4396410
Method
                  BLASTX
NCBI GI
                  g2232354
BLAST score
                  243
E value
                  3.0e-25
Match length
                  112
% identity
                  55
NCBI Description
                  (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
                  34060
Seq. No.
Contig ID
                  356041 1.R1040
5'-most EST
                  uC-gmflminsoy065c06b1
Method
                  BLASTN
NCBI GI
                  g3367637
BLAST score
                  36
E value
                  8.0e-11
Match length
                  48
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for monogalactosyldiacylglycerol
                  synthase
Seq. No.
                  34061
Contig ID
                  356063 1.R1040
5'-most EST
                  uC-gmflminsoy037d09b1
```

```
356152 1.R1040
Contig ID
                  uC-gmflminsoy040f09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1076545
BLAST score
                  458
                  1.0e-57
E value
                  162
Match length
                  71
% identity
NCBI Description
                  quanine nucleotide regulatory protein - fava bean
                  >gi 547478 emb CAA85733 (Z37503) guanine nucleotide
                  regulatory protein [Vicia faba] >gi_1098297_prf__2115367E
                  small GTP-binding protein [Vicia faba]
                  34063
Seq. No.
Contig ID
                  356212 1.R1040
5'-most EST
                  uC-gmflminsoy041e09b1
Seq. No.
                  34064
Contig ID
                  356238 1.R1040
5'-most EST
                  uC-qmropic067a12b1
Method
                  BLASTX
NCBI GI
                  q4544473
BLAST score
                  393
E value
                  3.0e-38
Match length
                  124
% identity
NCBI Description
                  (ACO06580) putative mei2 protein [Arabidopsis thaliana]
                  34065
Seq. No.
Contig ID
                  356254 1.R1040
5'-most EST
                  uC-gmflminsoy042b10b1
Method
                  BLASTX
NCBI GI
                  g1369852
BLAST score
                  567
E value
                  2.0e-58
Match length
                  146
% identity
NCBI Description
                  (L46702) kinesin heavy chain-like protein [Solanum
                  tuberosum]
                  34066
Seq. No.
                  356278 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy044h01b1
                  34067
Seq. No.
Contig ID
                  356297 1.R1040
5'-most EST
                  uC-qmflminsoy042q02b1
Method
                  BLASTX
NCBI GI
                  g417308
BLAST score
                  301
E value
                  3.0e-27
Match length
                  160
% identity
NCBI Description
                  PROBABLE HELICASE MOT1 >gi 283205 pir S22775 MOT1 protein
                  - yeast (Saccharomyces cerevisiae) >gi 171965 (M83224) Mot1
                  [Saccharomyces cerevisiae] >gi 1147612 (U41849) LPF4c;
```

Motlp is a probable helicase essential for vegetative

141

growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352 [Saccharo

Seq. No. 34068 356307 1.R1040 Contig ID 5'-most EST q4396674 Method BLASTX NCBI GI q4522004 BLAST score 525 E value 2.0e-53 Match length 189 % identity NCBI Description (AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No. 34069

Contig ID 356309_1.R1040

5'-most EST uC-gmflminsoy042h04b1

Seq. No. 34070

Contig ID 356334 1.R1040

5'-most EST uC-gmrominsoy177h07b1

Seq. No. 34071

Contig ID 356337_1.R1040

5'-most EST uC-gmflminsoy043b12b1

Seq. No. 34072

Contig ID 356375 1.R1040

5'-most EST uC-gmflminsoy100b12b1

Seq. No. 34073

Contig ID 356401 1.R1040

5'-most EST g5688034

Seq. No. 34074

Contig ID 356429_1.R1040

5'-most EST uC-gmflminsoy044c10b1

Method BLASTX
NCBI GI g3402687
BLAST score 346
E value 1.0e-32
Match length 91

% identity 71

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 34075

Contig ID 356450 1.R1040

5'-most EST uC-gmflminsoy053e01b1

Seq. No. 34076

Contig ID 356518_1.R1040

5'-most EST uC-gmrominsoy180a08b1

Method BLASTN NCBI GI g1326160

BLAST score 54

```
2.0e-21
E value
Match length
                   88
% identity
                   97
NCBI Description
                   Phaseolus vulgaris dehydrin mRNA, complete cds .
                   34077
Seq. No.
                   356556 1.R1040
Contig ID
5'-most EST
                   g5605939
Seq. No.
                   34078
                   356709 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy047h01b1
                   34079
Seq. No.
Contig ID
                   356715 1.R1040
5'-most EST
                   uC-gmflminsoy047h08b1
Seq. No.
                   34080
Contig ID
                   356770 1.R1040 ·
5'-most EST
                   q4286721
Method
                   BLASTX
NCBI GI
                   q1362112
BLAST score
                   469
E value
                   3.0e-65
Match length
                   169
                   76
% identity
                  protein kinase NPK2 (EC 2.7.1.-) - common tobacco
NCBI Description
                   >gi_862342_dbj_BAA06731_ (D31964) NPK2 [Nicotiana tabacum]
Seq. No.
                   356863 1.R1040
Contig ID
5'-most EST
                   uC-gmropic092e11b1
Method
                   BLASTX
NCBI GI
                   g3068704
BLAST score
                   535
E value
                   2.0e-54
Match length
                   232
% identity
                   49
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   34082
Seq. No.
Contig ID
                   356872 1.R1040
5'-most EST
                   uC-gmflminsoy053f11b1
Method
                   BLASTX
NCBI GI
                   g2245036
BLAST score
                   304
E value
                   2.0e-27
                   174
Match length
% identity
                   (Z97342) triacylglycerol lipase homolog [Arabidopsis
NCBI Description
                  thaliana]
                   34083
Seq. No.
Contig ID
                   356943 1.R1040
5'-most EST
                  uC-gmflminsoy054e08b1
```

34084

Seq. No.

BLAST score

376

```
356947 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy054e12b1
Seq. No.
                   34085
Contig ID
                   356949 1.R1040
5'-most EST
                   uC-qmflminsoy054f02b1
Seq. No.
                   34086
                                                    44
Contig ID
                   357074 1.R1040
5'-most EST
                   uC-gmropic050f10b1
Seq. No.
                   34087
Contig ID
                   357107 1.R1040
5'-most EST
                   uC-gmflminsoy056f07b1
Method
                   BLASTX
NCBI GI
                   g3941448
BLAST score
                   582
E value
                   4.0e-60
                   116
Match length
% identity
                   (AF062878) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   34088
Seq. No.
                   357154 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy057c04b1
Seq. No.
                   34089
                   357197 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy057g02b1
Method
                   BLASTX
NCBI GI
                   g2342682
BLAST score
                   221
E value
                   7.0e-23
Match length
                   81
% identity
                   (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                  protein kinase (gb_X95577). [Arabidopsis thaliana]
                   34090
Seq. No.
                   357236_1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy058b11b1
Method
                   BLASTX
NCBI GI
                   g4176557
BLAST score
                   419
E value
                   3.0e-41
Match length
                   132
% identity
                   58
                   (AL035259) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   34091
Seq. No.
                   357404_1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy263b11b1
Method
                  BLASTX
NCBI GI
                  g320161-7
```

NCBI Description

```
4.0e-36
E value
Match length
                  94
% identity
NCBI Description
                  (AC004669) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  34092
Contig ID
                  357499 1.R1040
5'-most EST
                  uC-gmropic105e10b1
Method
                  BLASTX
NCBI GI
                  g728905
BLAST score
                  257
E value
                  3.0e-27
Match length
                  128
% identity
NCBI Description
                  PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC
                  RETICULUM CA2+-ATPASE) >gi 1078206 pir S51995 probable
                  ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)
                  >gi 171114 (L01795) ATPase [Saccharomyces cerevisiae]
                  >gi 595560 (U12980) Drs2p: Membrane spanning
                  Ca-ATPase(P-type), member of the cation transport(E1-E2)
                  ATPase [Saccharomyces cerevisiae]
                  34093
Seq. No.
Contig ID
                  358040: 1.R1040
                  uC-gmropic087b10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3687246
BLAST score
                  241
                  2.0e-20
E value
Match length
                  61
% identity
                  (AC005169) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana]
                  34094
Seq. No.
                  358071 1.R1040
Contig ID
                  uC-gmflminsoy109f01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3450842
BLAST score
                  506
E value
                  3.0e-51
Match length
                  136
% identity
NCBI Description
                  (AF080436) mitogen activated protein kinase kinase [Oryza
                  sativa]
                  34095
Seq. No.
Contig ID
                  358140 1.R1040
5'-most EST
                  uC-gmflminsoy079a04b1
Method
                  BLASTX
NCBI GI
                  g3510251
BLAST score
                  190
                  2.0e-14
E value
Match length
                  70
% identity
```

(AC005310) unknown protein [Arabidopsis thaliana]

NCBI Description

34102

Seq. No.

```
34096
Seq. No.
Contig ID
                   358221 1.R1040
5'-most EST
                   uC-gmflminsoy074e07b1
Method
                   BLASTX
NCBI GI
                   g3004555
BLAST score
                   221
E value
                   5.0e-18
Match length
                   140
% identity
                   (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                   34097
Seq. No.
Contig ID
                   358345 1.R1040
5'-most EST
                  uC-gmrominsoy273a10b1
Method
                  BLASTX
NCBI GI
                  g3292826
BLAST score
                   655
E value
                   2.0e-68
                  137
Match length
% identity
                  80
NCBI Description
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34098
                   358380 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy076d06b1
Seq. No.
                   34099
                  358447_1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy077c01b1
Method
                  BLASTX
NCBI GI
                  g3152598
BLAST score
                  348
                  7.0e-33
E value
Match length
                  116
                  57
% identity
                   (AC002986) Contains similarity to C2-HC type zinc finger
NCBI Description
                  protein C.e-MyT1 gb_U67079 from C. elegans and to
                  hypersensitivity-related gene 201 isolog T28M21.14 from A.
                  thaliana BAC gb AF002109. [Arabidopsis thaliana]
Seq. No.
                  34100
                  358648 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir0001f05b1
Seq. No.
                  34101
                  358685 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy080b09b1
Method
                  BLASTX
NCBI GI
                  q4455232
BLAST score
                  617
                  3.0e-64
E value
                  190
Match length
% identity
                  61
```

(AL035523) putative protein [Arabidopsis thaliana]

```
Contig ID
                   358703 1.R1040
5'-most EST
                  uC-qmflminsoy080d03b1
Method
                  BLASTX
NCBI GI
                  q2149640
BLAST score
                  697
E value
                   1.0e-73
Match length
                   156
% identity
NCBI Description
                   (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                  34103
Contig ID
                   358725 1.R1040
5'-most EST
                  uC-gmflminsoy080g08b1
                   34104
Seq. No.
Contig ID
                   358731 1.R1040
5'-most EST
                  uC-gmronoir045a03b1
Method
                  BLASTX
NCBI GI
                  g1351676
BLAST score
                  185
E value
                   3.0e-30
Match length
                  153
% identity
                   43
NCBI Description
                  PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C
                  >gi 2130307 pir_ S62590 hypothetical protein SPAC21E11.05c
                   - fission yeast (Schizosaccharomyces pombe)
                  >gi_1067221_emb_CAA91964_ (Z67999) peptidyl-prolyl
                  cis-trans isomerase [Schizosaccharomyces pombe]
                  34105
Seq. No.
                  358867 1.R1040
Contig ID
                  uC-gmflminsoy082f08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3283026
BLAST score
                  343
E value .
                  4.0e-32
Match length .
                  173
% identity
NCBI Description
                  (AF051562) putative transposase [Arabidopsis thaliana]
                  34106
Seq. No.
                  358885 1.R1040
Contig ID
5'-most EST
                  g5607084
Seq. No.
                  34107
                  358918 1.R1040
Contig ID
5'-most EST
                  uC-gmropic097g07b1
Method
                  BLASTX
NCBI GI
                  q3482972
BLAST score
                  159
E value
                  1.0e-10
Match length
                  124
% identity
NCBI Description
                  (AL031369) putative protein [Arabidopsis thaliana]
Seq. No. -
                  34108
```

358964_1.R1040

Contig ID

```
5'-most EST
                    uC-gmflminsoy084e07b1
                    BLASTX
 Method
 NCBI GI
                    g1825766
 BLAST score
                    182
                    3.0e-13
 E value
Match length
                    138
 % identity
                    33
                    (U88314) similar to flavin-containing monooxygenases
NCBI Description
                    [Caenorhabditis elegans]
                    34109
 Seq. No.
                    359431 1.R1040
 Contig ID
 5'-most EST
                    uC-gmropic005e04b1
                    34110
 Seq. No.
                    359487 1.R1040
 Contig ID
 5'-most EST
                    uC-gmropic065f05b1
                    34111
Seq. No.
                    359935 1.R1040
Contig ID
 5'-most EST
                    uC-gmrominsoy0001a08a1
                    BLASTX
Method
NCBI GI
                    g4512698
BLAST score
                    180
E value
                    4.0e-13
                    53
Match length
 % identity
                    (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    34112
                    359960 1.R1040
Contig ID
 5'-most EST
                    g51266<del>5</del>3
 Seq. No.
                    34113
                    360036 1.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy025f05b1
Seq. No.
                    34114
                    360042 1.R1040
 Contig ID
 5'-most EST
                    uC-gmrominsoy055h08b1
Method
                    BLASTN
NCBI GI
                    g1235973
                    153
BLAST score
                    2.0e-80
E value
Match length
                    381
 % identity
                    80
NCBI Description
                   G.pallida mRNA for collagen
                    34115
 Seq. No.
                    360049 1.R1040
Contig ID
 5'-most EST
                    uC-gmrominsoy026a01b1
```

360160 1.R1040 Contig ID uC-gmropic042b09b1 5'-most EST

Method BLASTX NCBI GI g3415117

```
355
BLAST score
E value
                  1.0e-33
Match length
                  83
% identity
                  39
NCBI Description
                  (AF081203) villin 3 [Arabidopsis thaliana]
                  34117
Seq. No.
Contig ID
                  ..360252 1.R1040
5'-most EST
                  uC-qmrominsoy030e09b1
Method
                  BLASTX
NCBI GI
                  g400042
BLAST score
                  303
E value
                  1.0e-27
Match length
                  100
% identity
NCBI Description
                  TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521
                  >gi 539700 pir A38093 transformation-sensitive protein IEF
                  SSP 3521 - human >gi_184565 (M86752)
                  transformation-sensitive protein [Homo sapiens]
Seq. No.
                  34118
Contig ID
                  360262 1.R1040
5'-most EST
                  uC-gmrominsoy030g02b1
Seq. No.
                  34119
Contig ID
                  360279 1.R1040
5'-most EST
                  uC-gmrominsoy031b07b1
Method
                  BLASTX
NCBI GI
                  g1184072
BLAST score
                  353
                  2.0e-33
E value
Match length
                  97
% identity
NCBI Description
                  (U40766) COL-1 [Meloidogyne incognita]
Seq. No.
                  34120
                  360304 1.R1040
Contig ID
5'-most EST
                  uC-gmropic096c09b1
Seq. No.
                  34121
                  360433 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy038b12b1
Seq. No.
                  34122
                  360436 1.R1040
Contiq ID
5'-most EST
                  uC-gmrominsoy035b05b1
Method
                  BLASTX
NCBI GI
                  g3881546
BLAST score
                  177
E value
                  6.0e-13
Match length
                  72
% identity
                  43
                  (Z69904) Similarity to Human RAD23 protein homolog2 (PIR
NCBI Description
                  Acc. No. S44443); cDNA EST EMBL: D71787 comes from this
                  gene; cDNA EST EMBL:D72299 comes from this gene; cDNA EST
```

EMBL: D72362 comes from this gene; cDNA EST EMBL: D72820 co

5'-most EST

```
Seq. No.
                  34123
                  360643 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy169d02b1
Method
                  BLASTN
NCBI GI
                  g4220637
BLAST score
                  38
                  8.0e-12
E value
Match length
                  66
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIE1, complete sequence [Arabidopsis thaliana]
                  34124
Seq. No.
Contig ID
                  360732 1.R1040
5'-most EST
                  uC-qmrominsoy302b03b1
Method
                  BLASTX
NCBI GI
                  q563237
BLAST score
                  240
E value
                  3.0e-20
Match length
                  80
% identity
NCBI Description
                  (U16030) cuticular collagen Bmcol-2 [Brugia malayi]
Seq. No.
                  360773 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy046h09b1
Seq. No.
                  34126
                  360795 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy158b08b1
Seq. No.
                  34127
Contig ID
                  360835 1.R1040
5'-most EST
                  uC-gmrominsoy048c04b1
Seq. No.
                  34128
                  360866 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy049a05b1
Method
                  BLASTX
NCBI GI
                  g731834
BLAST score
                  204
                  5.0e-16
E value
Match length
                  74
% identity
                  HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION
NCBI Description
                  >gi 1077790 pir S49797 hypothetical protein YIL083c -
                  yeast (Saccharomyces cerevisiae) >gi_577131_emb_CAA86711.1_
                  (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17
                  [Saccharomyces cerevisiae]
                  34129
Seq. No.
                  360892 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy049f09b1
Seq. No.
                  34130
                  360936 1.R1040
Contig ID
```

-

uC-gmrominsoy052g10b1

grade to history has

```
Method
                  BLASTX
NCBI GI
                  g3600038
BLAST score
                   733
E value
                   6.0e-78
Match length
                   160
% identity
                   86
NCBI Description
                   (AF080119) similar to Saccharomyces cerevisiae
                   transcription regulator SPO8 (SW:P41833) [Arabidopsis
                   thaliana]
                   34131
Seq. No.
Contig ID
                   361015 1.R1040
5'-most EST
                  uC-gmronoir007e08b1
Seq. No.
                   34132
Contig ID
                   361051 1.R1040
5'-most EST
                  uC-gmrominsoy094b01b1
Method
                  BLASTX
NCBI GI
                  g2459587
BLAST score
                  227
E value
                   1.0e-18
Match length
                  118
% identity
NCBI Description
                   (U77675) 22 upper [Onchocerca volvulus]
                  34133
Seq. No.
Contig ID
                   361135 1.R1040
5'-most EST
                  uC-gmrominsoy060a01b1
Seq. No.
                  34134
Contig ID
                  361145 1.R1040
5'-most EST
                  uC-gmronoir043g06b1
Method
                  BLASTX
NCBI GI
                  g1707276
BLAST score
                  509
                   1.0e-51
E value
Match length
                  118
% identity
NCBI Description
                   (U80931) similar to ADP/ATP translocase [Caenorhabditis
                  elegans]
Seq. No.
                  34135
Contiq ID
                  361161 1.R1040
5'-most EST
                  uC-gmrominsoy060e06b1
Seq. No.
                  34136
Contig ID
                  361211 1.R1040
5'-most EST
                  uC-gmrominsoy061f12b1
Method
                  BLASTX
NCBI GI
                  q627424
BLAST score
                  300
E value
                  2.0e-27
Match length
                  85
% identity
NCBI Description
                  dolichyl-diphosphooligosaccharide--protein glycotransferase
```

Large De Charge

(EC 2.4.1.119) 50kD subunit - human >gi_2135018_pir__S66254 dolichyl-diphosphooligosaccharide--protein glycotransferase

(EC 2.4.1.119) 50K chain - human

```
Seq. No.
                   34137
 Contig ID
                   361222 1.R1040
 5'-most EST
                   uC-gmrominsoy062a10b1
 Method
                   BLASTX
                   q1184072
 NCBI GI
 BLAST score
                   370
                   1.0e-35
 E value
 Match length
                   82
 % identity
                   (U40766) COL-1 [Meloidogyne incognita]
 NCBI Description
 Seq. No.
                   34138
 Contig ID
                   361236 1.R1040
 5'-most EST
                   uC-gmrominsoy062c03b1
 Seq. No.
                   34139
 Contig ID
                   361259 1.R1040
 5'-most EST
                   uC-gmrominsoy090g08b1
Seq. No.
                   34140
 Contig ID
                   361289 1.R1040
 5'-most EST
                   uC-gmrominsoy064b09b1
Method
                   BLASTX
NCBI GI
                   q547837
BLAST score
                   259
E value
                   2.0e-22
Match length
                   136
 % identity
                   L-LACTATE DEHYDROGENASE >gi_480440_pir__S36863 L-lactate
NCBI Description
                   dehydrogenase (EC 1.1.1.27) - Thermotoga maritima
                   >gi_396281_emb_CAA52355_ (X74302) L-lactate dehydrogenase
                   [Thermotoga maritima]
Seq. No.
                   34141
Contig ID
                   361298 1.R1040
 5'-most EST
                   uC-gmrominsoy174d09b1
                   34142
Seq. No.
Contig ID
                   361446 1.R1040
 5'-most EST
                   uC-gmrominsoy069b09b1
Method
                   BLASTX
NCBI GI
                   g2129698
BLAST score
                   168
E value
                   9.0e-12
Match length
                   59
 % identity
                   protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 1054633 emb CAA63387 (X92728) protein kinase
                   [Arabidopsis thaliana]
                   34143
Seq. No.
Contig ID
                   361485 1.R1040
 5'-most EST
                   uC-gmrominsoy071f10b1
```

BLASTX

q3860249

Method NCBI GI

NCBI GI

BLAST score

```
273
BLAST score
E value
                   5.0e-24
Match length
                   129
% identity
                   50
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   34144
                   361506_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy071b11b1
Method
                   BLASTX
                   g630594
NCBI GI
BLAST score
                   269
E value
                   2.0e-23
Match length
                   161
% identity
                   40
NCBI Description
                   DNA topoisomerase II - Caenorhabditis elegans >gi 156413
                   (L07144) DNA topoisomerase II [Caenorhabditis elegans]
                   34145
Seq. No.
Contig ID
                   361526 1.R1040
5'-most EST
                   uC-gmrominsoy265e06b1
Method
                   BLASTX
NCBI GI
                   g2144165
BLAST score
                   159
E value
                   9.0e-11
Match length
                   99
% identity
NCBI Description
                   aspartic proteinase (EC 3.4.23.-) - dog hookworm
                   (Ancylostoma caninum) (fragment) >gi 1507725 (U34888)
                   aspartic protease [Ancylostoma caninum]
Seq. No.
                   34146
Contig ID
                   361682 1.R1040
5'-most EST
                   uC-gmrominsoy079h11b1
Seq. No.
                   34147
Contig ID
                   361687 1.R1040
5'-most EST
                   uC-gmrominsoy080h10b1
                   34148
Seq. No.
Contig ID
                   361748 1.R1040
5'-most EST
                   uC-gmrominsoy081c06b1
Method
                   BLASTX
NCBI GI
                   q3928008
BLAST score
                   618
E value
                   2.0e-64
Match length
                   140
% identity
                   (AJ130877) heat shock protein 60 (HSP60) [Plectus
NCBI Description
                   acuminatus]
Seq. No.
                   34149
Contig ID
                   361773 1.R1040
5'-most EST
                   uC-gmrominsoy081h05b1
Method
                   BLASTX
```

q2129820

494

```
6.0e-50
E value
Match length
                   130
% identity
                   67
NCBI Description
                   chitinase (EC 3.2.1.14) class II - peanut
                   >gi 1237025 emb CAA57773 (X82329) chitinase (class II)
                   [Arachis hypogaea]
Seq. No.
                   34150
Contig ID
                   361998 1.R1040
5'-most EST
                   uC-gmrominsoy090c07b1
Method
                   BLASTX
NCBI GI
                   g1125763
BLAST score
                   161
E value
                   6.0e-11
Match length
                   141
% identity
NCBI Description
                   (U42835) C. elegans vitellogenin 5 precursor, vit-5 (Spieth
                   et al., NAR 13:7129-7138(1985)) [Caenorhabditis elegans]
                                                        TT.
Seq. No.
                   362227 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy096e04b1
                   BLASTX
Method
NCBI GI
                   g3879811
BLAST score
                   305
                   8.0e-28
E value
Match length
                   140
                   49
% identity
NCBI Description
                   (Z66524) Homology with Squid retinal-binding protein (PIR
                  Acc. No. A53057) [Caenorhabditis elegans]
Seq. No.
                   34152
Contig ID
                   362292 1.R1040
                   uC-gmrominsoy307h02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4006915
BLAST score
                   314
                   7.0e-29
E value
                   138
Match length
% identity
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34153
Contig ID
                   362380 1.R1040
5'-most EST
                   uC-gmropic032c08b1
Method
                   BLASTX
NCBI GI
                   q123637
BLAST score
                   539
E value
                   3.0e-55
Match length
                   114
                   89
% identity
                  HEAT SHOCK 70 KD PROTEIN A >gi_72214_pir__HHKW7A heat shock
NCBI Description
                  protein 70 A - Caenorhabditis elegans >gi 156352 (M18540)
                  heat shock protein 70A [Caenorhabditis elegans]
                   34154
Seq. No.
Contig ID
                   362556 1.R1040
```

5'-most EST

```
5'-most EST
                  uC-gmropic107h01b1
Method
                  BLASTX
NCBI GI
                  g4454567
BLAST score
                  408
                  2.0e-39
E value
                  246
Match length
% identity
                  38
                  (AF128407) lipase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34155
Contig ID
                  362579 1.R1040
5'-most EST
                  uC-gmrominsoy105e11b1
Seq. No.
                  34156
Contig ID
                  362817 1.R1040
5'-most EST
                  uC-gmrominsoy111e03b1
Seq. No.
                  34157
Contig ID
                  362915 1.R1040
5'-most EST
                  uC-gmrominsoy114b03b1
Method
                  BLASTX
NCBI GI
                  g1311386
BLAST score
                  667
E value
                  4.0e-70
Match length
                  166
% identity
                  72
NCBI Description
                  Cyanogenic Beta-Glucosidase Mol id: 1; Molecule: Cyanogenic
                  Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21
Seq. No.
                  34158
Contig ID
                  363034 1.R1040
5'-most EST
                  uC-gmrominsoy116g04b1
Seq. No.
                  34159
Contig ID
                  363100 1.R1040
5'-most EST
                  q5510173
Seq. No.
                  34160
Contig ID
                  363117 1.R1040
5'-most EST
                  uC-gmrominsoy263f02b1
Method
                  BLASTX
NCBI GI
                  q4558666
BLAST score
                  148
E value
                  1.0e-09
Match length
                  92
% identity
NCBI Description
                  (AC007063) putative Na/H antiporter isolog [Arabidopsis
                  thaliana]
Seq. No.
                  34161
Contig ID
                  363212 1.R1040
5'-most EST
                  uC-gmrominsoy124h12b1
Seq. No.
                  34162
Contig ID
                  363220 1.R1040
```

uC-gmrominsoy122d11b1

BLAST score

E value

461

4.0e-46

```
34163
Seq. No.
Contig ID
                   363348 1.R1040
5'-most EST
                   uC-gmropic050c10b1
Method
                   BLASTX
NCBI GI
                   g4263818
BLAST score
                   275
E value
                   2.0e-24
Match length
                   99
% identity
                   (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
                   34164
Seq. No.
Contig ID
                   363645 1.R1040
5'-most EST
                   uC-gmrominsoy136a12b1
Seq. No.
                   34165
Contig ID
                   363693 1.R1040
5'-most EST
                   g5057607
                   BLASTX
Method
NCBI GI
                   g3004552
BLAST score
                   542
                   2.0e-55
E value
                   197
Match length
% identity
                   57
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34166
Contig ID
                   363719 1.R1040
5'-most EST
                   uC-gmrominsoy138d09b1
                   34167
Seq. No.
                   363809 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy141g09b1
Method
                   BLASTX
                   g4530126
NCBI GI
BLAST score
                   356
                   8.0e-34
E value
Match length
                   130
% identity
                   51
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                   34168
Contig ID
                   363820 1.R1040
5'-most EST
                   uC-gmrominsoy142a09b1
                   34169
Seq. No.
                   363992 1.R1040
Contiq ID
5'-most EST
                   uC-gmrominsoy188e05b1
                   34170
Seq. No.
Contig ID
                   363995 1.R1040
5'-most EST
                   uC-gmrominsoy214g07b1
Method
                   BLASTX
NCBI GI
                   g1703018
```

Contig ID 5'-most EST

800

```
118
Match length
                  73
% identity
                  6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING
NCBI Description
                  >gi 984325 (U30255) phosphogluconate dehydrogenase [Homo
                  sapiens] >gi 4505759 ref NP 002622.1 pPGD phosphogluconate
                  dehydrogenase
Seq. No.
                  34171
Contig ID
                  364106 1.R1040
5'-most EST
                  uC-gmrominsoy158g04b1
Method
                  BLASTX
NCBI GI
                  g1293848
BLAST score
                  206
E value
                  6.0e-16
Match length
                  205
% identity
                  (U56966) vitellogenin [Caenorhabditis elegans]
NCBI Description
                  34172
Seq. No.
Contig ID
                  364110 1.R1040
5'-most EST
                  uC-gmropic0001d12b1
Seq. No.
                  34173
                  364172 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy164g04b1
Seq. No.
                  34174
Contig ID
                  364175 1.R1040
5'-most EST
                  uC-gmrominsoy164h06b1
Method
                  BLASTX
NCBI GI
                  g730683
                  699
BLAST score
E value
                  8.0e-74
Match length
                  189
                  69
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ BINDING
NCBI Description
                  PROTEIN) >gi 476088 (U02370) 34/67 kD laminin binding
                  protein [Urechis caupo]
Seq. No.
                  34175
                  364334 1.R1040
Contig ID
5'-most EST
                  g56881<del>6</del>7
Seq. No.
                  34176
Contig ID
                  364364 1.R1040
5'-most EST
                  uC-gmronoir007a07b1
                  BLASTX
Method
NCBI GI
                  q1236781
                  272
BLAST score
E value
                  6.0e-24
Match length
                  82
% identity
                  (X96732) cuticular collagen [Ostertagia circumcincta]
NCBI Description
Seq. No.
                  34177
```

364537 1.R1040

uC-gmrominsoy213a06b1

```
Method
                   BLASTX
NCBI GI
                   g1184072
BLAST score
                   329
                   1.0e-30
E value
Match length
                   141
% identity
                   52
                   (U40766) COL-1 [Meloidogyne incognita]
NCBI Description
                   34178
Seq. No.
Contig ID
                   364634 1.R1040
                   uC-gmrominsoy179b05b1
5'-most EST
                   34179
Seq. No.
                   364656 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy179f10b1
Seq. No.
                   34180
Contig ID
                   364678 1.R1040
5'-most EST
                   uC-gmropic098a08b1
                   34181
Seq. No.
Contig ID
                   364764 1.R1040
5'-most EST
                   uC-gmrominsoy182h10b1
                   34182
Seq. No.
Contig ID
                   364773 1.R1040
5'-most EST
                   uC-gmropic088c05b1
Method
                   BLASTN
NCBI GI
                   g2618599
BLAST score
                   35
E value
                   4.0e-10
Match length
                   151
                   85
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
                   34183
Seq. No.
Contig ID
                   364787 1.R1040
5'-most EST
                   uC-gmrominsoy183e12b1
                   34184
Seq. No.
Contig ID
                   364861 1.R1040
5'-most EST
                   uC-gmrominsoy186g09b1
Seq. No.
                   34185
                   364988 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy192a01b1
Method
                   BLASTX
NCBI GI
                   g730692
BLAST score
                   225
E value
                   2.0e-18
Match length
                   121
% identity
                   44
                   RUBISCO-ASSOCIATED PROTEIN >gi_454179 (L28804) putative
NCBI Description
```

protein [Glycine max]

[Glycine max] >gi_1090839 prf_2019481A RuBisCO complex

NCBI Description

```
Seq. No.
                   34186
                   365032 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy193a03b1
Method
                   BLASTN
NCBI GI
                   g1235973
BLAST score
                   97
E value
                   4.0e-47
Match length
                   269
% identity
NCBI Description
                  G.pallida mRNA for collagen
                   34187
Seq. No.
Contig ID
                   365078 1.R1040
5'-most EST
                   uC-gmrominsoy194f11b1
Seq. No.
                   34188
Contig ID
                   365190 1.R1040
5'-most EST
                   uC-gmrominsoy198a01b1
                   34189
Seq. No.
                   365195 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir010a05b1
                  BLASTX
Method
NCBI GI
                   q4406777
BLAST score
                   254
                   1.0e-21
E value
Match length
                   56
% identity
                   (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34190
Contig ID
                   365282 1.R1040
5'-most EST
                   uC-gmrominsoy200g01b1
Method
                  BLASTX
NCBI GI
                   q625982
BLAST score
                  274
E value
                   5.0e-24
Match length
                  116
% identity
                   55
                  S-locus-specific glycoprotein S12 precursor - field mustard
NCBI Description
                  >gi 547238 bbs 149323 (S70937) S-glycoprotein [Brassica
                   campestris, S12S12 homozygotes, stigmas, Peptide, 436 aa]
                   [Brassica rapa] >gi_743639_prf__2013216A S glycoprotein
                   [Brassica rapa]
                   34191
Seq. No.
Contig ID
                   365373 1.R1040
5'-most EST
                  uC-gmrominsoy204a05b1
Method
                  BLASTX
                  g4220481
NCBI GI
BLAST score
                  236
                  1.0e-19
E value
Match length
                  89
% identity
```

(AC006069) unknown protein [Arabidopsis thaliana]

5'-most EST

```
34192
Seq. No.
                   365383 1.R1040
Contig ID
                   uC-gmrominsoy204c02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2464932
BLAST score
                   191
                   2.0e-14
E value
Match length
                   62
% identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34193
                   365387_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy204c06b1
                   34194
Seq. No.
Contig ID
                   365418_1.R1040
5'-most EST
                   uC-gmrominsoy205c02b1
                   34195
Seq. No.
                   365446 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy206a12b1
Seq. No.
                   34196
                   365486_1.R1040
Contig ID
5'-most EST
                   uC-gmropic117b11b1
                   BLASTX
Method
NCBI GI
                   g2827637
BLAST score
                   184
                   1.0e-13
E value
Match length
                   103
% identity
                   (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34197
                   365585 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy210d06b1
                   34198
Seq. No.
                   365586 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy210d08b1
                   34199
Seq. No.
Contig ID
                   365667_1.R1040
5'-most EST
                   uC-gmronoir008c01b1
Method
                   BLASTX
NCBI GI
                   g4206787
BLAST score
                   239
E value
                   4.0e-20
Match length
                   117
% identity
NCBI Description
                   (AF112863) syntaxin-related protein Nt-syr1 [Nicotiana
                   tabacum]
                   34200
Seq. No.
                   365851 1.R1040
Contig ID
```

uC-gmrominsoy217f08b1

Seq. No.

Contig ID

34209

366537_1.R1040

```
Method
                  BLASTX
NCBI GI
                   g1480453
BLAST score
                   258
E value
                   2.0e-22
Match length
                  104
% identity
                   47
                   (U41853) 150 kDa oxygen regulated protein [Rattus
NCBI Description
                  norvegicus]
Seq. No.
                   34201
                   365886 1.R1040
Contig ID
5'-most EST
                  uC-gmropic026e11b1
Seq. No.
                   34202
Contig ID
                   365946 1.R1040
5'-most EST
                  uC-gmrominsoy220b01b1
Seq. No.
                  34203
Contig ID
                   366080 1.R1040
5'-most EST
                  uC-gmrominsoy224e08b1
Seq. No.
                  34204
                  366146 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy227g11b1
Seq. No.
                  34205
Contig ID
                  366224 1.R1040
5'-most EST
                  uC-gmrominsoy229a12b1
Seq. No.
                  34206
                  366281 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy230d04b1
Method
                  BLASTX
NCBI GI
                  g1235974
BLAST score
                  356
                  8.0e-34
E value
                  92
Match length
% identity
NCBI Description
                  (X96713) collagen [Globodera pallida]
Seq. No.
                  34207
Contig ID
                  366326 1.R1040
5'-most EST
                  uC-gmrominsoy231f04b1
Method
                  BLASTX
NCBI GI
                  g3702340
BLAST score
                  374
E value
                  5.0e-36
Match length
                  122
% identity
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
                  34208
Seq. No.
                  366534 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy237a11b1
```

Method

BLASTX

```
5'-most EST
                   uC-gmrominsoy238b04b1
                   34210
Seq. No.
                   366539 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy238b07b1
Seq. No.
                   34211
                   366553 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy237e03b1
Method
                   BLASTX
NCBI GI
                   g2258315
BLAST score
                   174
E value
                   2.0e-12
Match length
                   103
                   44
% identity
                   (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                   esculentum]
                   34212
Seq. No.
                   366561 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy237g01b1
Method
                   BLASTX
NCBI GI
                   g3136056
BLAST score
                   1.64
E value
                   2.0e-11
Match length
                   125
                   34
% identity
                   (AL023592) RanBP7/importin-beta/Cselp superfamily protein
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   34213
                   366826 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy263c07b1
Method
                   BLASTX
NCBI GI
                   g2384956
BLAST score
                   284
                   1.0e-25
E value
Match length
                   85
% identity
NCBI Description
                   (AF022985) No definition line found [Caenorhabditis
                   elegans]
Seq. No.
                   34214
                   367470 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy275f10b1
Method
                   BLASTX
NCBI GI
                   g2213600
                   223
BLAST score
                   3.0e-18
E value
                   114
Match length
                   30
% identity
                   (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34215
                   367543 1.R1040
Contig ID
5'-most EST
                   q56058<del>5</del>1
```

```
NCBI GI
                   g1086586
BLAST score
                   243
E value
                   3.0e-20
Match length
                   187
% identity
NCBI Description
                   (U41007) similar to G beta repeats (PROSITE:PS00670)
                   [Caenorhabditis elegans]
                   34216
Seq. No.
Contig ID
                   367587 1.R1040
                  uC-gmrominsoy275d12b1
5'-most EST
                   34217
Seq. No.
Contig ID
                   367653 1.R1040
5'-most EST
                   uC-gmrominsoy276b03b1
Seq. No.
                   34218
Contig ID
                   367674 1.R1040
5'-most EST
                  uC-gmrominsoy276f01b1
Method
                  BLASTX
NCBI GI
                  g1458286
BLAST score
                  376
E value
                   4.0e-36
Match length
                  121
% identity
                   65
NCBI Description
                   (U64842) partial CDS, [Caenorhabditis elegans]
Seq. No.
                  34219
Contig ID
                   367833 1.R1040
5'-most EST
                  uC-gmrominsoy283g03b1
                   34220
Seq. No.
                  368031 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy298h11b1
Method
                  BLASTX
NCBI GI
                  g3378491
BLAST score
                  181
E value
                   2.0e-13
Match length
                  53
% identity
NCBI Description
                   (AJ007578) pRIB5 protein [Ribes nigrum]
                  34221
Seq. No.
Contig ID
                  368122 1.R1040
5'-most EST
                  uC-gmrominsoy304b01b1
Method
                  BLASTX
NCBI GI
                  q3879463
BLAST score
                  581
E value
                  3.0e-60
Match length
                  137
% identity
                  (Z68751) predicted using Genefinder; Similarity to Dog
NCBI Description
                  endoplasmin precursor GRP94 (SW:ENPL CANFA); cDNA EST
                  EMBL: D27273 comes from this gene; cDNA EST EMBL: D27275
```

gene

comes from this gene; cDNA EST EMBL: D27274 comes from this

```
Seq. No.
                  34222
                  368125 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy302c02b1
                  34223
Seq. No.
Contig ID
                  368201 1.R1040
5'-most EST
                  uC-gmrominsoy306g09b1
                  34224
Seq. No.
                  368247 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy306c10b1
                  34225
Seq. No.
                  368305 1.R1040
Contig ID
5'-most EST
                  uC-gmropic006h03b1
                  34226
Seq. No.
Contig ID
                  368305 2.R1040
5'-most EST
                  uC-gmrominsoy308b01b1
Seq. No.
                  34227
                  368454 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy312a05b1
Method
                  BLASTX
NCBI GI
                  g477280
                  277
BLAST score
                  2.0e-24
E value
Match length
                  74
% identity
                  68
                  mitochondrial processing peptidase (EC 3.4.99.41) 55K
NCBI Description
                  protein precursor - potato >gi_410633_bbs_136740 cytochrome
                  c reductase-processing peptidase subunit I, MPP subunit I,
                  P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  534 aa]
                  34228
Seq. No.
                  368472 1.R1040
Contig ID
5'-most EST
                  uC-gmropic034g02b1
Method
                  BLASTX
NCBI GI
                  g233489
BLAST score
                  158
E value
                  1.0e-10
                  100
Match length
% identity
NCBI Description
                  coagulation factor IX/factor X-binding protein A chain
                  [Trimeresurus flavoviridis, venom, Peptide, 129 aa]
                  >gi_3212543_pdb_1IXX_A Chain A, Crystal Structure Of
                  Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom
                  Of Habu Snake With A Heterodimer Of C-Type Lectin Domains
                  >gi 3212545 pdb 1IXX C Chain C, Crystal Structure Of
                  Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom
                  Of Habu Snake With A Heterodimer Of C-Type Lectin Domains
                  >gi_3212547 pdb 1IXX E Chain E, Crystal Structure Of
                  Coagulation Factors IxX-Binding Protein (IxX-Bp) From Venom
                  Of Habu Snake With A Heterodimer Of C-Type Lectin Domains
```

Seq. No.

34229

BLAST score

507

```
Contig ID
                   368656 1.R1040
5'-most EST
                   uC-gmrominsoy317b11b1
                   34230
Seq. No.
Contig ID
                   368700 1.R1040
5'-most EST
                   uC-gmrominsoy318c12b1
Method
                   BLASTN
NCBI GI
                   q16185
BLAST score
                   235
E value
                   1.0e-129
Match length
                   356
% identity
                   92
NCBI Description
                   A.thaliana atpgpl gene for P-glycoprotein, homologous to
                   mammalian mdr genes
Seq. No.
                   34231
Contig ID
                   368716 1.R1040
5'-most EST
                   uC-gmrominsoy318e06b1
Method
                   BLASTN
NCBI GI
                   g3738275
BLAST score
                   504
E value
                   0.0e + 00
Match length
                   516
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   34232
                   368730 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy318g09b1
Method
                   BLASTN
NCBI GI
                   g4006885
BLAST score
                   336
E value
                   0.0e + 00
Match length
                   372
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No .
Seq. No.
                   34233
Contig ID
                   368731 1.R1040
5'-most EST
                   uC-gmrominsoy318h12b1
Method
                   BLASTN
NCBI GI
                   g2244950
BLAST score
                   520
E value
                   0.0e+00 .
Match length
                   536
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   34234
Seq. No.
                   368740 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy318h09b1
Method
                   BLASTN
NCBI GI
                   q16473
```

```
E value
                   0.0e + 00
Match length
                   519
                   56
% identity
                  Arabidopsis thaliana 25S-18S ribosomal DNA spacer
NCBI Description
                   34235
Seq. No.
                   368757 1.R1040
Contig ID
                   uC-gmrominsoy319c02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2959759
BLAST score
                   163
E value
                   3.0e-11
Match length
                   80
                   38
% identity
                   (Y14704) galactokinase [Candida parapsilosis]
NCBI Description
                   34236
Seq. No.
                   368930 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir031b03b1
Seq. No.
                   34237
                   369042 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir005b08b1
                   34238
Seq. No.
                   369046 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir034b12b1
Method
                   BLASTX
NCBI GI
                   g3287946
BLAST score
                   515
E value
                   2.0e-52
Match length
                   130
                   75
% identity
NCBI Description
                   PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I
                   >gi 2330862 emb CAB11099 (Z98533) putative rna helicase
                   [Schizosaccharomyces pombe]
                   34239
Seq. No.
Contig ID
                   369048 1.R1040
5'-most EST
                   uC-gmronoir034c03b1
                   34240
Seq. No.
                   369129 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir059f03b1
Seq. No.
                   34241
                   369142 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir007g02b1
Method
                   BLASTX
NCBI GI
                   g3157932
BLAST score
                   353
                   5.0e-68
E value
Match length
                   222
% identity
                   (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
NCBI Description
```

from A. thaliana. [Arabidopsis thaliana]

```
34242
Seq. No.
Contig ID
                   369144 1.R1040
5'-most EST
                   uC-gmronoir007g05b1
                   BLASTX
Method
NCBI GI
                   g2597972
BLAST score
                   513
                   3.0e-52
E value
Match length
                   124
% identity
NCBI Description
                   (AJ001621) RAL-1 protein [Litomosoides sigmodontis]
                   34243
Seq. No.
                   369169 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir043b10b1
Method
                   BLASTX
NCBI GI
                   q1236781
BLAST score
                   308
E value
                   2.0e-28
Match length
                   95
% identity
                   (X96732) cuticular collagen [Ostertagia circumcincta]
NCBI Description
Seq. No.
                   34244
                   369195 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir057h07b1
                   34245
Seq. No.
Contig ID
                   369200_1.R1040
5'-most EST
                   uC-gmronoir009b06b1
Seq. No.
                   34246
Contig ID
                   369208 1.R1040
5'-most EST
                   uC-gmronoir054b12b1
                   34247
Seq. No.
Contig ID
                   369215 1.R1040
                  uC-gmronoir009e06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2982452
BLAST score
                   247
E value
                   5.0e-21
Match length
                   147
% identity
                   6
                   (AL022223) receptor protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  34248
Contig ID
                  369217 1.R1040
5'-most EST
                  uC-gmronoir035g05b1
Method
                  BLASTX
NCBI GI
                  g2500025
BLAST score
                  318
E value
                  2.0e-29
Match length
                  127
% identity
                   46
NCBI Description
                  PROBABLE ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE
```

k*

LIGASE) >gi 1825781 (U88315) Similar to adenylosuccinate

synthetase; coded for by C. elegans cDNA yk104b12.3; coded for by C. elegans cDNA yk12le6.3; coded for by C. elegans cDNA yk117a11.3; coded for by C. elegans cDNA yk19c6.3; coded for by C. elegans cDNA yk

Seq. No. 34249

Contig ID 369219_1.R1040 5'-most EST uC-gmronoir054f03b1

Seq. No. 34250

Contig ID 369222_1.R1040 5'-most EST uC-gmronoir057g11b1

Method BLASTX
NCBI GI g3096951
BLAST score 471
E value 2.0e-47
Match length 103
% identity 90

NCBI Description (AJ005784) heat shock protein 90 [Brugia pahangi]

Seq. No. 34251

Contig ID 369307_1.R1040 5'-most EST uC-gmronoir033e09b1

Seq. No. 34252

Contig ID 369326_1.R1040 5'-most EST uC-gmronoir012h12b1

Method BLASTX
NCBI GI g1706582
BLAST score 747
E value 1.0e-79
Match length 149
% identity 95

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_1072161 (U40935)

elongation-factor 1-alpha [Caenorhabditis elegans]

>gi_1255296 (U51994) coded for by C. elegans cDNA CEESE09R;

coded for by C. elegans cDNA CEESH59F; coded for by C. elegans cDNA CESAE06F; coded for by C. elegans cDNA

ykld11.3; coded for by C. elegans cDNA ykld11.5; coded for

by C. elegans cDNA yk17e7.3

Seq. No. 34253

Contig ID 369366_1.R1040 5'-most EST uC-gmronoir014a01b1

Seq. No. 34254

Contig ID 369430_1.R1040 5'-most EST uC-gmronoir040b12b1

Seq. No. 34255

Contig ID 369514_1.R1040 5'-most EST uC-gmronoir040d07b1

Seq. No. 34256

Contig ID 369567_1.R1040 5'-most EST uC-gmronoir052b03b1

Seq. No.

34267

```
34257
Seq. No.
Contig ID
                   369663 1.R1040
5'-most EST
                   uC-gmronoir026a08b1
Seq. No.
                   34258
Contig ID
                   369689 1.R1040
5'-most EST
                   uC-gmronoir054c09b1
                   34259
Seq. No.
Contig ID
                   369719 1.R1040
5'-most EST
                   uC-gmronoir054c11b1
Method
                   BLASTX
NCBI GI
                   g3877452
BLAST score
                   219
E value
                   7.0e-18
Match length
                   84
% identity
NCBI Description
                   (Z81086) predicted using Genefinder; Similarity to Human
                   platelet-endothelial tetraspan antigen (SWLPET3 HUMAN)
                   [Caenorhabditis elegans]
Seq. No.
                   34260
                   369770 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir030c08b1
Seq. No.
                   34261
Contig ID
                   369777 1.R1040
5'-most EST
                   uC-gmronoir030d11b1
Seq. No.
                   34262
                   369791 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir052h02b1
Seq. No.
                   34263
                   370067 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir038e06b1
Seq. No.
                   34264
                   370069 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir038f03b1
Seq. No.
                   34265
Contig ID
                   370078_1.R1040
5'-most EST
                   uC-gmronoir038h03b1
Method
                   BLASTX
NCBI GI
                   g1817584
BLAST score
                   267
E value
                   2.0e-23
Match length
                   137
% identity
NCBI Description
                   (Y08991) adaptor protein [Homo sapiens]
                   34266
Seq. No.
Contig ID
                   370163 1.R1040
                   g56881<del>0</del>1
5'-most EST
```

` .

E value

4.0e-58

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Contig ID
                   370363 1.R1040
5'-most EST
                   uC-gmropic075b08b1
                   34268
Seq. No.
Contig ID
                   370443 1.R1040
5'-most EST
                   uC-gmronoir050c02b1
                   34269
Seq. No.
Contig ID
                   370734 1.R1040
5'-most EST
                   uC-qmronoir059a02b1
Seq. No.
                   34270
Contig ID
                   371053 1.R1040
5'-most EST
                   uC-gmronoir070e12b1
Seq. No.
                   34271
Contig ID
                   371095 1.R1040
5'-most EST
                   uC-gmronoir073c02b1
Seq. No.
                   34272
                   371263 1.R1040
Contig ID
5'-most EST
                   uC-gmropic0001h09a1
Seq. No.
                   34273
                   371706 1.R1040
Contig ID
5'-most EST
                   uC-gmropic014c01b1
Seq. No.
                   34274
                   371818_1.R1040
Contig ID
5'-most EST
                   uC-gmropic106g05b1
Seq. No.
                   34275
Contig ID
                   372045 1.R1040
5'-most EST
                   uC-gmropic015c03b1
Seq. No.
                   34276
                   372149 1.R1040
Contig ID
5'-most EST
                   uC-gmropic016g08b1
Method
                   BLASTX
NCBI GI
                   g1707017
BLAST score
                   533
E value
                   1.0e-54
Match length
                   115
% identity
NCBI Description
                   (U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.
                   34277
                   372556 1.R1040
Contig ID
5'-most EST
                   uC-gmropic022f01b1
Seq. No.
                   34278
                   373030 1.R1040
Contig ID
5'-most EST
                   uC-gmropic028g01b1
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   563
```

```
Match length
                   122
% identity
                   83
NCBI Description
                   (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                   34279
Contig ID
                   373180 1.R1040
5'-most EST
                  uC-gmropic065g01b1
Method
                  BLASTX
NCBI GI
                  g4467124
BLAST score
                  201
E value
                   2.0e-15
Match length
                  222
% identity
NCBI Description
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   373469 1.R1040
5'-most EST
                  uC-gmropic034b01b1
Seq. No.
                  34281
                   373646 1.R1040
Contig ID
5'-most EST
                  uC-gmropic036d03b1
Seq. No.
                  34282
                  373888 1.R1040
Contig ID
5'-most EST
                  uC-gmropic039e06b1
Seq. No.
                  34283
                  374364_1.R1040
Contig ID
5'-most EST
                  uC-gmropic101f01b1
Method
                  BLASTX
NCBI GI
                  g2465925
BLAST score
                  397
E value
                  1.0e-38
Match length
                  135
                   57
% identity
NCBI Description
                   (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
                  34284
Seq. No.
                  375029 1.R1040
Contig ID
5'-most EST
                  uC-gmropic059f08b1
Seq. No.
                  34285
                  375324 1.R1040
Contig ID
5'-most EST
                  uC-gmropic063c06b1
Method
                  BLASTX
                  q4139038
NCBI GI
BLAST score
                  148
                  2.0e-09
E value
                  74
Match length
% identity
NCBI Description
                   (AF072272) resistance protein candidate RGC2K [Lactuca
                  sativa]
                  34286
Seq. No.
```

375970 1.R1040

Contig ID

Method

BLASTX

```
5'-most EST
                   uC-gmropic073a01b1
Seq. No.
                   34287
Contig ID
                   375993 1.R1040
5'-most EST
                   uC-qmropic096c05b1
Seq. No.
                   34288
Contig ID
                   376035 1.R1040
5'-most EST
                   uC-gmropic073g03b1
Method
                   BLASTX
NCBI GI
                   g2959320
BLAST score
                   271
E value
                   9.0e-24
Match length
                   59
% identity
NCBI Description
                   (Z97057) ANR1 , MADS-box protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   376073 1.R1040
5'-most EST
                   uC-qmropic074b06b1
Seq. No.
                   34290
                   376082 1.R1040
Contig ID
5'-most EST
                   g957409
Seq. No.
                   34291
Contig ID
                   376231 1.R1040
5'-most EST
                   uC-gmropic078f04b1
Seq. No.
                   34292
                   376326 1.R1040
Contig ID
5'-most EST
                   g5057783
Seq. No.
                   34293
                   376588 1.R1040
Contig ID
                   uC-gmropic090c06b1
5'-most EST
Method
                   BLASTX
                   g4371296
NCBI GI
BLAST score
                   318
                   3.0e-29
E value
Match length
                   141
% identity
NCBI Description
                   (AC006260) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   34294
Seq. No.
                   376624 1.R1040
Contig ID
5'-most EST
                   uC-gmropic090h02b1
Seq. No.
                   34295
                   376989 1.R1040
Contig ID
5'-most EST
                   uC-gmropic099b02b1
Seq. No.
                   34296
Contig ID
                   377209 1.R1040
5'-most EST
                   uC-gmropic102b02b1
```

```
g4469024
NCBI GI
BLAST score
                   817
E value
                   1.0e-87
Match length
                   222
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   34297
Seq. No.
                   377858 1.R1040
Contig ID
5'-most EST
                   uC-gmropic111c07b1
Seq. No.
                   34298
                   378085 1.R1040
Contig ID
5'-most EST
                   uC-qmropic114q03b1
Method
                   BLASTX
NCBI GI
                   q4530126
BLAST score
                   218
E value
                   1.0e-17
Match length
                   153
% identity
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
                   34299
Seq. No.
Contig ID
                   378116 1.R1040
5'-most EST
                   uC-gmropic115g05b1
Method
                   BLASTN
NCBI GI
                   g47594
BLAST score
                   359
E value
                   0.0e + 00
Match length
                   424
% identity
                   Synechocystis sp. ndhE gene (partial), psaC gene for
NCBI Description
                  photosystem I iron-sulfur protein and ndhD-like ORF
                   34300
Seq. No.
Contig ID
                   378324 1.R1040
5'-most EST
                   g4260005
                   34301
Seq. No.
Contig ID
                   378379 1.R1040
5'-most EST
                   q4260076
Seq. No.
                   34302
Contig ID
                   378384 1.R1040
5'-most EST
                   q42601\overline{2}4
Method
                   BLASTX
NCBI GI
                   q4104929
BLAST score
                   570
E value
                   2.0e-61
Match length
                   152
% identity
                   (AF042195) auxin response factor 7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34303
Contig ID
```

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378427 1.R1040

a4260128

5'-most EST

Seq. No.

Contig ID

34310

380046 1.R1040

```
BLASTX
Method
                   g1495804 .
NCBI GI
BLAST score
                    442
                    4.0e-44
E value
Match length
                   110
% identity
                    75
                    (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                    34304
Seq. No.
                    378666 1.R1040
Contig ID
5'-most EST
                   g4260450
                    34305
Seq. No.
                    378715 1.R1040
Contig ID
5'-most EST
                   g4277028
Seq. No.
                   34306
Contig ID
                   379005 1.R1040
5'-most EST
                   g4292087
Method
                   BLASTX
NCBI GI
                   g3549691
BLAST score
                   1112
E value
                   1.0e-122
                   209
Match length
                   89
% identity
                   (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
NCBI Description
                   34307
Seq. No.
                   379147 1.R1040
Contig ID
5'-most EST
                   g55089\overline{2}1
Method
                   BLASTX
NCBI GI
                   g1170601
BLAST score
                   169
E value
                    6.0e-12
Match length
                   119
                    42
% identity
                   FRUIT PROTEIN PKIWI502 >qi 1085869 pir S48036 hypothetical
NCBI Description
                   protein - kiwi fruit >gi 4\overline{5}0237 (L\overline{2}780\overline{9}) pKIWI502
                   [Actinidia deliciosa]
Seq. No.
                   34308
                   379387 1.R1040
Contig ID
5'-most EST
                   g4290656
Seq. No.
                   34309
                   379614 1.R1040
Contig ID
5'-most EST
                   g4284382
Method
                   BLASTX
NCBI GI
                   g4580470
BLAST score
                   172
                   9.0e-12
E value
Match length
                   141
% identity
                   (AC006081) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

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```
5'-most EST
                   g4405639
Method
                   BLASTX
NCBI GI
                   q4415942
BLAST score
                   178
E value
                   7.0e-13
Match length
                   92
% identity
NCBI Description
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34311
                   380240 1.R1040
Contig ID
5'-most EST
                   g4295003
Method
                   BLASTX
NCBI GI
                   q431154
BLAST score
                   229
E value
                   6.0e-21
Match length
                   159
% identity
                   35
NCBI Description (D21813) ORF [Lilium longiflorum]
Seq. No.
                   34312
Contig ID
                   380280 1.R1040
5'-most EST
                   g4313610
Method
                  BLASTX
NCBI GI
                   q4220482
BLAST score
                   431
E value
                   2.0e-42
Match length
                  188
                   48
% identity
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34313
                   380619_1.R1040
Contig ID
5'-most EST
                   g4292476
Method
                  BLASTX
NCBI GI
                   q2864615
BLAST score
                  389
E value
                  1.0e-37
Match length
                  141
% identity
                   60
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
                   34314
Seq. No.
Contig ID
                   380785 1.R1040
5'-most EST
                  g42932<del>6</del>7
Seq. No.
                  34315
Contig ID
                  381119 1.R1040
5'-most EST
                  g4295745
Method
                  BLASTX
NCBI GI
                  g3738293
BLAST score
                  362
                  2.0e-40
E value
                  129
Match length
                   68
% identity
                   (AC005309) putative CCAAT-binding transcription factor
NCBI Description
```

subunit A (CBF-A) [Arabidopsis thaliana]

Match length

84

```
Seq. No.
                   34316
Contig ID
                   381329 1.R1040
5'-most EST
                   q42972\overline{9}2
Method
                   BLASTN
NCBI GI
                   q508560
BLAST score
                   118
E value
                   3.0e-60
Match length
                   126
% identity
                   98
NCBI Description
                   Solanum tubersum mitochondrial 26S ribosomal RNA (rrn26)
                   34317
Seq. No.
                   381636 1.R1040
Contig ID
5'-most EST
                   g4299653
Method
                   BLASTN
NCBI GI
                   g312886
BLAST score
                   368
                   0.0e + 00
E value
                   509
Match length
% identity
                   95
NCBI Description
                   T.reesei tefl gene for translation elongation factor la
                   34318
Seq. No.
Contig ID
                   381672 1.R1040
5'-most EST
                   g4305559
Method
                   BLASTX
NCBI GI
                   g123544
BLAST score
                   209
E value
                   1.0e-16
Match length
                   91
                   45
% identity
NCBI Description
                   18.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.5)
                   >gi 81788 pir S00646 heat shock protein 18.5-C - soybean
                   >gi 18654 emb CAA30154 (X07160) hsp18.5-C protein (AA 1 -
                   161) [Glycine max]
Seq. No.
                   34319
Contig ID
                   381710 1.R1040
5'-most EST
                   g4303261
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   161
E value
                   2.0e-85
Match length
                   293
                   91
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   34320
Seq. No.
                   381934 1.R1040
Contig ID
5'-most EST
                   g43018<del>9</del>0
Method
                   BLASTX
NCBI GI
                   g2499773
BLAST score
                   134
E value
                   2.0e-12
```

5'-most EST

 $q55102\overline{3}7$

```
% identity
                   49
NCBI Description
                   46 KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL
                  CIS-TRANS ISOMERASE) (PPIASE) >gi 1079010 pir A55320
                   immunophilin FKBP46 - fall armyworm >gi 595845 (U15038)
                   immunophilin FKBP46 [Spodoptera frugiperda]
                   34321
Seq. No.
Contig ID
                   381949 1.R1040
5'-most EST
                   q4307437
Method
                  BLASTX
NCBI GI
                  g3929383
BLAST score
                  152
E value
                   7.0e-10
Match length
                  71
                   45
% identity
NCBI Description
                  SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR
                  SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)
                  >gi_1405747_emb_CAA67134_ (X98511) PR264/SC35 [Mus
                  musculus]
                   34322
Seq. No.
Contig ID
                   381980 1.R1040
5'-most EST
                  g4302233
Method
                  BLASTX
NCBI GI
                  g2500047
BLAST score
                  221
E value
                   6.0e-18
Match length
                  50
                  82
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi 534916_emb_CAA85362_
                   (Z36894) soluble inorganic pyrophosphatase [Solanum
                  tuberosum]
                  34323
Seq. No.
                  382296 1.R1040
Contig ID
5'-most EST
                  g4304627
Method
                  BLASTX
NCBI GI
                  g4580469
BLAST score
                  324
E value
                   4.0e-30
Match length
                  110
% identity
                  52
NCBI Description
                   (AC006081) putative zinc finger protein [Arabidopsis
                  thaliana]
                  34324
Seq. No.
                  382950 1.R1040
Contig ID
5'-most EST
                  g4313493
                  34325
Seq. No.
                  383013 1.R1040
Contig ID
5'-most EST
                  q56057\overline{3}1
Seq. No.
                  34326
Contig ID
                  383813 1.R1040
```

Contig ID

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34327
Seq. No.
Contig ID
                   384008 1.R1040
5'-most EST
                   g5509051
Seq. No.
                   34328
Contig ID
                   384210 1.R1040
5'-most EST
                   q4396317
Method
                   BLASTX
NCBI GI
                   q3876615
BLAST score
                   348
E value
                   1.0e-32
Match length
                   134
% identity
                   (Z74031) Similarity to Yeast D-lactate dehydrogenase
NCBI Description
                   (SW:DLD1 YEAST); cDNA EST EMBL:C12235 comes from this gene;
                   cDNA EST EMBL:C12916 comes from this gene; cDNA EST
                   EMBL:C10532 comes from this gene; cDNA EST EMBL:C10979
                   comes f
                   34329
Seq. No.
                   384227 1.R1040
Contig ID
5'-most EST
                   g4396334
                                                   ....
Method
                   BLASTX
NCBI GI
                   g2760326
BLAST score
                   225
E value
                   7.0e-19
Match length
                   145
% identity
                   43
NCBI Description
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.
                   34330
                   384574 1.R1040
Contig ID
                   q4396695
5'-most EST
                   34331
Seq. No.
                   384885 1.R1040
Contig ID
5'-most EST
                   g4397027
                   34332
Seq. No.
                   385189 1.R1040
Contig ID
5'-most EST
                   g4397355
Method.
                   BLASTN
NCBI GI
                   g556899
BLAST score
                   57
E value
                   4.0e-23
Match length
                   121
% identity
                   87
NCBI Description
                  L.esculentum (cv. Rentita) mRNA for 54-kD signal
                   recognition particle (SRP) specific protein
                   34333
Seq. No.
                   385852 1.R1040
Contig ID
5'-most EST
                   g4437084
Seq. No.
                   34334
```

386922 1.R1040 ...

E value

9.0e-24

```
g5058552
5'-most EST
Method
                  BLASTN
NCBI GI
                   q1055367
BLAST score
                   68
E value
                   1.0e-29
Match length
                   236
% identity
NCBI Description
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                   34335
Contig ID
                   387116 1.R1040
5'-most EST
                   g5605923
Method
                  BLASTX
NCBI GI
                   g480997
BLAST score
                   434
E value
                   7.0e-43
Match length
                   164
                  54
% identity
                  beta-fructofuranosidase (EC 3.2.1.26) class 1 - carrot
NCBI Description
                  >gi 407055 emb CAA53097
                                            (X75351) beta-fructofuranosidase
                   [Daucus carota] >gi 4454117 emb CAA77267 (Y18707)
                  beta-fructofuranosidase, isoform I [Daucus carota]
Seq. No.
                   34336
                   387221 1.R1040
Contig ID
5'-most EST
                  g5606037
Seq. No.
                   34337
Contig ID
                   388056 1.R1040
5'-most EST
                   g5509015
Method
                  BLASTX
NCBI GI
                  g2828285
BLAST score
                   273
E value
                   3.0e-24
Match length
                   62
% identity
NCBI Description
                   (AL021687) putative protein [Arabidopsis thaliana]
                   34338
Seq. No.
                  388187 1.R1040
Contig ID
5'-most EST
                  g5509057
Method
                  BLASTX
NCBI GI
                  g629858
BLAST score
                  175
E value
                  8.0e-13
Match length
                  34
% identity
NCBI Description protein kinase C inhibitor - maize
                  34339
Seq. No.
                  388197 1.R1040
Contig ID
5'-most EST
                  g55090<del>6</del>7
Method
                  BLASTX
NCBI GI
                  g3421413
BLAST score
                  231
                                                                   4.,7
```

```
99
Match length
                   57
% identity
                   (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                   subunit [Oryza sativa] >gi 3421415 (AF081923) protein
                   phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
                   34340
Seq. No.
                   388215 1.R1040
Contig ID
5'-most EST
                   g5509087
Seq. No.
                   34341
                   388218 1.R1040
Contig ID
5'-most EST
                   g5509090
                   34342
Seq. No.
Contig ID
                   388357 1.R1040
5'-most EST
                   g55092\overline{4}2
Seq. No.
                   34343
                   388363 1.R1040
Contig ID
5'-most EST
                   g5509248
                   34344
Seq. No.
                   388387 1.R1040
Contig ID
5'-most EST
                   g5509272
                   34345
Seq. No.
Contig ID
                   388419 1.R1040
5'-most EST
                   g5509308
                   34346
Seq. No.
                   388436 1.R1040
Contig ID
5'-most EST
                   g5509327
Seq. No.
                   34347
                   388884 1.R1040
Contig ID
5'-most EST
                   g5677195
Method
                   BLASTX
NCBI GI
                   q285636
BLAST score
                   407
E value
                   2.0e-39
Match length
                   165
% identity
                   55
NCBI Description
                   (D14161) ORF [Hordeum vulgare]
Seq. No.
                   34348
                   388936 1.R1040
Contig ID
5'-most EST
                   g5666960
                   BLASTX
Method
NCBI GI
                   g2826820
BLAST score
                   527
E value
                   9.0e-54
Match length
                   167
                   62
% identity
                   (Y15171) ribosomal protein L7a [Fugu rubripes]
NCBI Description
```

34349

Seq. No.

```
389018 1.R1040
Contig ID
5'-most EST
                   g5126360
                   34350
Seq. No.
                   389061 1.R1040
Contig ID
5'-most EST
                   q51265\overline{1}4
Seq. No.
                   34351
                   389140 1.R1040
Contig ID
5'-most EST
                   g5126480
                   34352
Seq. No.
                   389171 1.R1040
Contig ID
                   g51265\overline{1}3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539293
BLAST score
                   220
                   6.0e-37
E value .
Match length
                   129
% identity
                   65
NCBI Description
                   (AL049480) putative membrane transporter [Arabidopsis
                   thaliana]
                   34353
Seq. No.
                   389354 1.R1040
Contig ID
5'-most EST
                   q5126676
Seq. No.
                   34354
                   389381 1.R1040
Contig ID
5'-most EST
                   q5126692
Seq. No.
                   34355
                   389420 1.R1040
Contig ID
5'-most EST
                   g5126727
Seq. No.
                   34356
                   389578 1.R1040
Contig ID
5'-most EST
                   q5126845
Method
                   BLASTX
NCBI GI
                   q3451074
BLAST score
                   599
E value
                   1.0e-100
Match length
                   208
% identity
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   34357
                   389721 1.R1040
Contig ID
5'-most EST .
                   q5126901
Method
                   BLASTX
NCBI GI
                   q2829910
BLAST score
                   254
E value
                   1.0e-24
Match length
                   155
% identity
                   38
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                   chromosome condensation motifs [Arabidopsis thaliana]
```

Contig ID 5'-most EST

Seq. No.

Contig ID 5'-most EST

34358 Seq. No. 389736 1.R1040 Contig ID 5'-most EST g5126906 34359 Seq. No. Contig ID 390118 1.R1040 5'-most EST g5607175 34360 Seq. No. 390135 1.R1040 Contig ID 5'-most EST q5607195 Method BLASTX NCBI GI g3176664 BLAST score 489 E value 4.0e-49 147 Match length % identity 61 -(AC004393) Contains similarity to beta scruin gb Z47541 NCBI Description from Limulus polyphemus. ESTs gb T04493 and gb AA585955 come from this gene. [Arabidopsis thaliana] Seq. No. 34361 390140 1.R1040 Contig ID g5607200 5'-most EST Seq. No. 34362 Contig ID 5'-most EST g5752876 Seq. No. 34363 Contig ID 5'-most EST g5752967 Seq. No. 34364 Contig ID 5'-most EST g5509519 Seq. No. 34365 Contig ID 5'-most EST g5342384, Seq. No. 34366 Contig ID 5'-most EST g5509632 Seq. No. 34367 Contig ID 5'-most EST g5509635 Seq. No.

390196 1.R1040 390256 1.R1040 390386 1.R1040 390429 1.R1040 390578 1.R1040 390581 1.R1040 34368 390634 1.R1040 $g55101\overline{9}0$ 34369 390646 1.R1040 g5509650

Contig ID

```
34370
Seq. No.
                   390674 1.R1040
Contig ID
5'-most EST
                   g5753183
                   34371
Seq. No.
                   390745 1.R1040
Contig ID
                   g55097\overline{2}4
5'-most EST
Method
                   BLASTX
                   g3335366
NCBI GI
BLAST score
                   327
                   4.0e-30
E value
Match length
                   105
% identity
                   58
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   34372
Seq. No.
                   390815 1.R1040
Contig ID
5'-most EST
                   q55097\overline{4}2
                   34373
Seq. No.
                   390845 1.R1040
Contig ID
5'-most EST
                   g5509799
Method
                   BLASTX
                   q2979551
NCBI GI
BLAST score
                   147
                   3.0e-09
E value
Match length
                   82
% identity
NCBI Description
                    (AC003680) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   34374
Contig ID
                   390904 1.R1040
5'-most EST
                   g5510258
                   34375
Seq. No.
                   390916 1.R1040
Contig ID
5'-most EST
                   g5509800
Method
                   BLASTN
NCBI GI
                   g13154
BLAST score
                   293
E value
                   1.0e-164
Match length
                   444
                   91
% identity
NCBI Description
                   Nicotiana tabacum mitochondrial DNA for ORF
                   34376
Seq. No.
                   390940 1.R1040
Contig ID
5'-most EST
                   g55102<del>9</del>3
Seq. No.
                   34377
                   391025 1.R1040
Contig ID
5'-most EST
                   956770\overline{5}6
                   34378
Seq. No.
                   391040 1.R1040
```

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NCBI GI

```
5'-most EST
                   g5510310
                   34379
Seq. No.
                   391062 1.R1040
Contig ID
5'-most EST
                   g55098<del>5</del>1
Seq. No.
                   34380
                   391100 1.R1040
Contig ID
5'-most EST
                   g5510049
                   34381
Seq. No.
                   391112 1.R1040
Contig ID
5'-most EST
                   g5677115
Method
                   BLASTX
NCBI GI
                   g2245026
BLAST score
                   223
                   3.0e-18
E value
Match length
                   62
% identity
                   66
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34382
                   391131 1.R1040
Contig ID
5'-most EST
                   g5676954
                   34383
Seq. No.
                   391165 1.R1040
Contig ID
                   g55103<del>6</del>2
5'-most EST
Seq. No.
                   34384
                   391177 1.R1040
Contig ID
5'-most EST
                   g5510366
Method
                   BLASTN
NCBI GI
                   g1304226
BLAST score
                   54
E value
                   1.0e-21
                   98
Match length
% identity
                   89
                   Soybean mRNA for epoxide hydrolase, complete cds
NCBI Description
                   34385
Seq. No.
                   391178 1.R1040
Contig ID
5'-most EST
                   g5510069
Seq. No.
                   34386
                   391205_1.R1040
Contig ID
5'-most EST
                   g5510395
                   34387
Seq. No.
Contig ID
                   391259 1.R1040
5'-most EST
                   g5676991
                   34388
Seq. No.
                   391956 1.R1040
Contig ID
                   g5342392
5'-most EST
Method
                   BLASTX
```

g3688284

Method

BLASTX

```
BLAST score
                   157
                   2.0e-10
E value
Match length
                   38
                   79
% identity
                   (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                   lanata]
                   34389
Seq. No.
                   392276 1.R1040
Contig ID
5'-most EST
                   g5677448
Seq. No.
                   34390
                   392704 1.R1040
Contig ID
                   g5677731
5'-most EST
Seq. No.
                   34391
                   392824_1.R1040
Contig ID
5'-most EST
                   g56781\overline{5}6
Method
                   BLASTN
NCBI GI
                   g2943791
BLAST score
                   34
                   1.0e-09
E value
Match length
                   70
% identity
                   87
NCBI Description
                  Cucurbita sp. mRNA for PV72, complete cds
Seq. No.
                   34392
                   392855 1.R1040
Contig ID
                   g5342437
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3482913
BLAST score
                   560
E value
                   1.0e-57
Match length
                   171
% identity
                   58
                   (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
                   34393
Seq. No.
                   393033 1.R1040
Contig ID
5'-most EST
                   g5342645
                   34394
Seq. No.
                   393085 1.R1040
Contig ID
5'-most EST
                   g5342660
                   34395
Seq. No.
                   393712 1.R1040
Contig ID
5'-most EST
                   g5175420
Seq. No.
                   34396
                   394354 1.R1040
Contig ID
5'-most EST
                   g5752568
                   34397
Seq. No.
Seq. ID
                   2DA-01-Q1-B1-A4
```

% identity

94

```
NCBI GI
                   g1155090.,.
BLAST score
                   231
E value
                   2.0e-19
Match length
                   67
% identity
NCBI Description
                   (X94986) beta glucosidase [Manihot esculenta]
Seq. No.
                   34398
Seq. ID
                   2DA-01-Q1-B1-B2
Method
                   BLASTN
NCBI GI
                   g2264316
BLAST score
                   51
                   4.0e-20
E value
                   82
Match length
                   72
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRO11, complete sequence [Arabidopsis thaliana]
                   34399
Seq. No.
Seq. ID
                   2DA-01-Q1-B1-D3
Method
                   BLASTX
NCBI GI
                   q4539395
BLAST score
                   415
E value
                   6.0e-41
Match length
                   112
                   71
% identity
                   (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                   34400
Seq. No.
                   2DA-01-Q1-B1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1495366
BLAST score
                   207
E value
                   1.0e-16
Match length
                   99
% identity
                   38
                   (Z69370) nitrite transporter [Cucumis sativus]
NCBI Description
Seq. No.
                   34401
Seq. ID
                   2DA-01-Q1-B1-G11
Method
                   BLASTX
                   g4322421
NCBI GI
BLAST score
                   250
E value
                   2.0e-21
Match length
                   66
% identity
                   74
NCBI Description
                   (AF085230) cadmium resistance factor 1 [Arabidopsis
                   thaliana] -
                   34402
Seq. No.
Seq. ID
                   2DA-01-Q1-B1-G2
Method
                   BLASTN
NCBI GI
                   g986968
                   180
BLAST score
E value
                   1.0e-96
Match length
                   242
```

Seq. ID

```
NCBI Description
                  Glycine max TGACG-motif binding protein (STGA1) mRNA,
                  complete cds
                   34403
Seq. No.
Seq. ID
                   2DA-02-Q1-B1-A10
                  BLASTX
Method
NCBI GI
                  g2146742
                   495
BLAST score
E value
                   3.0e-50
Match length
                  129
% identity
                   74
                  pattern-formation protein GNOM - Arabidopsis thaliana
NCBI Description
                  >gi 1209631 (U36432) GNOM gene product [Arabidopsis
                  thaliana]
Seq. No.
                   34404
Seq. ID
                  2DA-02-Q1-B1-A12
Method
                  BLASTX
NCBI GI
                  g4539386
BLAST score
                  203
                   6.0e-16
E value
Match length
                  85
% identity
                   (AL035526) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                  34405
Seq. No.
Seq. ID
                  2DA-02-Q1-B1-B1
Method
                  BLASTX
NCBI GI
                  g3970652
BLAST score
                  109
E value
                  8.0e-13
Match length
                  120
% identity
                   42
NCBI Description
                   (X77499) amino acid permease [Arabidopsis thaliana]
                  34406
Seq. No.
Seq. ID
                  2DA-02-Q1-B1-C11
Method
                  BLASTN
NCBI GI
                  g1335998
BLAST score
                  36
E value
                   4.0e-11
Match length
                  132
                  83
% identity
NCBI Description
                  Arabidopsis thaliana EMB30 gene, complete cds
Seq. No.
                  34407
Seq. ID
                  2DA-02-Q1-B1-F4
                  BLASTN
Method
NCBI GI
                  g296442
BLAST score
                  37
E value
                  2.0e-11
                  93
Match length
                  90
% identity
NCBI Description
                  G.max ADR11 mRNA
Seq. No.
                  34408
```

2DA-02-Q1-B1-H8

E value

```
BLASTN
Method
NCBI GI
                   g1143321
BLAST score
                   53
                   3.0e-21
E value
Match length
                   151
% identity
                   89
                   Glycine max alfa-carboxyltransferase (accA-2) precursor
NCBI Description
                   mRNA, complete cds
                   34409
Seq. No.
Seq. ID
                   2DC-01-Q1-B1-E8
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   109
E value
                   2.0e-54
Match length
                   309
% identity
                   86
NCBI Description
                   Glycine max nodulin-26 mRNA, complete cds
                   34410
Seq. No.
Seq. ID
                   2DC-01-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   177
                   6.0e-13
E value
Match length
                   60
% identity
                   57
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
                   34411
Seq. No.
Seq. ID
                   2DC-01-Q1-E1-B9
Method
                   BLASTN
NCBI GI
                   g3452136
BLAST score
                   214
                   1.0e-117
E value
                   256
Match length
% identity
                   96
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
Seq. No.
                   34412
Seq. ID
                   2DC-02-Q1-B1-A9 ·
Method
                   BLASTX
NCBI GI
                   g3402686
BLAST score
                   326
                   2.0e-30
E value
                   115
Match length
                   57
% identity
                   (AC004697) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   34413
Seq. No.
Seq. ID
                   2DC-02-Q1-B1-B8
Method
                   BLASTX
NCBI GI
                   g3688600
BLAST score
                   328
```

5.0e-42

Match length

68

```
Match length
                   129
% identity
                   66
                   (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   34414
Seq. No.
Seq. ID
                   2DC-02-Q1-B1-D10
                   BLASTN
Method
NCBI GI
                   q609224
BLAST score
                   156
                   2.0e-82
E value
Match length
                   296
% identity
                   88
                   P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB
NCBI Description
                   Pisum sativum S-adenosylmethionine synthase mRNA, complete
                   cds
Seq. No.
                   34415
Seq. ID
                   2DC-02-Q1-B1-D2
Method
                   BLASTX
NCBI GI
                   g1711618
BLAST score
                   375
E value
                   3.0e-36
Match length
                  107
% identity
                   68
                  LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir S51765
NCBI Description
                  low affinity sulphate transporter - Stylosanthes hamata
                   >gi 607188 emb_CAA57831_ (X82454) low affinity sulphate
                   transporter [Stylosanthes hamata]
                   34416
Seq. No.
Seq. ID
                   2DC-02-Q1-B1-F11
Method
                  BLASTX
                  g2832682
NCBI GI
BLAST score
                  200
E value
                   1.0e-15
Match length .
                  69
% identity
                   (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34417
Seq. ID
                   2DC-02-Q1-B1-F4
                  BLASTN
Method
                  g3790440
NCBI GI
BLAST score
                  134
E value
                   3.0e-69
                  382
Match length
% identity
                  84
                  Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear
NCBI Description
                  gene encoding chloroplast protein, complete cds
Seq. No.
                   34418
                  2DC-02-Q1-B1-H12
Seq. ID
                  BLASTX
Method
                  g3355476
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
```

Seq. ID

```
% identity
NCBI Description
                   (AC004218) unknown protein [Arabidopsis thaliana]
                   34419
Seq. No.
                   2DC-02-Q1-B1-H9
Seq. ID
Method
                   BLASTN
                   g457569
NCBI GI
BLAST score
                   50
                   2.0e-19
E value
Match length
                   114
                   86
% identity
NCBI Description
                   Soybean mRNA for endo-xyloglucan transferase, partial cds
                   34420
Seq. No.
Seq. ID
                   6HA-01-Q1-B1-A10
Method
                   BLASTN
NCBI GI
                   g18764
BLAST score
                   366
E value
                   0.0e+00
Match length
                   366
                   100
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   34421
Seq. No.
                   6HA-01-Q1-B1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129844
                   170
BLAST score
                   1.0e-23
E value
                   94
Match length
                   65
% identity
NCBI Description
                   stress-induced protein stil - soybean
Seq. No.
                   34422
Seq. ID
                   6HA-01-Q1-B1-C9
Method
                   BLASTX
NCBI GI
                   g4510342
BLAST score
                   550
                   1.0e-56
E value
Match length
                   117
% identity
                   85
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   34423
Seq. No.
Seq. ID
                   6HA-01-Q1-B1-D12
Method
                  BLASTX
NCBI GI
                   g3738153
BLAST score
                   201
E value
                   9.0e-16
Match length
                  112
                   37
% identity
                   (AL031852) putative cleavage and polyadenylation
NCBI Description
                   specificity factor [Schizosaccharomyces pombe]
                   34424
Seq. No.
```

6HA-01-Q1-B1-G9

BLAST score

```
Method
                   BLASTX
NCBI GI
                   g2781355
BLAST score
                   306
                   5.0e-28
E value
Match length
                   122
% identity
                   58
NCBI Description
                   (AC003113) F2401.11 [Arabidopsis thaliana]
                   34425
Seq. No.
Seq. ID
                   6HA-01-Q1-B1-H1
Method
                  BLASTX
NCBI GI
                   q3914667
BLAST score
                   235
E value
                   1.0e-19
Match length
                   94
                   55
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
                  >gi 2459427 (AC002332) putative chloroplast 50S ribosomal
                  protein L28 [Arabidopsis thaliana]
Seq. No.
                  34426
Seq. ID
                   6HA-01-Q1-B1-H11
Method
                  BLASTX
NCBI GI
                  g2656003
BLAST score
                  231
                 -2.0e-19
E value
                                                     44.
Match length
                   63
% identity
NCBI Description
                   (Z98980) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  34427
Seq. ID
                   6HA-01-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g2588608
BLAST score
                  189
E value
                   1.0e-102
Match length
                  193
                   99
% identity
                  Human BAC clone RG385F02 from 7p15, complete sequence [Homo
NCBI Description
                  sapiens]
                  34428
Seq. No.
Seq. ID
                   6HA-01-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  g392590
BLAST score
                  106
                  2.0e-52
E value
Match length
                  296
                  95
% identity
NCBI Description
                  Human immunoglobulin heavy chain variable region (clone
                  Amuld4-3) mRNA, partial cds
                  34429
Seq. No.
Seq. ID
                  6HA-01-Q1-E1-D12
Method
                  BLASTN
NCBI GI
                  g392865
```

E value Match length

```
0.0e + 00
E value
Match length
                   424
% identity
                  Human neutrophil oxidase factor (NCF2) gene, exon 16
NCBI Description
                  34430
Seq. No.
                   6HA-01-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g457569
BLAST score
                  138
                  1.0e-71
E value
Match length
                  214
                  92
% identity
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
                  34431
Seq. No.
Seq. ID
                   6HA-01-Q1-E1-E10
                  BLASTN
Method
NCBI GI
                  g37495
                  389
BLAST score
E value
                  0.0e+00
                  413
Match length
                  99
% identity
                  Human mRNA for translationally controlled tumor protein
NCBI Description
                  >qi 4507668 ref NM 003295.1 TPT1 Homo sapiens tumor
                  protein, translationally-controlled 1 (TPT1) mRNA
                  34432
Seq. No.
Seq. ID
                   6HA-01-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  g3900847
BLAST score
                  263
E value
                  1.0e-146
Match length
                  371
                  50
% identity
                  Homo sapiens BAC clone GS421I03 from Xq25-q26, complete
NCBI Description
                  sequence [Homo sapiens]
Seq. No.
                  34433
Seq. ID
                   6HA-01-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                  g736399
BLAST score
                  322
E value
                  0.0e+00
Match length
                  377
                   95
% identity
NCBI Description Human cofilin mRNA, partial cds
                  34434
Seq. No.
                  6HA-01-Q1-E1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3282242
BLAST score
                  198
```

% identity NCBI Description Human alpha enolase like 1 (ENOIL1) mRNA, partial cds

1.0e-107

273

```
34435
Seq. No.
Seq. ID
                    6HA-01-Q1-E1-F10
Method
                   BLASTN
NCBI GI
                   g187237
BLAST score
                    405
E value
                    0.0e + 00
Match length
                    416
                    99
% identity
                   Human lymphocyte-specific protein 1 (LSP1) mRNA, complete
NCBI Description
                    34436
Seq. No.
Seq. ID
                    6HA-01-Q1-E1-G12
Method
                   BLASTN
NCBI GI
                   g1764087
BLAST score
                    411
E value
                    0.0e + 00
Match length
                    426
                    99
% identity
NCBI Description
                   Human cosmid LL12NC01-15A4, ETV6 gene, exon 1A and partial
                   cds
Seq. No.
                    34437
Seq. ID
                    6HA-01-Q1-E1-H10
Method
                   BLASTN
NCBI GI
                   g2393735
BLAST score
                   33
                    6.0e-09
E value
Match length
                   37
                    97
% identity
                   Human BAC clone RG043K06 from 7q21-q22, complete sequence
NCBI Description
                    [Homo sapiens]
Seq. No.
                    34438
Seq. ID
                    6HA-01-Q1-E1-H3
Method
                   BLASTN
NCBI GI
                   g1161251
BLAST score
                   98
                   7.0e-48
E value
Match length
                   254
% identity
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   34439
Seq. ID
                    6HA-01-Q1-E1-H9
Method
                   BLASTN
NCBI GI
                   g177899
BLAST score
                   338
                   0.0e + 00
E. value
Match length
                   413
                    96
% identity
                   Homo sapiens differentiation-dependent A4 protein mRNA,
NCBI Description
                   complete cds. >gi_4505892_ref_NM_002668.1_PLP2_ Homo sapiens proteolipid protein 2 (colonic epithelium-enriched)
```

(PLP2) mRNA

```
34440
Seq. No.
Seq. ID
                   6HA-02-Q1-B1-A5
Method
                   BLASTX
NCBI GI
                   g1865677
BLAST score
                   329
E value
                   5.0e - 31
Match length
                   84
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   34441
Seq. No.
Seq. ID
                   6HA-02-Q1-B1-A6
Method
                   BLASTX
NCBI GI
                   g4038055
BLAST score
                   172
E value
                   2.0e-12
Match length -
                   102
% identity
                   38
NCBI Description
                   (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
                   >gi 4557077 gb AAD22516.1 AC007045 16 (AC007045) putative
                   cytochrome p450 [Arabidopsis thaliana]
                   34442
Seq. No.
Seq. ID
                   6HA-02-Q1-B1-A8
Method
                   BLASTX
NCBI GI
                   g4455274
BLAST score
                   438
E value
                   2.0e-43
Match length
                   111
% identity
                   78
NCBI Description
                   (AL035527) spliceosome associated protein-like [Arabidopsis
                   thaliana]
                   34443
Seq. No.
Seq. ID
                   6HA-02-Q1-B1-B2
Method
                   BLASTX
NCBI GI
                   q2388577
BLAST score
                   392
E value
                   4.0e-38
Match length
                   128
% identity
NCBI Description
                   (AC000098) Similar to Arabidopsis putative ion-channel
                   PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
Seq. No.
                   34444
Seq. ID
                   6HA-02-Q1-B1-C11
Method
                   BLASTX
NCBI GI
                   g3242708
BLAST score
                   141
E value
                   1.0e-08
Match length
                   90
% identity
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
```

[Arabidopsis thaliana]

Seq. ID

```
Seq. No.
                   34445
Seq. ID
                   6HA-02-Q1-B1-D3
Method
                  BLASTX
NCBI GI
                   g3337367
BLAST score
                  268
E value
                   1.0e-23
Match length
                   109
                   48
% identity
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34446
Seq. No.
Seq. ID
                   6HA-02-Q1-B1-D6
                  BLASTX
Method
NCBI GI
                  g3024021
BLAST score
                  165
                   1.0e-14
E value
Match length
                  81
                  57
% identity
                  INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225883 dbj BAA20878 (AB004825) eukaryotic initiation
                  factor 5A4 [Solanum tuberosum]
Seq. No.
                  34447
Seq. ID
                   6HA-02-Q1-B1-E2
Method
                  BLASTX
                  g1657615
NCBI GI
BLAST score
                  381
E value
                  8.0e-37
Match length
                  87
% identity
                  82
                   (U72502) Glp [Arabidopsis thaliana] >gi 3068706 (AF049236)
NCBI Description
                  putative transmembrane protein Glp [Arabidopsis thaliana]
Seq. No.
                  34448
Seq. ID
                   6HA-02-Q1-B1-F6
Method
                  BLASTX
NCBI GI
                  g3176686
BLAST score
                  240
                  2.0e-20
E value
Match length
                   65
% identity
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                  HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
Seq. No.
                  34449
Seq. ID
                  6HA-02-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  g2252843
BLAST score
                  207
E value
                  2.0e-16
Match length
                  109
% identity
                  48
                   (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34450
```

6HA-02-Q1-B1-H6

NCBI GI

g419760

```
Method
                   BLASTX
NCBI GI
                   g99741
BLAST score
                   268
                   1.0e-23
E value
                   91
Match length
                   62
% identity
NCBI Description
                  P-glycoprotein pgp1 - Arabidopsis thaliana
                   34451
Seq. No.
Seq. ID
                   6HA-02-Q1-E1-A5
                   BLASTX
Method
                   g1865677
NCBI GI
BLAST score
                   187
                   4.0e-14
E value
                   49
Match length
                   73
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   34452
Seq. No.
Seq. ID
                   6HA-02-Q1-E1-B2
Method
                   BLASTX
NCBI GI:
                   g2388577
BLAST score
                   170
E value
                   5.0e-12
Match length
                   94
% identity
NCBI Description
                   (AC000098) Similar to Arabidopsis putative ion-channel
                   PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]
                   34453
Seq. No.
                   6HA-02-Q1-E1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2465015
BLAST score
                   180
E value
                   3.0e-13
                   97
Match length
                  39
% identity
                   (AJ001449) ripening-induced protein [Fragaria vesca]
NCBI Description
Seq. No.
                   34454
                   6HA-02-Q1-E1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123554
BLAST score
                   288
E value
                   6.0e-26
Match length
                   64
% identity
                  18.1 KD CLASS I HEAT SHOCK PROTEIN >gi 99978 pir S16248
NCBI Description
                   heat shock protein 18 (clone pMsHsp18.1) - alfalfa
                   (fragment) >gi 19616 emb CAA41546 (X58710) heat shock
                   protein [Medicago sativa]
                   34455
Seq. No.
Seq. ID
                   6HA-02-Q1-E1-H6
                  BLASTX
Method
```

```
BLAST score
                  360
E value
                  2.0e-34
Match length
                  82
                  49
% identity
NCBI Description
                  P-glycoprotein atpgpl - Arabidopsis thaliana
                  >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
                  [Arabidopsis thaliana]
Seq. No.
                  34456
Seq. ID
                  6HC-01-Q1-B1-B10
Method
                  BLASTX
NCBI GI
                  q282899
BLAST score
                  188
E value
                  1.0e-26
Match length
                  131
% identity
                  11
                  embryonic abundant protein, 59K - soybean >gi 170010
NCBI Description
                  (M80664) maturation polypeptide [Glycine max]
                  >gi_384333_prf__1905420A late embryogenesis abundant
                  protein [Glycine max]
Seq. No.
                  34457
Seq. ID
                  6HC-01-Q1-B1-B7
Method
                  BLASTX
NCBI GI
                  q4336436
BLAST score
                  186
E value
                  3.0e-14
Match length
                  89
                  39
% identity
NCBI Description
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
Seq. No.
                  34458
Seq. ID
                  6HC-01-Q1-B1-D1
Method
                  BLASTN
NCBI GI
                  q1022364
BLAST score
                  201
E value
                  1.0e-109
Match length
                  349
                  89
% identity
NCBI Description
                  V.faba mRNA for sucrose phosphate synthase
Seq. No.
                  34459
Seq. ID
                  6HC-01-Q1-B1-E10
Method
                  BLASTX
NCBI GI
                  g2119848
BLAST score
                  163
E value
                  2.0e-11
Match length
                  80
                  47
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
NCBI Description
                  Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
```

[Arabidopsis thaliana]

Seq. No.

```
34460
Seq. No.
                   6HC-01-Q1-B1-G7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g166421
BLAST score
                   61
E value
                   1.0e-25
Match length
                   181
                   92
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   34461
Seq. No.
                   6HC-01-Q1-E1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g549637
BLAST score
                   161
E value
                   4.0e-11
                   92
Match length
                   40
% identity
                   HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION
NCBI Description
                   >gi_539278_pir__S38156 hypothetical protein YKR079c - yeast
                   (Saccharomyces cerevisiae) >gi 486557 emb CAA82158_
                   (Z28304) ORF YKR079c [Saccharomyces cerevisiae]
                   34462
Seq. No.
                   6HC-01-Q1-E1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1432056
BLAST score
                   272
E value
                   3.0e-24
Match length
                   61
% identity
NCBI Description
                   (U56834) WRKY3 [Petroselinum crispum]
Seq. No.
                   34463
Seq. ID
                   6HC-02-Q1-B1-A9
Method
                   BLASTX
NCBI GI
                   g4538939
BLAST score
                   139
E value
                   5.0e-09
                   53
Match length
% identity
                   (ALO49483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34464
Seq. ID
                   6HC-02-Q1-B1-B8
                   BLASTN
Method
NCBI GI
                   g2661020
BLAST score
                   89
E value
                   1.0e-42
                   201
Match length
% identity
                   86
                  Glycine max catalase (cat4) mRNA, complete cds
NCBI Description
```

Method

```
Seq. ID
                    ASG32442DA-01-Q1-E1-A11
Method
                    BLASTN
NCBI GI
                    g169936
BLAST score
                    134
                    2.0e-69
E value
Match length
                    221
                    91
% identity
NCBI Description
                    Glycine max chalcone synthase (chs7) gene, complete cds
Seq. No.
Seq. ID
                    ASG32442DA-01-Q1-E1-C10
Method
                    BLASTX
NCBI GI
                    g1076283
BLAST score
                    193
                    7.0e-15
E value
                    56
Match length
                    66
% identity
NCBI Description
                    adenylylsulfate kinase (EC 2.7.1.25) precursor -
                    Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS
                    kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS
                    kinase [Arabidopsis thaliana]
Seq. No.
                    344.67
                    ASG32442DA-01-Q1-E1-D7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4539395
BLAST score
                    143
E value
                    4.0e-09
Match length
                    36
% identity
NCBI Description
                    (AL035526) putative protein [Arabidopsis thaliana]
Seq. No.
                    34468
Seq. ID
                    ASG32442DA-01-Q1-E1-E7
Method
                    BLASTX
NCBI GI
                    q1621539
BLAST score
                    223
E value
                    3.0e-18
Match length
                    55
% identity
                    (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    34469
Seq. ID
                    ASG32442DA-01-Q1-E1-F11
Method
                    BLASTX
NCBI GI
                    q3461848
BLAST score
                    206
E value
                    2.0e-16
Match length
                    65
% identity
NCBI Description
                    (AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.
                    34470
Seq. ID
                    ASG32442DA-02-Q1-E1-A8
```

BLASTN

E value

3.0e-29

```
g56539
 NCBI GI
 BLAST score
                    76
                    1.0e-34
 E value
 Match length
                    265
                    92
 % identity
 NCBI Description
                    R.norvegicus gene encoding prolactin, exon 5
                    >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                    : exon v and flanks
                    34471
 Seq. No.
 Seq. ID
                    ASG32442DA-02-Q1-E1-F2
 Method
                    BLASTX
 NCBI GI
                    q2282586
 BLAST score
                    253
 E value
                    7.0e-22
                    73
 Match length
 % identity
                    63
                    (U82011) methyltransferase [Prunus armeniaca]
 NCBI Description
 Seq. No.
                    34472
 Seq. ID
                    ASG32442DA-02-Q1-E1-G8
 Method
                    BLASTN
 NCBI GI
                    g169069
 BLAST score
                    38
 E value
                    5.0e-12
 Match length
                    70
 % identity
                    89
 NCBI Description
                    Pea Cu-Zn superoxide dismutase mRNA, complete cds
                    34473
 Seq. No.
 Seq. ID
                    ASG3244V4L-01-Q1-E1-G1
 Method
                    BLASTX
 NCBI GI
                    g4115939
 BLAST score
                    163
 E value
                    6.0e-12
 Match length
                    47
 % identity
                    40
 NCBI Description
                    (AF118223) contains similarity to Methanobacterium
                    thermoautotrophicum transcriptional regulator (GB:AE000850)
                    [Arabidopsis thaliana]
                    34474
 Seq. No.
 Seq. ID
                    ASG3244V4R-02-Q1-E1-A8
 Method
                    BLASTN
                    g3776081
 NCBI GI
                    77
 BLAST score
 E value
                    3.0e-35
 Match length
                    179
                    91
 % identity
 NCBI Description
                   Medicago truncatula mRNA for MtN30 gene, partial
                    34475
 Seq. No.
                    LIB3027-001-Q1-B1-D7
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    g18628
                    67
"BLAST score
```

```
% identity
                   85
                   Soybean mRNA for A5A4B3 subunits of glycinin
NCBI Description
                   >gi_2170692 dbj_E02461_E02461 cDNA encoding glycinine
                   subunit A5A4B3 precursor
Seq. No.
                   34476
Seq. ID
                   LIB3027-001-Q1-B1-E4
Method
                   BLASTN
NCBI GI
                   q206371
BLAST score
                   103
                   8.0e-51
E value
Match length
                   140
% identity
                   100
                   Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
NCBI Description
Seq. No.
                   34477
Seq. ID
                  LIB3027-001-Q1-B1-E6
Method
                   BLASTN
NCBI GI
                   g2305019
BLAST score
                   219
E value
                   1.0e-120
Match length
                   291
% identity
                   94
NCBI Description
                  Glycine max 2S albumin pre-propeptide mRNA, complete cds
Seq. No.
                   34478
                   LIB3027-001-Q1-B1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g169962
BLAST score
                   92
E value
                   3.0e-44
Match length
                   96
% identity
                   99
NCBI Description
                  Soybean 16 kDa seed maturation protein (gGmpm9) gene exons
                   1-2, complete cds
Seq. No.
                   34479
Seq. ID
                  LIB3027-001-Q1-B1-H4
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  280
E value
                   2.0e-43
Match length
                  128
% identity
                   73
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  34480
Seq. ID
                  LIB3027-002-Q1-B1-D1
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  77
                  3.0e-35
E value
```

316

Match length

Match length

% identity

```
% identity
NCBI Description
                  R.norvegicus gene encoding prolactin, exon 5
                  >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                  34481
Seq. No.
Seq. ID
                  LIB3027-002-Q1-B1-D2
Method
                  BLASTN
                  q2920665
NCBI GI
BLAST score
                  300
                  1.0e-168
E value
Match length
                  304
                  100
% identity
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                  34482
Seq. ID
                  LIB3027-003-Q1-B1-A4
Method
                  BLASTX
NCBI GI
                  g3249066
BLAST score
                  148
E value
                  1.0e-09
Match length
                  103
% identity
                  37
NCBI Description
                   (AC004473) Similar to S. cerevisiae SIK1P protein
                  qb 984964. ESTs qb F15433 and qb AA395158 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  34483
Seq. ID
                  LIB3027-003-Q1-B1-B7
Method
                  BLASTN
NCBI GI
                  g2305019
BLAST score
                  71
E value
                   5.0e-32
Match length
                  75
% identity
                  99
                  Glycine max 2S albumin pre-propeptide mRNA, complete cds
NCBI Description
Seq. No.
                  34484
Seq. ID
                  LIB3027-003-Q1-B1-C5
Method
                  BLASTN
NCBI GI
                  g206371
BLAST score
                  103
E value
                   9.0e-51
                  292
Match length
% identity
                  96
NCBI Description
                  Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
Seq. No.
                  34485
                  LIB3027-003-Q1-B1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q206371
BLAST score
                  40
E value
                  3.0e-13
Match length
                  52
```

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Seq. ID

```
Seq. No.
                   34486
Seq. ID
                   LIB3027-004-Q1-B1-A4
Method
                   BLASTX
NCBI GI
                   g4262162
                   429
BLAST score
E value
                   2.0e-42
Match length
                   122
% identity
                   60
NCBI Description
                   (AC005275) putative glycosylation enzyme [Arabidopsis
                   thaliana]
Seq. No.
                   34487
Seq. ID
                   LIB3027-004-Q1-B1-A5
Method
                   BLASTN
NCBI GI
                   g736001
BLAST score
                   230
E value
                   1.0e-126
Match length
                   270
% identity
                   97
NCBI Description
                  G.soja (SH1) Gy5 mRNA for glycinin
Seq. No.
                   34488
Seq. ID
                   LIB3027-004-Q1-B1-D11
Method
                   BLASTN
NCBI GI
                   q18535
BLAST score
                   307
E value
                   1.0e-172
Match length
                   310
                   100
% identity
NCBI Description
                   Soybean mRNA for the alpha subunit of beta-conglycinin
                   34489
Seq. No.
Seq. ID
                   LIB3027-004-Q1-B1-D3
Method
                   BLASTN
NCBI GI
                   q56539
BLAST score
                   60
E value
                   3.0e-25
Match length
                   184
                   90
% identity
NCBI Description
                   R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   34490
Seq. ID
                   LIB3027-004-Q1-B1-D6
Method
                   BLASTN
NCBI GI
                   q2160543
BLAST score
                   121
E value
                   1.0e-61
Match length
                   293
% identity
NCBI Description
                   Pisum sativum ent-kaurene synthase A (LS) mRNA, complete
                   cds
                   344.91
Seq. No.
```

LIB3027-004-Q1-B1-G6

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   g4469005
BLAST score
                   214
                   3.0e-17
E value
Match length
                   84
                   54
% identity
NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34492
Seq. ID
                   LIB3027-005-Q1-B1-B5
Method
                   BLASTN
NCBI GI
                   g169972
BLAST score
                   401
                   0.0e + 00
E value
Match length
                   405
                   100
% identity
                   Soybean glycinin A-la-B-x subunit mRNA, complete cds
NCBI Description
Seq. No.
                   34493
Seq. ID
                   LIB3027-005-Q1-B1-D10
Method
                   BLASTN
NCBI GI
                   g56539
BLAST score
                   99
                   2.0e-48
E value
Match length
                   302
% identity
                   94
NCBI Description
                   R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   34494
                   LIB3027-006-Q1-B1-C11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g56539
BLAST score
                   62
                   2.0e-26
E value
Match length
                   241
% identity
                   91
NCBI Description
                   R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   34495
Seq. ID
                   LIB3027-006-Q1-B1-D10
Method
                  BLASTX
NCBI GI
                   g4056415
BLAST score
                   208
E value
                   2.0e-23
                   70
Match length
% identity
NCBI Description
                   (AC005322) Similar to the end of DNA repair protein
                   gb X74615 (rad8) gene. [Arabidopsis thaliana]
Seq. No.
                  LIB3027-006-Q1-B1-D12
Seq. ID
Method
                  BLASTN
```

g531828

```
BLAST. score
                   43
                  2.0e-15
E value
Match length
                  87
                  87
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
Seq. No.
                   34497
Seq. ID
                  LIB3027-006-Q1-B1-E10
Method
                  BLASTN
NCBI GI
                   g736001
BLAST score
                   155
E value
                   7.0e-82
Match length
                   243
% identity
                   91
NCBI Description
                  G.soja (SH1) Gy5 mRNA for glycinin
                   34498
Seq. No.
Seq. ID
                  LIB3027-006-Q1-B1-E7
Method
                  BLASTN
NCBI GI
                  q18749
BLAST score
                   144
                   2.0e-75
E value
Match length
                   202
% identity
                   96
                  G.max mRNA for seed maturation polypeptide
NCBI Description
                   34499
Seq. No.
                  LIB3027-006-01-B1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                   q12974
BLAST score
                   51
                   8.0e-20
E value
Match length
                   51
                   100
% identity
                   Soybean mitochondrial COII gene for cytochrome oxidase
NCBI Description
                   subunit II and tRNA-Met (CAT) gene (upstream)
Seq. No.
                   34500
                  LIB3027-006-Q1-B1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g18535
BLAST score
                   76
E value
                   7.0e-35
Match length
                  88
                   97
% identity
                  Soybean mRNA for the alpha subunit of beta-conglycinin
NCBI Description
Seq. No.
                   34501
Seq. ID
                  LIB3027-006-Q1-B1-H3
                  BLASTN
Method
NCBI GI
                  a56539
BLAST score
                   33
E value
                   4.0e-09
Match length
                  152
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
```

: exon v and flanks

```
Seq. No.
                   34502
Seq. ID
                   LIB3027-006-Q1-B1-H5
Method
                   BLASTX
NCBI GI
                   g138364
BLAST score
                   384
E value
                   1.0e-57
Match length
                   135
% identity
                   83
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   34503
Seq. No.
Seq. ID
                   LIB3027-007-Q1-B1-A2
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   338
E value
                   5.0e-32
Match length
                   91
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34504
Seq. ID
                   LIB3027-007-Q1-B1-H5
Method
                   BLASTX
NCBI GI
                   q633890
BLAST score
                   276
E value
                   2.0e-24
                   75
Match length
% identity
NCBI Description
                   ($72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
Seq. No.
                   34505
Seq. ID
                   LIB3027-008-Q1-B1-E1
Method
                   BLASTX
NCBI GI
                   q3912997
BLAST score
                   256
E value
                   3.0e-22
Match length
                   72
                   69
% identity
                   FLORAL HOMEOTIC PROTEIN AGL15 >gi 2129535 pir S71200 AGL15
NCBI Description
                   protein - Arabidopsis thaliana >g\bar{i}_790635 (U2\overline{25}28) AGL15
                   [Arabidopsis thaliana]
Seq. No.
                   34506
Seq. ID
                   LIB3027-008-Q1-B1-G2
Method
                   BLASTN
NCBI GI
                   q4324966
BLAST score
                   227
                   1.0e-125
E value
Match length
                   227
% identity
                   100
NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
```

Seq. No.

```
34507
Seq. No.
Seq. ID
                   LIB3027-008-Q1-B1-H7
Method
                   BLASTX
NCBI GI
                   g3413170
BLAST score
                   171
                   3.0e-12
E value
Match length
                   101
% identity
                   42
                  (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]
NCBI Description
Seq. No.
                   34508
                   LIB3027-010-Q1-B1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1794171
BLAST score
                   101
E value
                   1.0e-49
Match length
                   289
% identity
                   84
NCBI Description
                  Glycine max lipoxygenase-3 mRNA, complete cds
                   34509
Seq. No.
                   LIB3027-010-Q1-B1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1389896
BLAST score
                   32
E value
                   1.0e-08
Match length
                   184
                   80
% identity
                  Glycine max 68 kDa LEA protein mRNA, complete cds
NCBI Description
                   34510
Seq. No.
                   LIB3027-010-Q1-B1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193306
BLAST score
                   484
E value
                   6.0e-49
Match length
                   126
                   79
% identity
                   (AF069300) contains similarity to Arabidopsis
NCBI Description
                   membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
                   34511
Seq. No.
                  LIB3027-010-Q1-B1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g138364
BLAST score
                   119
E value
                   4.0e-15
Match length
                   67
% identity
                   53
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M ·
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
```

```
LIB3027-010-Q1-B1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913425
                   635
BLAST score
                   1.0e-66
E value
                   125
Match length
                   94
% identity
                   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                   HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
                   34513
Seq. No.
Seq. ID
                   LIB3027-011-Q1-B1-C6
Method
                   BLASTN
NCBI GI
                   g3452136
BLAST score
                   168
                   1.0e-89
E value
Match length
                   184
% identity =
                   99
NCBI Description
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
                   partial
Seq. No.
                   34514
                   LIB3027-011-Q1-B1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170746
BLAST score
                   246
                   2.0e-21
E value
                   78
Match length
% identity
                   64
                   DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi 472850
NCBI Description
                   (U08108) putative desiccation protectant protein, homolog
                   of Lea14, GenBank Accession Number M88321 [Glycine max]
Seq. No.
                   34515
Seq. ID
                   LIB3028-001-Q1-B1-A3
Method
                   BLASTX
NCBI GI
                   q3769472
BLAST score
                   418
E value
                   4.0e-41
Match length
                   109
% identity
                   68
                   (AF064732) putative phospholipase A2 [Dianthus
NCBI Description
                   caryophyllus]
Seq. No.
                   34516
Seq. ID
                   LIB3028-001-Q1-B1-B2
Method
                   BLASTX
NCBI GI
                   g282964
BLAST score
                   195
                   5.0e-15
E value
Match length
                   136
% identity
                   50
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                   petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia
```

46.

x hybrida]

```
Seq. No.
                   34517
Seq. ID
                   LIB3028-001-Q1-B1-E4
Method
                   BLASTX
NCBI GI
                   g4107099
BLAST score
                   283
E value
                   2.0e-25
Match length
                  102
% identity
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
Seq. No.
                   34518
Seq. ID
                   LIB3028-002-Q1-B1-A11
Method
                   BLASTX
                   g2739374
NCBI GI
BLAST score
                   145
E value
                   4.0e-09
Match length
                   58
% identity
                   11
NCBI Description
                   (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34519
Seq. ID
                   LIB3028-002-Q1-B1-C11
Method
                   BLASTX-
NCBI GI
                   q3128224
BLAST score
                   523
                   2.0e-53
E value
Match length
                   115
% identity
NCBI Description
                   (AC004077) putative protein serine/threonine kinase
                   [Arabidopsis thaliana]
                   34520
Seq. No.
                   LIB3028-002-Q1-B1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g303900
BLAST score
                   93
E value
                   7.0e-45
Match length
                   309
% identity
                   41
NCBI Description
                   Soybean gene for ubiquitin, complete cds
                   34521
Seq. No.
                   LIB3028-002-Q1-B1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3540180
BLAST score
                   320
E value
                   1.0e-29
Match length
                   116
% identity
                   53
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   34522
                   LIB3028-003-Q1-B1-B12
Seq. ID
Method
                   BLASTX
```

g3201617

NCBI GI .

Match length

```
BLAST score
                   419
E value
                   3.0e-41
Match length
                   130
                   58
% identity
                   (AC004669) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34523
Seq. No.
Seq. ID
                  LIB3028-003-Q1-B1-C3
Method
                   BLASTX
NCBI GI
                   g4455169
BLAST score
                   159
                   9.0e-11
E value
Match length
                   92
                   39
% identity
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   34524
Seq. No.
                  LIB3028-003-Q1-B1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160189
BLAST score
                   353
                   1.0e-33
E value
                   126
Match length
% identity
                   (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   34525
Seq. ID
                   LIB3028-003-Q1-B1-F2
Method
                   BLASTX
NCBI GI
                   g4467110
BLAST score
                   599
E value
                   2.0e-62
Match length
                   124
                   89
% identity
NCBI Description
                   (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   34526
Seq. ID
                  LIB3028-003-Q1-B1-G10
Method
                  BLASTN
NCBI GI
                   g2564336
BLAST score
                   104
E value
                   2.0e-51
Match length
                   284
% identity
                   84
NCBI Description
                  Brassica campestris mRNA for Tat binding protein 1,
                  complete cds
                  34527
Seq. No.
                  LIB3028-003-Q1-B1-G11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g609224
BLAST score
                  186
                   1.0e-100
E value
```

```
% identity
                  P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB
NCBI Description
                  Pisum sativum S-adenosylmethionine synthase mRNA, complete
                  34528
Seq. No.
Seq. ID
                  LIB3028-003-Q1-B1-G2
Method
                  BLASTX
                                       1.5
NCBI GI
                  q3043529
BLAST score
                  147
E value
                  2.0e-09
Match length
                  38
% identity
                   (AJ002204) polyamine oxidase [Zea mays]
NCBI Description
                  34529
Seq. No.
                  LIB3028-003-Q1-B1-H12
Seq. ID
                  BLASTN
Method
                  q2606080
NCBI GI
BLAST score
                  157
                  4.0e-83
E válue
                  313
Match length
% identity
                  88
                  Glycine max sucrose synthase (SS) mRNA, complete cds
NCBI Description
                  34530
Seq. No.
                  LIB3028-004-Q1-B1-E11
Seq. ID
Method
                  BLASTX
                  g3135264
NCBI GI
BLAST score
                  353
E value
                  2.0e-33
Match length
                  89
                  76
% identity
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                  34531
Seq. No.
Seq. ID
                  LIB3028-004-Q1-B1-H12
Method
                  BLASTN
                 ,g516853
NCBI GI
BLAST score
                  254
E value
                  1.0e-141
Match length
                  346
                  27
% identity
                  Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
                  34532
Seq. No.
                  LIB3028-005-Q1-B1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168196
BLAST score
                  210
                   6.0e-17
E value
                  67
Match length
                  67
% identity
                  14-3-3-LIKE PROTEIN >qi 555974 (U15036) 14-3-3-like protein
NCBI Description
                   [Pisum sativum]
```

34533

Seq. No.

Seq. No.

```
Seq. ID
                   LIB3028-005-Q1-B1-B8
Method
                   BLASTX
NCBI GI
                   q1771162
BLAST score
                   163
E value
                   2.0e-13
Match length
                   65
% identity
                   66
NCBI Description
                   (X98930) SBT2 [Lycopersicon esculentum]
                   >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
Seq. ID
                   LIB3028-005-Q1-B1-C6
Method
                   BLASTX
NCBI GI
                   q4335745
BLAST score
                   174
E value
                   2.0e-12
Match length
                   103
                   43
% identity
NCBI Description
                   (AC006284) putative hydrolase (contains an
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                   34535
Seq. ID
                   LIB3028-005-01-B1-D2
Method
                   BLASTN
NCBI GI
                   a3377793
BLAST score
                   140
E value
                   6.0e-73
Match length
                   284
% identity
                   87
NCBI Description
                   Glycine max proteasome IOTA subunit mRNA, complete cds
Seq. No.
                   34536
Seq. ID
                   LIB3028-005-Q1-B1-D5
Method ·
                   BLASTX
NCBI GI
                   a2498706
BLAST score
                   142
E value
                   7.0e-09
Match length
                   73
                   41
% identity
NCBI Description
                   ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1113103
                   (U40269) at Orc2p [Arabidopsis thaliana] > gi 32362\overline{3}9
                   (AC004684) origin recognition complex protein [Arabidopsis
                   thaliana]
Seq. No.
                   34537
Seq. ID
                   LIB3028-005-Q1-B1-D7
Method
                   BLASTX
NCBI GI
                   q1001708
BLAST score
                   314
E value
                   7.0e-29
Match length
                   139
% identity
                   49
NCBI Description
                   (D64004) NifS [Synechocystis sp.]
```

Method

BLASTX

```
Seq. ID
                   LIB3028-006-Q1-B1-A10
Method
                   BLASTX
NCBI GI
                   q115797
BLAST score
                   285
E value
                   1.0e-25
Match length
                   94
                   57
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                   (CAB-215) (LHCP) >gi_100026_pir__S16592 chlorophyll
                   a/b-binding protein - garden pea >gi_20658_emb_CAA40365_
                   (X57082) chlorophyll a/b-binding protein [Pisum sativum]
                   34539
Seq. No.
Seq. ID
                   LIB3028-006-Q1-B1-A5
Method
                   BLASTN
NCBI GI
                   q1944318
BLAST score
                   284
                   1.0e-158
E value
                   326
Match length
% identity
                  Glycine max mRNA for cysteine proteinase inhibitor,
NCBI Description
                   complete cds
                   34540
Seq. No.
Seq. ID
                   LIB3028-006-Q1-B1-C5
Method
                   BLASTX
                   g1350720
NCBI GI
BLAST score
                   216
E value
                   1.0e-17
Match length
                   91
                   50
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L32
                   34541
Seq. No.
                   LIB3028-006-Q1-B1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1669341
                   262
BLAST score
E value
                   8.0e-23
Match length
                   118
                   47
% identity
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
                   34542
Seq. No.
                  LIB3028-006-Q1-B1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3176098
BLAST score
                   341
E value
                   3.0e-32
                  107
Match length
% identity
                   67
                   (Y15036) annexin [Medicago truncatula]
NCBI Description
                   34543
Seq. No.
                  LIB3028-006-Q1-B1-G7
Seq. ID
```

BLAST score

```
NCBI GI
                   g3128218
BLAST score
                   395
E value
                   2.0e-38
Match length
                   119
% identity
                   66
                   (AC004077) putative end13 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   LIB3028-006-Q1-B1-H1
Method
                   BLASTX
NCBI GI
                   g123650
BLAST score
                   301
E value
                   1.0e-27
Match length
                   109
% identity
                   58
                   HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir S03250 heat
NCBI Description
                   shock protein 70 (clone pMON9743) - garden petunia
                   >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
                   34545
Seq. No.
Seq. ID
                   LIB3028-007-Q1-B1-A4
Method
                   BLASTX
NCBI GI
                   q3738299
BLAST score
                   363
E value
                   1.0e-34
Match length
                   101
% identity
                   (AC005309) putative glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   >gi 4249395 (AC006072) putative glutaredoxin [Arabidopsis
                   thaliana)
                   34546
Seq. No.
                   LIB3028-007-Q1-B1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2935449
BLAST score
                   73
E value
                   6.0e - 33
Match length
                   109
                   92
% identity
                  Malus domestica histone H2B mRNA, partial cds
NCBI Description
Seq. No.
                   34547
Seq. ID
                  LIB3028-007-Q1-B1-B8
Method
                  BLASTX
NCBI GI
                   q4558673
BLAST score
                  244
E value
                   9.0e-21
Match length
                   125
% identity
                   (AC007063) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34548
Seq. ID
                  LIB3028-007-Q1-B1-C7
Method
                  BLASTN
NCBI GI
                  q2760168
                                                          37
```

% identity

```
1.0e-15
E value
Match length
                   215
% identity
                   81
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MEE6, complete sequence [Arabidopsis thaliana]
                   34549
Seq. No.
Seq. ID
                   LIB3028-007-Q1-B1-D10
Method
                   BLASTX
NCBI GI
                   q2894606
                   208
BLAST score
                   2.0e-16
E value
Match length
                   76
% identity
                   55
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seg. No.
                   34550
Seq. ID
                   LIB3028-007-Q1-B1-E7
Method
                   BLASTX
NCBI GI
                   g267079
BLAST score
                   505
E value
                   2.0e-51
Match length
                   131
                   75
% identity
NCBI Description
                  TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
                   chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6
                   tubulin [Arabidopsis thaliana]
Seq. No.
                   34551
Seq. ID
                   LIB3028-007-Q1-B1-H4
Method
                   BLASTN
NCBI GI
                   g18551
BLAST score
                   289
E value
                   1.0e-162
Match length
                   364
% identity
                   95
NCBI Description
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                   protein
Seq. No.
                   34552
Seq. ID
                   LIB3028-008-Q1-B1-A10
Method
                   BLASTX
NCBI GI
                   q3608479
BLAST score
                   240
E value
                   2.0e-20
Match length
                   60
% identity
NCBI Description
                   (AF088912) ribosomal protein L15 [Petunia x hybrida]
Seq. No.
                   34553
Seq. ID
                   LIB3028-008-Q1-B1-B2
Method
                   BLASTX
NCBI GI
                   q1488255
BLAST score
                   172
E value
                   2.0e-12
Match length
                   59 -
```

NCBI Description

```
(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
NCBI Description
                   >gi 2961381 emb CAA18128 (AL022141) ferulate-5-hydroxylase
                   (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                   ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3028-008-Q1-B1-F2
Method
                   BLASTX
NCBI GI
                   g2642154
BLAST score
                   162
                   8.0e-14
E value
                   91
Match length
                   55
% identity
NCBI Description
                   (AC003000) unknown protein [Arabidopsis thaliana]
                   >gi 3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
Seq. No.
                   34555
Seq. ID
                   LIB3028-008-Q1-B1-G7
Method
                   BLASTN
NCBI GI
                   g312988
BLAST score
                   130
E value
                   6.0e-67
Match length
                   258
% identity
                   88
NCBI Description
                   G.max mRNA for beta-tubulin, partial; cds
                   34556
Seq. No.
Seq. ID
                   LIB3028-009-Q1-B1-A6
Method
                   BLASTX
NCBI GI
                   g549986
BLAST score
                   541
E value
                   2.0e-55
Match length
                   141
% identity
NCBI Description
                   (U13149) possible apospory-associated protein [Pennisetum
                   ciliare]
Seq. No.
                   34557
                   LIB3028-009-Q1-B1-B1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g303900
BLAST score.
                   209
E value
                   1.0e-114
                   293
Match length
% identity
                   28
NCBI Description
                   Soybean gene for ubiquitin, complete cds
Seq. No.
                   34558
                   LIB3028-009-Q1-B1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522929
BLAST score
                   339
E value
                   6.0e-32
Match length
                   78
% identity
```

(AC002535) putative dTDP-glucose 4-6-dehydratase

BLAST score

Match length

% identity

E value

449

66

1.0e-44 134

```
Seq. No.
                  34559
                  LIB3028-009-Q1-B1-C6
Seq. ID
Method
                  BLASTX
                  q462138
NCBI GI
                  299
BLAST score
E value
                  3.0e-27
                  83
Match length
% identity
                  67
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_169091 (L07500) glyceraldehyde-3-phosphate
                  dehydrogenase [Pisum sativum] >gi 1345567 emb_CAA51675_
                   (X73150) glyceraldehyde 3-phosphate dehydrogenase
                   (phosphorylating) [Pisum sativum]
                  34560
Seq. No.
Seq. ID
                  LIB3028-009-Q1-B1-D2
Method
                  BLASTX
NCBI GI
                  g3834322
BLAST score
                  271
                  7.0e-24
E value
                  96
Match length
                  56
% identity
                   (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  34561
Seq. No.
Seq. ID
                  LIB3028-009-Q1-B1-F7
Method
                  BLASTX
                  g3695063.
NCBI GI
BLAST score
                  341
                  5.0e-32
E value
Match length
                  144
% identity
NCBI Description
                   (AF064789) rac GTPase activating protein 3 [Lotus
                  japonicus]
                  34562
Seq. No.
Seq. ID
                  LIB3028-009-Q1-B1-G12
Method
                  BLASTN
NCBI GI
                  g3059094
BLAST score
                  125
                  6.0e-64
E value
                  184
Match length
                  92
% identity
                  Glycine max mRNA for magnesium chelatase subunit
NCBI Description
Seq. No.
                  34563
Seq. ID
                  LIB3028-009-Q1-B1-G6
Method
                  BLASTX
NCBI GI
                  g2739000
```

[Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Method

BLASTN

```
NCBI Description
                   (AF022459) CYP71D10p [Glycine max]
Seq. No.
                   34564
Seq. ID
                  LIB3028-009-Q1-B1-H10
Method
                  BLASTX
NCBI GI
                   g3335376
BLAST score
                   203
E value
                   5.0e-16
Match length
                   79
% identity
                   44
NCBI Description
                   (AC003028) putative ammonium transporter [Arabidopsis.
                   thaliana]
Seq. No.
                   34565
Seq. ID
                  LIB3028-010-Q1-B1-A12
Method
                  BLASTX
NCBI GI
                   g1565225
BLAST score
                   172
E value
                   2.0e-12
Match length
                   43
% identity
NCBI Description
                   (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                   34566
Seq. ID
                  LIB3028-010-Q1-B1-D1
Method
                   BLASTN
NCBI GI
                   q3869087
BLAST score
                   48
E value
                   3.0e-18
Match length
                   96
% identity
                  Nicotiana paniculata mRNA for elongation factor-1 alpha,
NCBI Description
                   complete cds
                   34567
Seq. No.
Seq. ID
                  LIB3028-010-Q1-B1-E3
Method
                  BLASTN
NCBI GI
                   q303900
BLAST score
                   224
E value
                   1.0e-123
Match length
                   334
% identity
                  Soybean gene for ubiquitin, complete cds
NCBI Description
                  34568.
Seq. No.
                  LIB3028-010-Q1-B1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1314277
BLAST score
                  149
                   1.0e-09
E value
Match length
                  111
% identity
                   (U34919) white homolog [Homo sapiens]
NCBI Description
                  34569
Seq. No.
                  LIB3028-011-Q1-B1-E12
Seq. ID
```

Match length

```
q170087
NCBI GI
BLAST score
                   91
E value
                   7.0e-44
Match length
                   171
                   88
% identity
NCBI Description
                  G.max vegetative storage protein mRNA (VSP25 gene)
                   34570
Seq. No.
Seq. ID
                  LIB3028-011-Q1-B1-E8
Method
                  BLASTN
NCBI GI
                   g310575
BLAST score
                   254
E value
                   1.0e-141
Match length
                   413
% identity
                   93
NCBI Description
                  Glycine max nodulin-26 mRNA, complete cds
                   34571
Seq. No.
                  LIB3028-011-Q1-B1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3176715
BLAST score
                   381
E value . '
                   8.0e-37
                  117
Match length
% identity
NCBI Description
                   (AC002392) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   34572
Seq. ID
                  LIB3028-011-Q1-B1-G8
Method
                  BLASTX
                   g2088643
NCBI GI
BLAST score
                   237
E value
                   4.0e-20
Match length
                   64
                   36
% identity
NCBI Description
                   (AF002109) transcription factor SF3 isolog [Arabidopsis
                   thaliana]
                  34573
Seq. No.
Seq. ID
                  LIB3028-011-Q1-B1-H2
Method
                  BLASTN
                  g1408470
NCBI GI
BLAST score
                  38
E value
                  3.0e-12
Match length
                  110
                  84
% identity
NCBI Description
                  Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1)
                  mRNA, complete cds
                  34574
Seq. No.
                  LIB3028-012-Q1-B1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539333
BLAST score
                  345
                  1.0e-32
E value
```

```
% identity
                   (AL035539) putative amino acid transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   34575
Seq. No.
Seq. ID
                   LIB3028-012-Q1-B1-G12
Method
                   BLASTX
NCBI GI
                   g1171642
BLAST score
                   216 -
E value
                   2.0e-17
                   90
Match length
                   50
% identity
                   PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
NCBI Description
                   >gi 481206_pir__S38326 protein kinase - Arabidopsis
                   thaliana >gi 166809 (L07248) protein kinase [Arabidopsis
                   thaliana]
                   34576
Seq. No.
Seq. ID
                   LIB3028-013-Q1-B1-A11
Method
                   BLASTX
NCBI GI
                   g2129889
BLAST score
                   269
E value
                   5.0e-31
'Match length
                   95 :
                   76
% identity
NCBI Description
                  methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
Seq. No.
                   34577
                   LIB3028-013-Q1-B1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2505884
BLAST score
                   282
                   3.0e-25
E value
                   90
Match length
                   59
% identity
                   (Y12776) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34578
                   LIB3028-013-Q1-B1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q951449
BLAST score
                   214
                   6.0e-25
E value
Match length
                   96
                   59
% identity
NCBI Description
                   (L46681) aspartic protease precursor [Lycopersicon
                   esculentum]
Seq. No.
                   34579
                   LIB3028-013-Q1-B1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   a2463568
BLAST score
                   48
                   3.0e-18
E value
Match length
                  173
% identity
                   81
```

NCBI Description Glycine max mRNA for squalene synthase, complete cds

```
34580
Seq. No.
                  LIB3028-013-Q1-B1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4049632
BLAST score
                  520
E value
                  4.0e-53
Match length
                  129
% identity
NCBI Description
                  (AF039406) pyruvate dehydrogenase kinase [Arabidopsis
                  thaliana]
Seq. No.
                  34581
                  LIB3028-014-Q1-B1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1781299
BLAST score
                  185
                  9.0e-14
E value
                  55
Match length
                  62
% identity
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  34582
Seq. ID
                  LIB3028-014-Q1-B1-B3
Method
                  BLASTX
NCBI GI
                  q3122671
BLAST score
                  259
E value
                  1.0e-22
Match length
                  85
% identity
                  HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241
NCBI Description
                  probable export protein - Arabidopsis thaliana >gi 1297188
                  (U53501) Theoretical protein with similarity to Swiss-Prot
                  Accession Number P41838 poly A+ RNA export protein
                  [Arabidopsis thaliana]
                  34583
Seq. No.
Seq. ID
                  LIB3028-014-Q1-B1-B4
Method
                  BLASTX
NCBI GI
                  g4544419
BLAST score
                  249
E value
                  3.0e-21
Match length
                  67
% identity
NCBI Description
                  (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                  34584
Seq. ID
                  LIB3028-014-Q1-B1-C5
Method
                  BLASTX
NCBI GI
                  q4406781
BLAST score
                  161
E value
                  4.0e-11
Match length
                  120
                  42
% identity
NCBI Description
                  (AC006532) putative Na+/H+ antiporter [Arabidopsis
```

thaliana]

```
34585 -
Seq. No.
Seq. ID
                  LIB3028-014-Q1-B1-D1
Method
                  BLASTN
NCBI GI
                  q2570122
BLAST score
                  33
E value
                  5.0e-09
Match length
                  41
% identity
                  95
NCBI Description
                  S.latifolia mRNA, clone CCLS 30.1-21
                  34586
Seq. No.
                  LIB3028-014-Q1-B1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4572673
BLAST score
                  297
                  5.0e-27
E value
Match length
                  103
% identity
                  54
                  (AC006954) putative sarcosine oxidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34587
                  LIB3028-014-Q1-B1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1515454
BLAST score
                  147
                  1.0e-09
E value
Match length
                  69
                  46
% identity
                  (U64448) lac repressor [Cloning vector pCMVLacI]
NCBI Description
                  34588
Seq. No.
                  LIB3028-015-Q1-B1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267124
BLAST score
                  184
E value
                  4.0e-23
Match length
                  96
% identity
                  THIOREDOXIN H-TYPE 1 (TRX-H1) >gi 100387 pir S16590
NCBI Description
                  thioredoxin h1 - common tobacco >gi 20047 emb CAA41415
                  (X58527) thioredoxin [Nicotiana tabacum]
Seq. No.
                  34589
Seq. ID
                  LIB3028-015-Q1-B1-C5
Method
                  BLASTX
NCBI GI
                  g1172664
BLAST score
                  383
E value
                  4.0e-37
Match length
                  118
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_419791_pir__S31165 photosystem I chain III precursor -
                  Flaveria trinervia >gi_298482_bbs_127083 photosystem I
                  reaction center subunit III, PSI-RC PsaF [Flaveria
```

NCBI Description

34595

Seq. No.

```
I subunit III [Flaveria trinervīa]
                    34590
 Seq. No.
 Seq. ID
                    LIB3028-015-Q1-B1-D2
 Method
                    BLASTX
 NCBI GI
                    g2746719
 BLAST score
                    210
                    7.0e-17
 E value
                    102
 Match length
 % identity
                    48
                    (AF038386) histone H2B [Capsicum annuum]
 NCBI Description
 Seq. No.
                    34591
 Seq. ID
                    LIB3028-015-Q1-B1-E10
 Method
                    BLASTN
 NCBI GI
                    g2815245
 BLAST score
                    75
 E value
                    5.0e-34
                    203
 Match length
 % identity
                    84
 NCBI Description
                    C.arietinum mRNA for class I type 2 metallothionein (clone:
                    CanMT-2)
 Seq. No.
                    34592
                    LIB3028-015-Q1-B1-G11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2252824
 BLAST score
                    407
 E value
                    7.0e-40
                    104
 Match length
 % identity
                    73
 NCBI Description
                    (AF013293) No definition line found [Arabidopsis thaliana]
 Seq. No.
                    34593
 Seg. ID
                    LIB3028-016-Q1-B1-A11
 Method
                    BLASTX
 NCBI GI
                    q1076634
 BLAST score
                    186
 E value
                    4.0e-14
 Match length
                    78
 % identity
                    50
                    protein-serine/threonine kinase NPK15 - common tobacco
 NCBI Description
                    >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine
                    kinase [Nicotiana tabacum]
Seq. No.
                    34594
 Seq. ID
                    LIB3028-016-Q1-B1-A9
 Method
                    BLASTN
 NCBI GI
                    q18761
 BLAST score
                    7.7
 E value
                    3.0e-35
 Match length
                    249
 % identity
                    89
```

trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem

Soybean stem mRNA for 31 kD glycoprotein

NCBI GI

```
LIB3028-016-Q1-B1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3183088
BLAST score
                  164
E value
                  2.0e-11
Match length
                  94
% identity
                   38
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi 629658_pir__S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  34596
Seq. No.
Seq. ID
                  LIB3028-016-Q1-B1-D10
Method
                  BLASTX
NCBI GI
                  g4510383
BLAST score
                  256
                  1.0e-22
E value
Match length
                  67
                  79
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34597
                  LIB3028-017-Q1-B1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2983814
BLAST score
                  151
E value
                  4.0e-10
Match length
                  78
% identity
                  41
                   (AE000739) tryptophan synthase beta subunit [Aquifex
NCBI Description
                  aeolicus]
                  34598
Seq. No.
Seq. ID
                  LIB3028-017-Q1-B1-G10
Method
                  BLASTX
NCBI GI
                  g3063691
BLAST score
                  267
E value
                  2.0e-23
Match length
                  68
% identity
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
                  34599
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-A4
                  BLASTX
Method
NCBI GI
                  g2911073
BLAST score
                  177
                  4.0e-13
E value
Match length
                  66
% identity
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
                  34600
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-A8
Method
                  BLASTX
```

q1871182

Match length

```
BLAST score
                   300
E value
                   1.0e-27
Match length
                   84
                   67
% identity
                   (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34601
Seq. ID
                   LIB3028-018-Q1-B1-B1
Method
                   BLASTN
NCBI GI
                   g3021484
BLAST score
                   36
E value
                   7.0e-11
                   68
Match length
                   88
% identity
                  Lycopersicon esculentum H2B-3 mRNA for histone H2B
NCBI Description
                   34602
Seq. No.
                   LIB3028-018-Q1-B1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129879
                   190
BLAST score
E value
                   1.0e-17
                   108
Match length
                   50
% identity
                   chlorophyll a/b-binding protein type II precursor,
NCBI Description
                   photosystem I - garden pea >gi 602359 emb CAA57492
                   (X81962) Type II chlorophyll a/b binding protein from
                   photosystem I [Pisum sativum]
Seq. No.
                   34603
                   LIB3028-018-Q1-B1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2764803
BLAST score
                   122
E value
                   4.0e-62
Match length
                   310
                   85
% identity
NCBI Description
                   G.max mRNA for epoxide hydrolase
                   34604
Seq. No.
                   LIB3028-018-Q1-B1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2618705
                   257
BLAST score
E value
                   2.0e-26
Match length
                   93
% identity
                   43
                   (AC002510) putative ABC transporter, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   34605
Seq. No.
                   LIB3028-018-Q1-B1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455276
                   393
BLAST score
E value
                   3.0e-38
```

NCBI Description

thaliana]

```
% identity
NCBI Description
                   (AL035527) peptide transporter-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  34606
Seq. ID
                  LIB3028-018-Q1-B1-G10
Method
                  BLASTX
                  q3004564
NCBI GI
BLAST score
                  272
                  4.0e-24
E value
Match length
                  106
% identity
                   51
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  34607
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-G11
Method
                  BLASTN
NCBI GI
                  g456567
BLAST score
                  109
                  3.0e-54
E value
                  205
Match length
                  88
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  34608
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-H12
Method
                  BLASTX
NCBI GI
                  g2618699
BLAST score
                  267
                  2.0e-23
E value
                  71
Match length
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                  34609
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-H5
Method
                  BLASTN
NCBI GI
                  g1053215
BLAST score
                  165
E value
                  9.0e-88
                  357
Match length
                  87
% identity
NCBI Description
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
                  nuclear gene encoding chloroplast protein, complete cds
                  34610
Seq. No.
Seq. ID
                  LIB3028-018-Q1-B1-H8
Method
                  BLASTX
                  g4455259
NCBI GI
                  355
BLAST score
E value
                  8.0e-34
Match length
                  119
                  59
% identity
```

...

(AL035523) putative Ser/Thr protein kinase [Arabidopsis

Method

BLASTX

```
34611
Seq. No.
Seq. ID
                   LIB3028-019-Q1-B1-A12
Method
                   BLASTX
NCBI GI
                   g2708331
BLAST score
                   286
E value
                   1.0e-25
Match length
                   94
% identity
                   (AF038557) ligand gated channel-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34612
Seq. ID
                   LIB3028-019-Q1-B1-A7
Method
                   BLASTN
NCBI GI
                   g1256365
BLAST score
                   41
E value
                   6.0e-14
                   65
Match length
                   91
% identity
                  Promoter-trapping vector pdeltagusBin19
NCBI Description
Seq. No.
                  34613
Seq. ID
                   LIB3028-019-Q1-B1-B11
Method
                   BLASTX
NCBI GI
                   g2832640
BLAST score
                   347
                   6.0e-33
E value
                   105
Match length
% identity
                   65
                   (AL021710) neoxanthin cleavage enzyme - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   34614
Seq. ID
                   LIB3028-019-Q1-B1-B6
Method
                   BLASTX
NCBI GI
                   g309673
BLAST score
                   213
E value
                   2.0e-17
Match length
                   81
% identity
NCBI Description
                   (L19651) light harvesting protein [Pisum sativum]
Seq. No.
                   34615
Seq. ID
                   LIB3028-019-Q1-B1-B7
Method
                   BLASTN
NCBI GI
                   g1399379
BLAST score
                   106
E value
                   9.0e-53
                   122
Match length
                   97
% identity
NCBI Description
                   Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
                   methyltransferase mRNA, complete cds
Seq. No.
                   34616
                   LIB3028-019-Q1-B1-C5
Seq. ID
```

Seq. No.

. 34621

```
g542005
NCBI GI
BLAST score
                  181
E value
                  1.0e-13
Match length
                  71
% identity
                  56
NCBI Description
                  endoxyloglucan transferase - adzuki bean
                  >gi 469510 dbj BAA03925 (D16458) endo-xyloglucan
                  transferase [Vigna angularis]
Seq. No.
                  34617
Seq. ID
                  LIB3028-019-Q1-B1-C6
Method
                  BLASTN
NCBI GI
                  q18551
BLAST score
                  132
E value
                  3.0e-68
Match length
                  236
% identity
                  89
NCBI Description
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
Seq. No.
                  34618
Seq. ID
                  LIB3028-019-Q1-B1-D1
Method
                  BLASTX
NCBI GI-
                  g1346701
BLAST score
                  284
E value
                  2.0e-25
Match length
                  110
% identity
                  48
NCBI Description
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
                  (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 421831 pir S34199 exopolygalacturonase (clone GBGe184)
                  - Arabidopsis thaliana >gi 313682 emb CAA51032 (X72291)
                  exopolygalacturonase [Arabidopsis thaliana]
                  >gi_3004440_emb_CAA76127_ (Y16230) polygalacturonase
                  [Arabidopsis thaliana]
                  34619
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-E11
Method
                  BLASTX
NCBI GI
                  g4100433
BLAST score
                  234
E value
                  1.0e-19
Match length
                  50
% identity
NCBI Description (AF000378) beta-glucosidase [Glycine max]
                  34620
Seq. No.
Seq. ID
                  LIB3028-019-Q1-B1-F5
Method
                  BLASTN
NCBI GI
                  q18557
BLAST score
                  84
E value
                  1.0e-39
Match length
                  136
                  91
% identity
NCBI Description G.max mRNA for ACC synthase
```

E value

3.0e-13

```
LIB3028-019-Q1-B1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2055228
BLAST score
                   143
                   6.0e-09
E value
Match length
                   78
% identity
                   41
NCBI Description
                   (AB000129) SRC1 [Glycine max]
                   34622 -
Seq. No.
                  LIB3028-019-Q1-B1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3461821
BLAST score
                   184
                   9.0e-14
E value
Match length
                   91
                   46
% identity
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   34623
Seq. No.
                  LIB3028-020-Q1-B1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                   315
E value
                   4.0e-29
                  108
Match length
% identity
                   58
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   34624
Seq. ID
                  LIB3028-020-Q1-B1-A7
Method
                  BLASTX
NCBI GI
                   g4049354
BLAST score
                   154
                   3.0e-10
E value
                   62
Match length
                   47
% identity
                   (AL034567) glycine hydroxymethyltransferase (EC
NCBI Description
                   2.1.2.1)-like protein [Arabidopsis thaliana]
Seq. No.
                   34625
Seq. ID
                  LIB3028-020-Q1-B1-D2
Method
                  BLASTX
NCBI GI
                  g4239692
BLAST score
                  270
E value
                   9.0e-24
                  54
Match length
% identity
                  81
                   (AJ132745) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34626
                  LIB3028-020-Q1-B1-E3
Seq. ID
                  BLASTX
Method
                  g1408296
NCBI GI
BLAST score
                  176
```

```
45
Match length
% identity
                   69
                   (U61984) phosphoglucomutase A [Dictyostelium discoideum]
NCBI Description
                  34627
Seq. No.
                  LIB3028-020-Q1-B1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1669599
BLAST score
                  180
E value
                   3.0e-13
                  99
Match length
                   40
% identity
                   (D88746) AR791 [Arabidopsis thaliana]
NCBI Description
                  34628
Seq. No.
                  LIB3028-020-Q1-B1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4572671
BLAST score
                   416
                   3.0e-54
E value
Match length
                  133
% identity
                   81
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   34629
                  LIB3028-020-Q1-B1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206122
BLAST score
                   344
E value
                   2.0e-32
Match length
                   123
% identity
NCBI Description
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                   crystallinum]
Seq. No.
                   34630
Seq. ID
                  LIB3028-021-Q1-B1-B1
Method
                  BLASTX
NCBI GI
                  q2244924
BLAST score
                  164
E value
                   2.0e-11
                  53
Match length
% identity
                   (Z97339) glutaredoxin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34631
Seq. ID
                  LIB3028-021-Q1-B1-B5
Method
                  BLASTX
NCBI GI
                  g4160441
BLAST score
                  123
E value
                   6.0e-09
                  106
Match length
% identity
                   (AF098674) lateral suppressor protein [Lycopersicon
NCBI Description
```

esculentum]

E value

6.0e-48

```
34632
Seq. No.
Seq. ID
                   LIB3028-021-Q1-B1-B9
Method
                   BLASTX
NCBI GI
                   g4377374
                   251
BLAST score
                   1.0e-21
E value
                   122
Match length
% identity
                   39
NCBI Description
                   (AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate
                   Aminotransferase [Chlamydia pneumoniae]
Seq. No.
Seq. ID
                   LIB3028-022-Q1-B1-C4
Method
                   BLASTX
NCBI GI
                   q4490736
BLAST score
                   164
                   7.0e-12
E value
Match length
                   53
% identity
                   37
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   34634
Seq. ID
                   LIB3028-022-Q1-B1-D12
Method
                   BLASTX
NCBI GI
                   q2244929
BLAST score
                   293
E value
                   2.0e-26
Match length
                   128
                   50
% identity
NCBI Description
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
                   34635
Seq. No.
Seq. ID
                   LIB3028-022-Q1-B1-D4
Method
                   BLASTX
NCBI GI
                   q4432814
BLAST score
                   187
E value
                   1.0e-14
Match length
                   53
% identity
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
Seq. No.
                   34636
Seq. ID
                   LIB3028-022-Q1-B1-E9
Method
                   BLASTX
NCBI, GI
                   g3702327
BLAST score
                   160
E value
                   7.0e-11
Match length
                   62
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                   34637
Seq. No..
Seq. ID
                   LIB3028-022-Q1-B1-F1
Method
                   BLASTN
NCBI GI
                   g255578
BLAST score
                   98
```

```
209
Match length
% identity
                    90
                    small auxin up RNA gene cluster: orf X10A [Glycine
 NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 666 nt]
                    34638
 Seq. No.
 Seq. ID
                    LIB3028-022-Q1-B1-F3
Method
                    BLASTX
NCBI GI
                    g1350720
BLAST score
                    136
                    1.0e-08
E value
Match length
                    44
                    61
 % identity
                    60S RIBOSOMAL PROTEIN L32
NCBI Description
                    34639
 Seq. No.
 Seq. ID
                   LIB3028-022-Q1-B1-F6
Method
                    BLASTN
NCBI GI
                    g1431628
BLAST score
                    118
E value
                    9.0e-60
Match length
                    335
 % identity
                    87
                   V.radiata mRNA for pectinacetylesterase
NCBI Description
Seq. No.
                   34640
Seq. ID
                   LIB3028-022-Q1-B1-G9
Method
                   BLASTX
NCBI GI
                    g2739044
BLAST score
                    405
E value
                    1.0e-39
Match length
                    111
 % identity
                    68
NCBI Description
                    (AF024651) polyphosphoinositide binding protein Sshlp
                    [Glycine max]
Seq. No.
                    34641
Seq. ID
                   LIB3028-022-Q1-B1-H3
Method
                   BLASTX
NCBI GI
                    q3738339
BLAST score
                   174
E value
                    5.0e-16
                    90
Match length
 % identity
NCBI Description
                    (AC005170) putative kinase [Arabidopsis thaliana]
Seq. No.
                   34642
                   LIB3028-023-Q1-B1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4200122
BLAST score
                   357
E value
                   5.0e-34
                   109
Match length
% identity
                   61
NCBI Description
                    (AJ009555) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34643
```

E value

```
LIB3028-023-Q1-B1-C5
Seq. ID
Method 🚟
                   BLASTX
NCBI GI
                   g2104536
BLAST score
                   141
                   1.0e-08
E value
Match length
                   56
% identity
NCBI Description
                   (AF001308) predicted glycosyl transferase [Arabidopsis
                   thaliana]
                   34644
Seq. No.
                   LIB3028-024-Q1-B1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2182285
                   57
BLAST score
                   3.0e-23
E value
                   125
Match length
                   86
% identity
NCBI Description
                   Sequence of BAC F5I14 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   34645
                   LIB3028-024-Q1-B1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4522012
BLAST score
                   158
E value
                   1.0e-10
                   93
Match length
% identity
                   41
NCBI Description
                   (AC007069) hypothetical protein [Arabidopsis thaliana]
                   34646
Seq. No.
                   LIB3028-024-Q1-B1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006827
BLAST score
                   313
E value
                   7.0e-29
Match length
                   115
% identity
NCBI Description
                   (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   34647
                   LIB3028-024-Q1-B1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3152613
BLAST score
                   280
E value
                   5.0e-25
Match length
                   113
% identity
                   52
                   (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34648
Seg. No.
                   LIB3028-024-Q1-B1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2828280
BLAST score
                   192
```

7.0e-15

Match length

```
Match length
                   47
                   74
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2832633 emb_CAA16762 (AL021711) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   34649
Seq. ID
                  LIB3028-024-Q1-B1-H8
Method
                  BLASTX
NCBI GI
                  g3402684
BLAST score
                  150
                   7.0e-10
E value
                   40
Match length
                   72
% identity
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34650
Seq. No.
                  LIB3028-025-Q1-B1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345785
BLAST score
                  536
E value
                   1.0e-56
                  126
Match length
                   94
% identity
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                  >gi 567935 dbj BAA05640 (D26593) chalcone synthase
                   [Camellia sinensis]
                   34651
Seq. No.
                  LIB3028-025-Q1-B1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2982431
BLAST score
                  203
E value
                   6.0e-16
Match length
                  125
% identity
                   (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   34652
Seq. No.
Seq. ID
                  LIB3028-026-Q1-B1-A4
                  BLASTX
Method
NCBI GI
                  g3176874
                  179
BLAST score
E value
                   4.0e-13
Match length
                   45
% identity
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
                  34653
Seq. No.
                  LIB3028-026-Q1-B1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4468993
                  543
BLAST score
                  8.0e-56
E value
```

Seq. No.

```
% identity
NCBI Description
                   (AL035605) putative protein [Arabidopsis thaliana]
                  34654
Seq. No.
Seq. ID
                  LIB3028-026-Q1-B1-H9
Method
                  BLASTX
NCBI GI
                  g3608155
BLAST score
                   402
                  3.0e-39
E value
Match length
                  124
% identity
NCBI Description
                   (AC005314) putative RNA helicase [Arabidopsis thaliana]
                  34655
Seq. No.
                  LIB3028-027-Q1-B2-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3885334
                  335
BLAST score
                  2.0e-31
E value
Match length
                  121
% identity
NCBI Description
                   (AC005623) putative argonaute protein [Arabidopsis
                  thaliana]
Seq. No.
                  34656
Seq. ID
                  LIB3028-027-Q1-B2-D9
Method
                  BLASTX
NCBI GI
                  g2911797
BLAST score
                  142
                  7.0e-09
E value
Match length
                  82
                   49
% identity
                   (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera
NCBI Description
                  subsp. trichocarpa X Populus deltoides}
Seq. No.
                  34657
Seq. ID
                  LIB3028-027-Q1-B2-G6
Method
                  BLASTN
NCBI GI
                  g1841474
BLAST score
                  91
E value
                  9.0e-44
Match length
                  171
                  89
% identity
NCBI Description
                  P.sativum mRNA for Myb-like protein (Myb26)
Seq. No.
                  34658
Seq. ID
                  LIB3028-028-Q1-B1-B12
Method
                  BLASTX
NCBI GI
                  q2829910
BLAST score
                  352
E value
                  2.0e-33
Match length
                  119
                  11
% identity
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
```

Method

BLASTX

```
LIB3028-028-Q1-B1-B2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3860312
BLAST score
                   44
E value
                   1.0e-15
Match length
                   70
% identity
NCBI Description
                   Cicer arietinum mRNA for hypothetical protein, clone Can144
                   34660
Seq. No.
Seq. ID
                   LIB3028-028-Q1-B1-B6
Method
                   BLASTX
                   g1903357
NCBI GI
BLAST score
                   366
E value
                   4.0e-35
Match length
                   112
% identity
NCBI Description
                   (AC000104) Strong similarity to Arabidopsis 2A6
                   (gb X83096). [Arabidopsis thaliana]
Seq. No.
                   34661
Seq. ID
                   LIB3028-028-Q1-B1-B7
Method
                   BLASTX
NCBI GI
                   q1903357
                                                                   ٠٠٠.
BLAST score
                   223
E value
                   2.0e-18
Match length
                   74
% identity
                   59
                   (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb X83096). [Arabidopsis thaliana]
Seq. No.
                   34662
Seq. ID
                   LIB3028-028-Q1-B1-F10
Method
                   BLASTN
NCBI GI
                   g56539
BLAST score
                   75
E value
                   4.0e-34
Match length
                   234
% identity
                   93
NCBI Description
                   R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   34663
Seq. ID
                   LIB3028-028-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   g4539326
BLAST score
                   439
E value
                   1.0e-43
Match length
                   108
% identity
NCBI Description
                   (AL035679) putative zinc finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   34664
Seq. ID
                   LIB3028-028-Q1-B1-H6
```

```
NCBI GI
                  g123620
                  196
BLAST score
E value
                   4.0e-15
Match length
                  106
                  49
% identity
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
                  heat shock cognate protein 70 - tomato
                  >gi_19258 emb CAA37971_ (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  34665
Seq. No.
Seq. ID
                  LIB3028-029-Q1-B1-B11
Method
                  BLASTX
NCBI GI
                  g3367522
BLAST score
                  180
                  5.0e-20
E value
                  125
Match length
% identity
                  40
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  34666
Seq. No.
Seq. ID
                  LIB3028-029-Q1-B1-D10
Method
                  BLASTN
NCBI GI
                  g18551
BLAST score
                  397
                  0.0e + 00
E value
                  397
Match length
                  100
% identity
NCBI Description
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
                  34667
Seq. No.
Seq. ID
                  LIB3028-029-Q1-B1-D11
Method
                  BLASTX
NCBI GI
                  g128592
BLAST score
                  309
E value
                  2.0e-28
                  89
Match length
                  64
% identity
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                  >gi_82190_pir_ S22495 pollen-specific protein precursor -
                  common tobacco >gi 19902 emb CAA43454 (X61146) pollen
                  specific protein [Nicotiana tabacum]
Seq. No.
                  34668
Seq. ID
                  LIB3028-029-Q1-B1-E5
Method
                  BLASTX
NCBI GI
                  g1730107
BLAST score
                  241
E value
                  2.0e-20
Match length
                  53
% identity
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi_421870_pir__S33144 anthocyanidin
                  hydroxylase - apple tree >gi 296844 emb CAA50498 (X71360)
```

3.

anthocyanidin hydroxylase [Malus sp.]

```
Seq. No.
                  34669
Seq. ID
                  LIB3028-029-Q1-B1-F4
Method
                  BLASTX
NCBI GI
                  g2662077
BLAST score
                  166
E value
                  1.0e-11
Match length
                  111
% identity
                  (AB007858) KIAA0398 [Homo sapiens] >gi 3450836 (AF067791)
NCBI Description
                  mRNA 5' cap guanine-N-7 methyltransferase [Homo sapiens]
                  >gi 4200033 dbj BAA74464 (AB022604) mRNA
                   (quanine-7-)methyltransferase [Homo sapiens]
                  >gi 4506567 ref_NP_003790.1_pRNMT_ UNKNOWN
                  34670
Seq. No.
Seq. ID
                  LIB3028-029-Q1-B1-H9
Method
                  BLASTX
NCBI GI
                  g2245394
BLAST score
                  268
E value
                  2.0e-27
                  95
Match length
% identity
NCBI Description
                   (U89771) ARF1-binding protein [Arabidopsis thaliana]
                  34671
Seq. No.
                  LIB3028-030-Q1-B1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220633
BLAST score
                  51
E value
                  1.0e-19
Match length
                  264
                  84
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  34672
Seq. ID
                  LIB3028-030-Q1-B1-A9
Method
                  BLASTX
NCBI GI
                  g3142303
BLAST score
                  222
E value
                  3.0e-18
                  109
Match length
% identity
                  (AC002411) Strong similarity to MRP-like ABC transporter
NCBI Description
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb L49379 from Rattus norvegicus.
                   [Arabidopsis thaliana]
                  34673
Seq. No.
Seq. ID
                  LIB3028-030-Q1-B1-B2
Method
                  BLASTX
NCBI GI
                  g1666171
BLAST score
                  353
E value
                  4.0e-34
Match length
                  108
% identity
                  66
```

```
NCBI Description (Y09105) unknown [Nicotiana plumbaginifolia]
Seq. No.
                   34674
                   LIB3028-030-Q1-B1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3550661
BLAST score
                   139
E value
                   2.0e-16
Match length
                   92
% identity
NCBI Description
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
                   tuberosum]
                   34675
Seq. No.
Seq. ID
                   LIB3028-030-Q1-B1-D7
Method
                   BLASTN
NCBI GI
                   g56539
BLAST score
                   87
E value
                   3.0e-41
Match length
                   285
% identity
                   94
NCBI Description
                   R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene .
                   : exon v and flanks
                   34676
Seq. No.
                  LIB3028-030-Q1-B1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2347088
BLAST score
                   142
E value
                   6.0e-15
Match length
                   78
% identity
NCBI Description
                   (U72765) non-specific lipid transfer protein PvLTP-24
                   [Phaseolus vulgaris]
Seq. No.
                   34677
Seq. ID
                  LIB3028-030-Q1-B1-H12
Method '
                   BLASTX
NCBI GI
                   g3785971
BLAST score
                   232
E value
                   1.0e-19
Match length
                   96
% identity
NCBI Description
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
                  >gi_4262248_gb_AAD14541_ (AC006200) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                  34678
Seq. ID
                  LIB3028-030-Q1-B1-H8
Method
                  BLASTX
NCBI GI
                  g3.986172
BLAST score
                  316
                   2.0e-29
E value
Match length
                  95
% identity
                   (AB015428) EXGT1 [Pisum sativum]
NCBI Description
```

Seq. ID

```
34679
Seq. No.
Seq. ID
                  LIB3028-031-Q1-B1-C12
Method
                  BLASTX
NCBI GI
                   g4204268
BLAST score
                   235
E value
                   9.0e-20
                   118
Match length
% identity
                   (AC005223) 62134 [Arabidopsis thaliana]
NCBI Description
                   34680
Seq. No.
                  LIB3028-031-Q1-B1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g126307
BLAST score
                  167
                   1.0e-11
E value
Match length
                   132
                   38
% identity
NCBI Description
                  TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, LINGUAL)
                  >gi_67160_pir__LIRTT triacylglycerol lipase (EC 3.1.1.3)
                  precursor, lingual - rat >gi_56596_emb_CAA26179_ (X02309)
                  lipase precursor [Rattus norvegicus]
Seq. No.
                   34681
                  LIB3028-031-Q1-B1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  210
E value
                   9.0e-17
                   67
Match length
                   60
% identity
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
Seq. No.
                   34682
                  LIB3028-031-Q1-B1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832616
BLAST score
                  210 -
                   9.0e-17
E value
                   46
Match length
% identity
                   (AL021711) heat shock transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  34683
Seq. ID
                  LIB3028-032-Q1-B1-B2
Method
                  BLASTX
NCBI GI
                  g1946366
BLAST score
                  145
                   4.0e-09
E value
                  72
Match length
% identity
NCBI Description
                   (U93215) unknown protein [Arabidopsis thaliana]
                  34684
Seq. No.
```

LIB3028-032-Q1-B1-D2

BLAST score

E value

141

9.0e-09

```
Method
                    BLASTX
 NCBI GI
                     g913445
 BLAST score
                     511
                     5.0e-52
 E value
 Match length
                     125
 % identity
                     74
                     (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase
 NCBI Description
                     homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
 Seq. No.
                     34685
                     LIB3028-033-Q1-B1-A5
 Seq. ID
 Method
                     BLASTN
 NCBI GI
                     q1236948
 BLAST score
                     66
 E value
                     5.0e-29
 Match length
                     178
 % identity
                     86
NCBI Description
                     Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                     34686
 Seq. No.
                     LIB3028-034-Q1-B1-A7
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g3341443
 BLAST score
                     348
 E value
                     6.0e-33
 Match length
                     99
 % identity
                     (AJ223074) acid phosphatase [Glycine max]
 NCBI Description
 Seq. No.
                     34687
                     LIB3028-034-Q1-B1-C6
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g602292
 BLAST score
                     144
 E value
                     4.0e-09
 Match length
                     81
 % identity
                     (U17987) RCH2 protein [Brassica napus]
 NCBI Description
                     34688
 Seq. No.
 Seq. ID
                     LIB3028-034-Q1-B1-E12
 Method
                     BLASTX
 NCBI GI
                     g2920666
 BLAST score
                     258
 E value
                     2.0e-22
 Match length
                     96
 % identity
 NCBI Description
                     (AF048978) 2,4-D inducible glutathione S-transferase
                     [Glycine max].
                     34689
 Seq. No.
 Seq. ID
                     LIB3028-034-01-B1-F11
 Method
                     BLASTX
 NCBI GI
                     q4049350
```

```
Match length
                    84
                    33
% identity
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                    34690
 Seq. No.
 Seq. ID
                    LIB3028-034-Q1-B1-F12
Method
                    BLASTN
NCBI GI
                    g516853
BLAST score
                    181
                    2.0e-97
E value
                    317
Match length
                    38
 % identity
                    Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
                    34691
 Seq. No.
 Seq. ID
                    LIB3028-034-Q1-B1-H1
Method
                    BLASTX
NCBI GI
                    g3435096
BLAST score
                    381
E value
                    9.0e-37
Match length
                    98
                    73
 % identity
                    (AF033587) SRZ-80 [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    34692
Seq. ID
                    LIB3028-034-Q1-B1-H2
Method
                    BLASTX
NCBI GI
                    g1345132
                    323
BLAST score
                    4.0e-30
E value
                    108
Match length
                    62
 % identity
NCBI Description
                    (U47029) ERECTA [Arabidopsis thaliana]
                    >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                    protein kinase, ERECTA [Arabidopsis thaliana]
                    34693
 Seq. No.
 Seq. ID
                    LIB3028-035-Q1-B1-A4
Method
                    BLASTX
NCBI GI
                    g3063448
BLAST score
                    290
E value
                    4.0e-26
Match length
                    126
 % identity
                    47
NCBI Description
                    (AC003981) F22013.10 [Arabidopsis thaliana]
                    34694
Seq. No.
Seq. ID
                    LIB3028-035-Q1-B1-B2
Method
                    BLASTX
NCBI GI
                    q3776005
                    222
BLAST score
                    3.0e-18
E value
                    48
Match length
 % identity
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
```

Method

BLASTX

```
34695~
Seq. No.
Seq. ID
                   LIB3028-035-Q1-B1-C4
Method
                   BLASTX
NCBI GI
                   g3746060
BLAST score
                   377
                   2.0e-36
E value
                   83
Match length
% identity
                   78
NCBI Description
                   (AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.
                   34696
                   LIB3028-035-Q1-B1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1806145
BLAST score
                   113
                   1.0e-56
E value
                   289
Match length
% identity
                   85
NCBI Description
                  M.sativa mRNA for cdc2 kinase homologue, cdc2MsF
                   34697
Seq. No.
Seq. ID
                   LIB3028-035-Q1-B1-H6
Method
                   BLASTX
NCBI GI
                   q3980393
BLAST score
                   359
E value
                   3.0e-34
Match length
                   98
% identity
NCBI Description
                   (AC004561) putative glutathione S-transferase [Arabidopsis
                   thaliana]
Seq. No.
                   34698
Seq. ID
                   LIB3028-036-Q1-B1-A4
Method
                   BLASTX
NCBI GI
                   q2462758
BLAST score
                   234
E value
                   1.0e-19
Match length
                   92
% identity
                   (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34699
                   LIB3028-036-Q1-B1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3461836
BLAST score
                   422
E value
                   1.0e-41
Match length
                   123
% identity
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >qi 3927841 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   34700
                   LIB3028-036-Q1-B1-C9
Seq. ID
```

NCBI Description

```
NCBI GI
                  g2342735
BLAST score
                  184
E value
                  8.0e-14
Match length
                  81
% identity
NCBI Description
                   (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                  34701
                  LIB3028-036-Q1-B1-E5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g18761
BLAST score
                  171
                  2.0e-91
E value
                  255
Match length
                  92
% identity
                  Soybean stem mRNA for 31 kD glycoprotein
NCBI Description
                  34702
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-E9
                  BLASTX
Method
NCBI GI -
                  g886130
                  167
BLAST score
E value
                  8.0e-12
                  77
Match length
% identity
                  43
                  (U28148) putative pectinesterase [Medicago sativa]
NCBI Description
                  34703
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-F3
                  BLASTX
Method
                  g3746062
NCBI GI
                  284
BLAST score
E value
                  2.0e-25
Match length
                  114
% identity
                  4.8
NCBI Description
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
                  34704
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-G6
Method .
                  BLASTN
NCBI GI
                  g170087
                  233
BLAST score
                  1.0e-128
E value
Match length
                  356
                  92
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  34705
Seq. No.
Seq. ID
                  LIB3028-036-Q1-B1-H1
                  BLASTX
Method
NCBI GI
                  q1279640
BLAST score
                  426
E value
                  4.0e-42
                  93
Match length
                                              81
% identity
```

(X92204) NAM [Petunia x hybrida].

Seq. ID

```
34706
Seq. No.
Seq. ID
                   LIB3028-036-Q1-B1-H11
Method
                   BLASTN
NCBI GI
                   g309563
BLAST score
                   47
                   2.0e-17
E value
Match length
                   79
% identity
                   91
NCBI Description
                   Zea mays NADH dehydrogenase subunit 4 (complex I) (nad4)
                   gene, exon 3
                   34707
Seq. No.
Seq. ID
                   LIB3028-036-Q1-B1-H12
Method
                   BLASTN
NCBI GI
                   g3941288
BLAST score
                   63
E value
                   7.0e-27
Match length
                   107
% identity
                   90
NCBI Description
                   Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
Seq. No.
                   34708
Seq. ID
                   LIB3028-037-Q1-B1-F4
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   310
E value
                   2.0e-28
Match length
                   88
% identity
                   69
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
Seq. No.
                   34709
Seq. ID
                   LIB3028-037-Q1-B1-G7
Method
                   BLASTX
NCBI GI
                   q3386614
BLAST score
                   313
E value
                   7.0e-29
Match length
                   86
% identity
NCBI Description
                   (AC004665) putative transcription factor SF3 [Arabidopsis
                   thaliana]
Seq. No.
                   34710
Seq. ID
                   LIB3028-038-Q1-B1-H6
Method
                   BLASTX
NCBI GI
                   g2289003
BLAST score
                   442
E value
                   5.0e-44
Match length
                   126
% identity
NCBI Description
                   (AC002335) membrane transporter D1 isolog [Arabidopsis
                   thaliana]
Seq. No.
                   34711
```

LIB3028-038-Q1-B1-H9

E value

3.0e-69

```
Method
                   BLASTN
NCBI GI
                   g2827081
BLAST score
                   90
                   4.0e-43
E value
Match length
                   149
                   91
% identity
NCBI Description
                  Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,
                  complete cds
                   34712
Seq. No.
Seq. ID
                  LIB3028-039-Q1-B2-B1
Method
                  BLASTN
NCBI GI
                  g1173641
BLAST score
                  126
                   1.0e-64
E value
Match length
                  229
                   90
% identity
NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds
Seq. No.
                   34713
Seq. ID
                  LIB3028-039-Q1-B2-B9
Method
                  BLASTN
NCBI GI
                  g170089
BLAST score
                  268
E value
                   1.0e-149
Match length
                  324
% identity
                   96
                  G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
Seq. No.
                  34714
                  LIB3028-039-Q1-B2-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3033373
BLAST score
                  51
E value
                   6.0e-20
Match length
                  95
% identity
                  88
                  Arabidopsis thaliana chromosome II BAC F19I3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  34715
                  LIB3028-039-Q1-B2-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244956
                  231
BLAST score
E value
                  4.0e-19
Match length
                  83
% identity
NCBI Description
                   (Z97340) strong similarity to pectinesterase [Arabidopsis
                  thaliana]
Seq. No.
                  34716
                  LIB3028-039-Q1-B2-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1778371
BLAST score
                  134
```

```
373
  Match length
                    85
  % identity
  NCBI Description
                    Glycine max asparagine synthetase 1 (AS1) mRNA, complete
                    34717
  Seq. No.
                    LIB3028-039-Q1-B2-G9
  Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g1841474
  BLAST score
                    35
  E value
                    1.0e-10
 Match length
                    95
  % identity
                    84
 NCBI Description
                    P.sativum mRNA for Myb-like protein (Myb26)
                    34718
 Seq. No.
 Seq. ID
                    LIB3028-039-Q1-B2-H1
 Method
                    BLASTX
  NCBI GI
                    g3355483
 BLAST score
                    163
 E value
                    2.0e-11
 Match length
                    58
  % identity
                    48
NCBI Description
                     (AC004218) gibberellin-regulated protein (GASA5)-like
                     [Arabidopsis thaliana]
                    34719
 Seq. No.
 Seq. ID
                    LIB3028-040-Q1-B1-A8
 Method
                    BLASTX
 NCBI GI
                    g3402694
 BLAST score
                    439
 E value
                    1.0e-43
 Match length
                    131
  % identity
                    66
 NCBI Description
                    (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]
 Seq. No.
                    34720
 Seq. ID
                    LIB3028-040-Q1-B1-C4
 Method
                    BLASTX
 NCBI GI
                    q4539314
 BLAST score
                    141
 E value
                    1.0e-08
 Match length
                    53
  % identity
                    58
 NCBI Description
                    (AL035679) kinesin like protein [Arabidopsis thaliana]
 Seq. No.
                    34721
 Seq. ID
                    LIB3028-040-Q1-B1-D10
 Method
                    BLASTX
 NCBI GI
                    q2765093
 BLAST score
                    140
                    1.0e-08
 E value
 Match length
                    100
 % identity
                    (Y10983) putative cytochrome P450 [Glycine max]
 NCBI Description
```

34722

Seq. No.

NCBI GI

م الما به جونيف اوبود

```
Seq. ID
                  LIB3028-040-Q1-B1-D11
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  589
E value
                   3.0e-61
Match length
                  112
% identity
                  87
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  34723
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-A12
Method
                  BLASTX
NCBI GI
                  q1297189
                  329
BLAST score
                  8.0e-31
E value
Match length
                  107
                                                                            - GANGTON
                   62
% identity
                   (U53501) Theoretical protein with similarity to Swiss-Prot
NCBI Description
                  Accession Number P19456 plasma membrane ATPase 2 (proton
                  pump) [Arabidopsis thaliana]
                  34724
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-A8
Method
                  BLASTN
NCBI GE
                  g516853
BLAST score
                  134
                  3.0e-69
E value
Match length
                  287
% identity
                   45
                  Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
                  34725
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-B2
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  273
                   3.0e-24
E value
Match length
                  55
                  85
% identity
NCBI Description
                  metallothionein - soybean >gi 228682 prf 1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  34726
Seq. ID
                  LIB3028-041-Q1-B1-E12
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  141
E value
                  5.0e-09
Match length
                  44
% identity
NCBI Description
                   (AL031004) putative protein [Arabidopsis thaliana]
                  34727
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-E8
                  BLASTX
Method
```

q1568637

NCBI GI

```
BLAST score
                   186
                   5.0e-14
E value
Match length
                   109
                   42
% identity
                   (U69554) 6a-hydroxymaackiain methyltransferase [Pisum
NCBI Description
                   sativum]
                   34728
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  q1531758
BLAST score
                  174
E value
                   1.0e-12
Match length
                   42
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                   34729
Seq. No.
Seq. ID
                  LIB3028-041-Q1-B1-H9
Method
                  BLASTX
NCBI GI
                   g136057
BLAST score
                  233
E value
                  1.0e-19
Match length
                  81
                   56
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
Seq. No.
                   34730
Seq. ID
                  LIB3028-042-Q1-B1-A10
Method
                  BLASTX
NCBI GI
                  g2654095
BLAST score
                  214
                   3.0e-17
E value
                  87
Match length
% identity
                   51
NCBI Description
                   (AF034210) aspartate aminotransferase cytosolic isozyme
                  AAT2 [Glycine max]
Seq. No.
                  34731
Seq. ID
                  LIB3028-042-Q1-B1-B4
Method
                  BLASTX
NCBI GI
                  g2706515
BLAST score
                  210
                  7.0e-17
E value
                  86
Match length
% identity
                   48
                   (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                  paradisi]
                  34732
Seq. No.
                  LIB3028-042-Q1-B1-C12
Seq. ID
Method
                  BLASTX
```

g3892056

```
BLAST score
                   140
E value
                   8.0e-09
Match length
                   54
                   59
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                   34733
Seq. No.
Seq. ID
                   LIB3028-042-Q1-B1-D2
Method ...
                   BLASTX
NCBI GI
                   q294666
BLAST score
                   181
                   2.0e-13
E value
Match length
                   58
% identity
                   60
NCBI Description
                   (L13241) beta-ketoacyl-ACP synthase [Ricinus communis]
Seq. No.
                   34734
Seq. ID
                   LIB3028-042-Q1-B1-F7
Method
                   BLASTX
NCBI GI
                   g2880044
BLAST score
                   142
E value
                   7.0e-09
Match length
                   31
% identity --
                   94
NCBI Description
                   (AC002340) putative tropinone reductase [Arabidopsis
                   thaliana]
                   34735
Seq. No.
Seq. ID
                   LIB3028-043-Q1-B1-E3
Method
                   BLASTX
NCBI GI
                   g2760837
BLAST score
                   151
                   5.0e-10
E value
Match length
                   88
% identity
                   38
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   34736
Seq. ID
                   LIB3028-043-Q1-B1-E8
Method
                   BLASTX
NCBI GI
                   g2632105
BLAST score
                   150
E value
                   1.0e-09
                   37
Match length
                   78
% identity
NCBI Description
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
                   >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA
                   synthetase [Arabidopsis thaliana]
                   34737
Seq. No.
                   LIB3028-043-Q1-B1-G11
Seq. ID
Method
                  BLASTX
                   g2642450
NCBI GI
BLAST score
                   484
                   7.0e-49
E value
                  122
Match length
```

. .

75

% identity

NCBI Description

```
NCBI Description
                   (AC002391) putative metal ion transporter (Nramp)
                   [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
Seq. No.
                   34738
Seq. ID
                   LIB3028-043-Q1-B1-G3
Method
                   BLASTX
NCBI GI
                   g2792297
BLAST score
                   320
                   9.0e-30
E value
Match length
                   66
% identity
NCBI Description
                   (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                   34739
Seq. ID
                   LIB3028-043-Q1-B1-H3
Method
                   BLASTX
NCBI GI
                   g2244898
BLAST score
                   334
E value
                   2.0e-31
Match length
                   98
                   63
% identity
NCBI Description
                   (Z97338) strong similarity to protein phosphatase 2A
                   regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                   34740
Seq. ID
                  LIB3028-044-Q1-B1-C11
Method
                   BLASTX
NCBI GI
                   g3641252
BLAST score
                   571
E value
                   4.0e-59
Match length
                   117
% identity
NCBI Description
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
                   domestica]
Seq. No.
                   34741
Seq. ID
                  LIB3028-044-Q1-B1-F11
Method
                  BLASTX
NCBI GI
                   g4337196
BLAST score
                   202
                   7.0e-16
E value
Match length
                   123
% identity
NCBI Description
                   (AC006403) putative serine/threonine receptor kinase
                   [Arabidopsis thaliana]
                   34742
Seq. No.
Seq. ID
                  LIB3028-044-Q1-B1-G9
Method
                  BLASTX
NCBI GI
                  g2760319
BLAST score
                  188
E value
                   3.0e-14
Match length
                  107
% identity
                   50
```

(AC002130) F1N21.3 [Arabidopsis thaliana]

BLAST score

```
34743
Seq. No.
Seq. ID
                  LIB3028-045-Q1-B1-B12
                  BLASTX
Method
NCBI GI
                  g603074
BLAST score
                  228
E value
                  7.0e-19
Match length
                  122
                   39
% identity
                  (U18197) ATP:citrate lyase [Homo sapiens]
NCBI Description
                  34744
Seq. No.
Seq. ID
                  LIB3028-045-Q1-B1-B3
                  BLASTN
Method
NCBI GI
                  g2828182
BLAST score
                  47
                  2.0e-17
E value
Match length
                  95
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  34745
Seq. ID
                  LIB3028-045-Q1-B1-E1
Method
                  BLASTN
NCBI GI
                  g1326160
BLAST score
                  48
                   4.0e-18
E value
                  94
Match length
                  95
% identity
NCBI Description
                  Phaseolus vulgaris dehydrin mRNA, complete cds
                  34746
Seq. No.
Seq. ID
                  LIB3028-046-Q1-B1-A4
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  310
                  1.0e-174
E value
Match length
                  387
                  30
% identity
NCBI Description
                  Soybean gene for ubiquitin, complete cds
                  34747
Seq. No.
Seq. ID
                  LIB3028-046-Q1-B1-A9
                  BLASTX
Method
NCBI GI
                  q464365
BLAST score
                  205
E value
                  2.0e-16
Match length
                  62
                  63
% identity
                  PEROXIDASE P7 >gi 66306 pir OPNB7 peroxidase (EC 1.11.1.7)
NCBI Description
                  - turnip
                 34748
Seq. No.
                  LIB3028-046-Q1-B1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2687432
```

NCBI Description

```
6.0e-18
E value
Match length
                   48
                   100
% identity
                   Plumbago auriculata large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
Seq. No.
                   34749
Seq. ID
                   LIB3028-046-Q1-B1-C9
Method
                   BLASTX
NCBI GI
                   q4007792
BLAST score
                   283
E value
                   2.0e-25
Match length
                   96
                   62
% identity
                   (AL034463) Xenopus 14s cohesin smc1 subunit homolog
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   34750
Seq. ID
                   LIB3028-046-Q1-B1-D9
Method
                   BLASTX
NCBI GI
                   g4056433
BLAST score
                   142
E value
                   6.0e-09
                   95
Match length
% identity
                   40
NCBI Description
                   (AC005990) Similar to anter-specific proline-rich protein
                   (CEX) gb X60376 from Brassica napus. [Arabidopsis thaliana]
Seq. No.
                   34751
Seq. ID
                   LIB3028-046-Q1-B1-H1
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   127
E value
                   2.0e-09
Match length
                   77
% identity
                   56
NCBI Description
                   (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                   34752
Seq. ID
                  ·LIB3028-046-Q1-B1-H7
Method
                   BLASTX
NCBI GI
                   g3885329
BLAST score
                   333
E value
                   3.0e-31
Match length
                   83
% identity
NCBI Description
                   (AC005623) alien-like protein [Arabidopsis thaliana]
                   34753
Seq. No.
                   LIB3028-047-Q1-B1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244899
BLAST score
                   164
                   1.0e-11
E value
                   92 ...
Match length
% identity
                   43
```

(297338) similar to UFD1 protein [Arabidopsis thaliana]

```
34754
Seq. No.
Seq. ID
                   LIB3028-048-Q1-B1-B8
Method
                   BLASTX
NCBI GI
                   g3643608
BLAST score
                   197
E value
                   3.0e-15
Match length
                   100
% identity
                   43
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   34755
Seq. No.
Seq. ID
                   LIB3028-048-Q1-B1-D2
Method
                   BLASTX
NCBI GI
                   g2651314
BLAST score
                   148
E value
                   1.0e-11
Match length
                   43
% identity
                   (AC002336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   34756
Seq. ID
                   LIB3028-048-Q1-B1-D8
Method
                   BLASTN
NCBI GI
                   g391604
BLAST score
                   35
E value
                   3.0e-10
Match length
                   59
% identity
                   90
NCBI Description
                   Arabidopsis thaliana ATPK15D mRNA for casein kinase II
                   catalytic subunit, complete cds
Seq. No.
                   34757
Seq. ID
                   LIB3028-049-Q1-B1-A5
Method
                   BLASTX
NCBI GI
                   g1170619
BLAST score
                   219
E value
                   8.0e-18
Match length
                   52
% identity
                   83
NCBI Description
                   KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
                   kinesin-related protein katA - Arabidopsis thaliana
                  >gi_303502 dbj BAA01972 (D11371) kinesin-like motor
                   protein heavy chain [Arabidopsis thaliana]
                   >gi_2911084_emb_CAA17546_ (AL021960) kinesin-related protein katA [Arabidopsis thaliana]
Seq. No.
                   34758
Seq. ID
                   LIB3028-049-Q1-B1-B2
Method
                   BLASTN
NCBI GI
                   g2687725
BLAST score
                   382
                   0.0e + 00
E value
Match length
                   466
% identity
                   98-
NCBI Description Glycine max mRNA for putative 2-hydroxydihydrodaidzein
```

BLAST score

293

reductase

```
34759
Seq. No.
                   LIB3028-049-Q1-B1-C1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4098318
BLAST score
                   237
E value
                   1.0e-130
                   501
Match length
                   87
% identity
                  Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds
NCBI Description
                   34760
Seq. No.
                   LIB3028-050-Q1-B1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3935183
BLAST score
                   174
                   5.0e-13
E value
Match length
                   75
                   52
% identity
                   (AC004557) F17L21.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34761
                   LIB3028-050-Q1-B1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3551247
BLAST score
                   331
E value
                   6.0e-31
Match length
                   75
% identity
                   77
NCBI Description
                  (AB012703) 181 [Daucus carota]
Seq. No.
                   34762
Seq. ID
                   LIB3028-050-Q1-B1-H5
Method
                   BLASTN
NCBI GI
                   g624937
BLAST score
                   40
E value
                   3.0e-13
Match length
                   104
% identity
                   86
NCBI Description A.thaliana RPL16A gene
                   34763
Seq. No.
                   LIB3028-051-Q1-B1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827992
BLAST score
                   174
E value
                   9.0e-13
                   75
Match length
% identity
                  (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
Seq. No.
                   34764
                   LIB3028-051-Q1-B1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1871184
```

Match length

```
E value
                  2.0e-26
Match length
                  93
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34765
                  LIB3028-052-Q1-B1-G9
Seq. ID
Method
                  BLASTX
                  q1708025
NCBI GI
BLAST score
                  473
E value
                  1.0e-47
Match length
                  99
% identity
                  91
NCBI Description
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
                  >gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate
                  dehydrogenase (NAD+) [Cuphea lanceolata]
                  34766
Seq. No.
Seq. ID
                  LIB3028-052-Q1-B2-C11
                  BLASTX
Method
NCBI GI
                  g629641
BLAST score
                  239
E value
                  1.0e-20
                  58
Match length
                  79
% identity
NCBI Description PsHSC71.0 protein - garden pea >gi 1076530 pir S53500
                  HSC71.0 protein - garden pea >gi 473217 emb CAA83548
                  (Z32537) PsHSC71.0 [Pisum sativum]
Seq. No.
                  34767
Seq. ID
                  LIB3028-052-Q1-B2-C9
                  BLASTN
Method
NCBI GI
                  g303900
BLAST score
                  254
E value
                  1.0e-141
Match length
                  377
                  33
% identity
NCBI Description
                  Soybean gene for ubiquitin, complete cds
Seq. No.
                  34768
Seq. ID
                  LIB3028-052-Q1-B2-G4
Method
                  BLASTX
NCBI GI
                  g4049401
BLAST score
                  139
E value
                  6.0e-09
Match length
                  49
% identity
NCBI Description
                  (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
                  thaliana]
Seq. No.
                  34769
Seq. ID
                  LIB3028-052-Q1-B2-H9
Method
                  BLASTN
NCBI GI
                  g18551
BLAST score
                  387
E value
                  0.0e+00
```

E value

Match length

4.0e-09

```
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
Seq. No.
                   34770
Seq. ID
                   LIB3028-053-Q1-B1-A12
Method
                   BLASTX
NCBI GI
                   g3183088
BLAST score
                   252
E value
                   7.0e-22
                   93
Match length
% identity
                   54
NCBI Description
                   PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                   cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
                   34.771
Seq. No.
Seq. ID
                   LIB3028-053-Q1-B1-C1
Method
                   BLASTX
NCBI GI
                   g2827658
BLAST score
                   198
E value
                   8.0e-16
Match length
                   56
% identity
                   66
NCBI Description
                   (AL021637) putative protein [Arabidopsis thaliana]
Seq. No.
                   34772
                   LIB3028-053-Q1-B1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20728
BLAST score
                   54
E value
                   9.0e-22
                  134
Match length
% identity
                   85
NCBI Description
                   Pea chloroplast GAPA mRNA encoding
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
Seq. No.
                   34773
                   LIB3028-053-Q1-B1-D9
Seq. ID
Method
                   BLASTX
                   g4337196
NCBI GI
BLAST score
                   254
E value
                   4.0e-22
                   73
Match length
                   64
% identity
NCBI Description
                   (AC006403) putative serine/threonine receptor kinase
                   [Arabidopsis thaliana]
                   34774
Seq. No.
                  LIB3028-053-Q1-B1-F6
Seq. ID
Method
                  BLASTX
                  g4193382
NCBI GI
BLAST score
                  144
```

Method

BLASTN

```
% identity
NCBI Description
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
Seq. No.
                  34775
Seq. ID
                  LIB3028-053-01-B1-G12
Method
                  BLASTN
NCBI GI
                  g18551
BLAST score
                  148
E value
                  1.0e-77
Match length
                  219
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                  34776
Seq. ID
                  LIB3028-053-Q1-B1-G4
Method
                  BLASTX
NCBI GI
                  g3676469
BLAST score
                  176
E value
                  4.0e-13
Match length
                  60
% identity
                  53
NCBI Description
                  (AF053884) (R)-(+)-mandelonitrile lyase isoform MDL4
                  precursor [Prunus serotina] >gi 3676471 (AF053885)
                  (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus
                  serotina] >gi 4105127 (AF043186) (R)-(+)-mandelonitrile
                  lyase isoform MDL4 precursor [Prunus serotina] >gi_4105129
                  (AF043187) (R)-(+)-mandelonitrile lyase isoform MDL4
                  precursor [Prunus serotina]
Seq. No.
                  34777
                  LIB3028-053-Q1-B1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913808
BLAST score
                  268
                  1.0e-23
E value
Match length
                  64
% identity
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >gi_2429618_dbj_BAA22284 (AB007120)
                  ferrochelatase [Oryza sativa]
Seq. No.
                  34778
Seq. ID
                  LIB3028-053-Q1-B1-G7
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  132
E value
                  3.0e-68
Match length
                  213
                  34
% identity
                  Soybean gene for ubiquitin, complete cds
NCBI Description
Seq. No.
                  34779
Seq. ID
                  LIB3028-054-Q1-B1-A11
```

% identity

```
NCBI GI
                   g1173641
BLAST score -
                   94
E value
                   8.0e-46
Match length
                   152
% identity
                   91
NCBI Description
                   Glycine max lipoxygenase (lox7) mRNA, complete cds
Seq. No.
Seq. ID
                   LIB3028-054-Q1-B1-A12
Method
                   BLASTX
NCBI GI
                   q3367520
BLAST score
                   286
E value
                   1.0e-25
Match length
                   124
% identity
                   40
NCBI Description
                   (AC004392) Similar to protein kinase APK1A,
                   tyrosine-serine-threonine kinase gb D12522 from A.
                   thaliana. [Arabidopsis thaliana]
Seq. No.
                   34781
Seq. ID
                   LIB3028-054-Q1-B1-A3
Method
                   BLASTX
NCBI GI
                   q2642606
BLAST score
                   154
E value
                   1.0e-10
Match length
                   39
                   74
% identity
                   (AF031922) chalcone synthase [Raphanus sativus]
NCBI Description
Seq. No.
                   34782
Seq. ID
                   LIB3028-054-Q1-B1-B12
Method
                   BLASTX
NCBI GI
                   q629669
BLAST score
                   365
E value
                   5.0e-35
Match length
                   115
% identity
                   59
NCBI Description
                   hypothetical protein - tomato
Seq. No.
                   34783
Seq. ID
                   LIB3028-054-Q1-B1-B4
Method
                   BLASTX
NCBI GI
                   g3176710
BLAST score
                   205
E value
                   1.0e-19
Match length
                   95
% identity
                   56
NCBI Description
                   (AC002392) unknown protein [Arabidopsis thaliana]
                   34784
Seq. No.
                   LIB3028-054-Q1-B1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455276
BLAST score
                   298
E value
                   3.0e-36
Match length
                  116
```

% identity

```
NCBI Description
                     (AL035527) peptide transporter-like protein [Arabidopsis
                     thaliana]
                     34785
Seq. No.
Seq. ID
                     LIB3028-054-Q1-B1-D5
Method
                     BLASTX
NCBI GI
                     g2341032
BLAST score
                     210
E value
                     3.0e−17
Match length
                     47
% identity
                     83
                     (AC000104) EST gb ATTS0956 comes from this gene.
NCBI Description
                     [Arabidopsis thaliana]
                     34786
Seq. No.
Seq. ID
                     LIB3028-054-Q1-B1-H11
Method
                     BLASTX
NCBI GI
                     g3269285
BLAST score
                     360
                     2.0e-34
E value .
                     106
Match length
% identity
                     63
                     (AL030978) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     34787 -
Seq. ID
                     LIB3028-054-Q1-B1-H3
Method
                     BLASTX
NCBI GI
                     q1346118
BLAST score
                     384
E value
                     3.0e-37
                     107
Match length
% identity
                     69
NCBI Description
                     GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                     >gi_542101_pir__S40215 H-protein - Flaveria pringlei
>gi_2119599_pir__S60194 H-protein precursor (clone HFP4) -
Flaveria pringlei >gi_438001_emb_CAA81075_ (Z25856)
H-protein [Flaveria pringlei] >gi_3688301_emb_CAB16913_
                     (Z99764) H-protein [Flaveria pringlei]
Seq. No.
                     34788
Seq. ID
                     LIB3028-054-Q1-B1-H8
Method
                     BLASTX
NCBI GI
                     g4309758
BLAST score
                     148
E value
                     2.0e-09
Match length
                     37
% identity
                     (AC006217) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     34789
Seq. ID
                     LIB3028-055-Q1-B1-G5
Method
                     BLASTN
NCBI GI
                     g1055367
BLAST score
                     191
E value
                     1.0e-103
Match length
                     311
```

```
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  34790
                  LIB3028-056-Q1-B1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3114573
BLAST score
                  546
E value
                   4.0e-56
Match length
                  130
% identity
NCBI Description
                   (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
                  piperita]
Seq. No.
                  34791
Seq. ID
                  LIB3028-056-Q1-B1-D9
Method
                  BLASTN
                  g1370171
NCBI GI
BLAST score
                  47
E value
                  2.0e-17
Match length
                  59
% identity
NCBI Description
                  L.japonicus mRNA for small GTP-binding protein, RAB1X
Seq. No.
                  34792
Seq. ID
                  LIB3028-056-Q1-B1-F8
Method
                  BLASTN
NCBI GI
                  q56539
BLAST score
                  40
                  4.0e-13
E value
Match length
                  100
% identity
NCBI Description
                  R.norvegicus gene encoding prolactin, exon 5
                  >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
Seq. No.
                  34793
                  LIB3028-056-Q1-B1-G10
Seq. ID
Method
                  BLASTX
                  g3860247
NCBI GI
BLAST score
                  371
E value
                  1.0e-35
                  72
Match length
% identity
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  34794
Seq. ID
                  LIB3028-056-Q1-B1-H12
Method
                  BLASTX
NCBI GI
                  g4559330
                  240
BLAST score
                  2.0e-20
E value.
Match length
                  89
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
```

34795

Seq. No.

Seq. No.

Seq. ID

*1.

34800

LIB3029-002-Q1-B1-E3

```
Seq. ID
                  LIB3029-001-Q1-B1-B4
Method
                  BLASTX
NCBI GI
                  g731651
BLAST score
                  308
E value
                  3.0e-28
Match length
                  124
% identity
NCBI Description
                  HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN
                  PUT2-SRB2 INTERGENIC REGION >gi 626608 pir S46746
                  hypothetical protein YHR039c - yeast (Saccharomyces
                  cerevisiae) >gi 488180 (U00062) Yhr039cp [Saccharomyces
                  cerevisiae]
                  34796
Seq. No.
                  LIB3029-001-Q1-B1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244852
BLAST score
                  308
                  3.0e-28
E value
Match length
                  66
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  34797
Seq. No.
Seq. ID
                  LIB3029-002-Q1-B1-A4
Method
                  BLASTN
NCBI GI
                  g1431744
BLAST score
                  79
E value
                  8.0e-37
                  151
Match length
% identity
                  Glycine max sucrose binding protein (sbp) mRNA, complete
NCBI Description
                  cds
                  34798
Seq. No.
Seq. ID
                  LIB3029-002-Q1-B1-C3
Method
                  BLASTN
NCBI GI
                  q18540
BLAST score
                  139
E value
                  2.0e-72
Match length
                  285
                  87
% identity
NCBI Description
                  G.max BBI mRNA for proteinase inhibitor
Seq. No.
                  34799
Seq. ID
                  LIB3029-002-Q1-B1-D12
Method
                  BLASTX
NCBI GI
                  g1352345
BLAST score
                  161
E value
                  3.0e-15
Match length
                  90
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_18765_emb_CAA40182_ (X56856) eEF-la [Glycine max]
```

```
BLASTX
Method
NCBI GI
                   g4006897
BLAST score
                   132
E value
                   2.0e-11
Match length
                   122
% identity
                   40
NCBI Description
                   (Z99708) globulin-like protein [Arabidopsis thaliana]
                   34801
Seq. No.
Seq. ID
                  LIB3029-003-Q1-B1-D10
Method
                   BLASTX
NCBI GI
                   q3097321
BLAST score
                   215
                   2.0e-17
E value
Match length
                   80
                   57
% identity
NCBI Description
                  (AB013289) Bd 30K [Glycine max]
                   34802
Seq. No.
                  LIB3029-003-Q1-B1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4097880
BLAST score
                   126
E value
                   1.0e-13
Match length
                   110
                   45
% identity
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   34803
Seq. ID
                  LIB3029-003-Q1-B1-E4
Method
                  BLASTX
NCBI GI
                  g3036802
BLAST score
                  274
                   3.0e-24
E value
Match length
                  112
% identity
                   55
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805864 emb CAA21484 (AL031986) putative protein
                   [Arabidopsis thaliana]
                  34804
Seq. No.
Seq. ID
                  LIB3029-004-Q1-B1-D8
Method
                  BLASTN
NCBI GI
                  g516102
BLAST score
                  331
E value
                  0.0e + 00
                  412
Match length
                  95
% identity
NCBI Description
                  Soybean phytochrome B (phyB) gene exons 1-5, complete cds
Seq. No.
                  34805
Seq. ID
                  LIB3029-004-Q1-B1-F6
Method
                  BLASTN
NCBI GI
                  g2270991
BLAST score
                  105
E value
                  6.0e-52
```

Seq. No. Seq. ID

```
% identity
NCBI Description
                  Glycine max metallothionein-II protein mRNA, complete cds
Seq. No.
Seq. ID
                  LIB3029-004-Q1-B1-G12
Method
                   BLASTN
NCBI GI
                   g3097320
                   276
BLAST score
E value
                   1.0e-154
Match length
                   324
% identity
                   96
NCBI Description
                  Glycine max gene for Bd 30K, complete cds
                   34807
Seq. No.
Seq. ID
                  LIB3029-004-Q1-B1-G3
Method
                  BLASTN
NCBI GI
                   g886099
BLAST score
                   49
E value
                   6.0e-19
                   77
Match length
% identity
                   92
                  Glycine max putative water channel protein (Pipl) mRNA,
NCBI Description
                  complete cds
                   34808
Seq. No.
Seq. ID
                  LIB3029-004-Q1-B1-H8
Method
                  BLASTN
NCBI GI
                  g434060
BLAST score
                  85
                   4.0e-40
E value
Match length
                  153
                  89
% identity
                  Soybean DNA for basic 7S globulin, complete cds
NCBI Description
Seq. No.
                   34809
Seq. ID
                  LIB3029-005-Q1-B1-A10
Method
                  BLASTX
NCBI GI
                  g3894194
BLAST score
                  144
E value
                  1.0e-09
Match length
                   61
% identity
                   (AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  34810
Seq. ID
                  LIB3029-005-Q1-B1-B6
Method
                  BLASTN
NCBI GI
                  g2305019
BLAST score
                  104
E value
                  2.0e-51
Match length
                  271 -
% identity
                  97
NCBI Description
                  Glycine max 2S albumin pre-propeptide mRNA, complete cds
```

LIB3029-005-Q1-B1-E5

```
Method
                  BLASTX
NCBI GI
                  g2801536
BLAST score
                  328
                  1.0e-30
E value
                  121
Match length
                   54
% identity
NCBI Description
                   (AF039531) lysophospholipase homolog [Oryza sativa]
                  34812
Seq. No.
Seq. ID
                  LIB3029-005-Q1-B1-F12
Method
                  BLASTN
NCBI GI
                  g169972
BLAST score
                  344
E value
                  0.0e + 00
Match length
                  344
                  100
% identity
                  Soybean glycinin A-la-B-x subunit mRNA, complete cds
NCBI Description
Seq. No.
                  34813
Seq. ID
                  LIB3029-005-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  g1871526
BLAST score
                  359
E value
                  3.0e - 34
Match length
                  121
% identity
                  30
NCBI Description
                  (X81997) leucine-rich-repeat protein [Helianthus annuus]
Seq. No.
                  34814
Seq. ID
                  LIB3029-006-Q1-B1-A2
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  89
E value
                  2.0e-42
Match length
                  121
% identity
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  34815
Seq. ID
                  LIB3029-006-Q1-B1-B3
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  119
E value
                  3.0e-60
Match length
                  317
% identity
                  85
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  34816
Seq. ID
                  LIB3029-006-Q1-B1-D2
Method
                  BLASTN
NCBI GI
                  g2370311
BLAST score
                  125
E value
                  7.0e-64
```

% identity

```
NCBI Description
                  Medicago sativa mRNA for DnaJ-like protein
                   34817
                   LIB3029-006-Q1-B1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18540
BLAST score
                   188
E value
                   1.0e-101
                   377
Match length
                   88
% identity
                   G.max BBI mRNA for proteinase inhibitor
NCBI Description
Seq. No.
                   34818
Seq. ID
                   LIB3029-006-Q1-B1-F6
                   BLASTN
Method
NCBI GI
                   q4220638
BLAST score
                   43
E value
                   5.0e-15
Match length
                   143
                   83
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   34819
Seq. ID
                   LIB3029-007-Q1-B1-A9
Method
                   BLASTX
NCBI GI
                   q132944
BLAST score
                   485
E value
                   4.0e-49
Match length
                   102
                   87
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                   protein L3 (ARP2) - Arabidopsis thaliana >qi 806279
                   (M32655) ribosomal protein [Arabidopsis thalīana]
Seq. No.
                   34820
Seq. ID
                   LIB3029-007-Q1-B1-B12
Method
                   BLASTX
NCBI GI
                   q4539292
BLAST score
                   331
E value
                   5.0e-31
                   92
Match length
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   34821
                   LIB3029-007-Q1-B1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g138364
BLAST score
                   453
E value
                   7.0e-53
Match length
                   132
% identity
                   80
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
```

% identity

54

```
(M62738) coat protein [Bean pod mottle virus]
                  34822
Seq. No.
                  LIB3029-007-Q1-B1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519193
BLAST score
                  34
E value
                  1.0e-09
Match length
                  38
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                  34823
Seq. ID
                  LIB3029-007-Q1-B1-C3
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  265
                  8.0e-27
E value
                  99
Match length
% identity
                  69
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                  34824
Seq. No.
Seq. ID
                  LIB3029-007-Q1-B1-E12
Method
                  BLASTN
NCBI GI
                  g18551
BLAST score
                  56
E value
                  7.0e-23
Match length
                  188
% identity
                  82
NCBI Description
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
Seq. No.
                  34825
Seq. ID
                  LIB3029-007-Q1-B1-H4
Method
                  BLASTN
NCBI GI
                  g1199562
BLAST score
                  315
E value
                  1.0e-177
Match length
                  367
% identity
                  99
NCBI Description
                  Glycine max 34 kDa maturing seed vacuolar thiol protease
                  mRNA, complete cds
                  34826
Seq. No.
Seq. ID
                  LIB3029-008-Q1-B1-C4
Method
                  BLASTX
NCBI GI
                  q4337188
BLAST score
                  248
E value
                  3.0e-21
Match length
                  81
```

bean pod mottle virus (strain Kentucky G7) >gi 210812

```
NCBI Description
                  (AC006403) hypothetical protein [Arabidopsis thaliana]
                  34827
Seq. No.
Seq. ID
                  LIB3029-008-Q1-B1-C7
                  BLASTX
Method
NCBI GI
                  g2388937
BLAST score
                  204
E value
                  3.0e-16
                  72
Match length
                  50
% identity
                  (Z98977) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  34828
Seq. ID
                  LIB3029-008-Q1-B1-H6
Method
                  BLASTX
NCBI GI
                  g3913952
BLAST score
                  350
E value
                  3.0e-33
                  85
Match length
                  73
% identity
                  ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi 2351578
NCBI Description
                  (U82330) adenylate kinase homolog [Prunus armeniaca]
                  34829
Seq. No.
                  LIB3029-008-Q1-B1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3377507
BLAST score
                  462
E value
                  2.0e-46
Match length
                  125
                  69
% identity
NCBI Description
                  (AF056026) auxin transport protein EIR1 [Arabidopsis
                  thaliana] >gi 3661620 (AF093241) putative auxin efflux
                  carrier AGR [Arabidopsis thaliana] >gi 3746886 (AF087459)
                  polar-auxin-transport efflux component AGRAVITROPIC 1
                  [Arabidopsis thaliana] >gi 4206709 (AF086906) root
                  gravitropism control protein [Arabidopsis thaliana]
Seq. No.
                  34830
Seq. ID
                  LIB3029-009-Q1-B1-A7
Method
                  BLASTN
NCBI GI
                  g18535
                  299
BLAST score
E value
                  1.0e-167
Match length
                  365
% identity
                  91
NCBI Description
                  Soybean mRNA for the alpha subunit of beta-conglycinin
                  34831
Seq. No.
                  LIB3029-009-Q1-B1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3549626
                  180
BLAST score
                  8.0e-14
E value
Match length
                  58
                  53
% identity
                 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
```

NCBI GI

g210811

```
34832
Seq. No.
Seq. ID
                   LIB3029-009-Q1-B1-E5
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   351
E value
                   2.0e-33
                   99
Match length
% identity
                   71
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   34833
Seq. No.
                   LIB3029-009-Q1-B1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3097320
                   190
BLAST score
E value
                   1.0e-102
Match length
                   265
% identity
                   95
                   Glycine max gene for Bd 30K, complete cds
NCBI Description
Seq. No.
                   34834
Seq. ID
                   LIB3029-009-Q1-B1-H8
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   110 -
                   5.0e-55
E value
                   253
Match length
% identity
                   88
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   34835
Seq. ID
                   LIB3029-010-Q1-B1-A1
Method
                   BLASTX
NCBI GI
                   g2213594
BLAST score
                   221
E value
                   4.0e-18
Match length
                   73
% identity
NCBI Description
                   (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                   34836
Seq. ID
                   LIB3029-010-Q1-B1-B3
Method
                   BLASTN
NCBI GI
                   g2905771
BLAST score
                   144
E value
                   3.0e-75
                   156
Match length
% identity
                   98
                   Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                   (GAPDH) mRNA, partial cds
Seq. No.
                   34837
Seq. ID
                   LIB3029-010-Q1-B1-C10
Method
                   BLASTN
```

```
BLAST score
                   249
E value
                   1.0e-138
Match length
                   392
                   91
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   34838
Seq. No.
Seq. ID
                  LIB3029-010-Q1-B1-C7
Method
                   BLASTN
NCBI GI
                  g18535
BLAST score
                   147
                   5.0e-77
E value
                   219
Match length
                   92
% identity
                  Soybean mRNA for the alpha subunit of beta-conglycinin
NCBI Description
                   34839
Seq. No.
Seq. ID
                  LIB3029-010-Q1-B1-D3
Method
                  BLASTN
NCBI GI
                  g169972
                   349
BLAST score
                   0.0e + 00
E value
Match length
                   361
                  99
% identity
NCBI Description Soybean glycinin A-la-B-x subunit mRNA, complete cds
                  34840
Seq. No.
Seq. ID
                  LIB3029-010-Q1-B1-E7
Method
                  BLASTX
NCBI GI
                  g2495699
BLAST score
                   168
E value
                   7.0e-12
Match length
                   124
% identity
                   8
NCBI Description
                  HYPOTHETICAL PROTEIN KIAA0032 >gi 517115 dbj BAA04945
                   (D25215) KIAA0032 [Homo sapiens]
Seq. No.
                   34841
Seq. ID
                  LIB3029-010-Q1-B1-F12
Method
                  BLASTX
NCBI GI
                   g4263791
BLAST score
                  161
                   2.0e-16
E value
Match length
                   93
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  34842
Seq. No.
Seq. ID
                  LIB3029-010-Q1-B1-F6
Method
                  BLASTX
NCBI GI
                  g135859
                  203
BLAST score
                  6.0e-16
E value
Match length .
                  59.
                  69
% identity
```

```
TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                    '>gi_282919_pir__S26742 tonoplast intrinsic protein - kidney
bean >gi_21055_emb_CAA44669_ (X62873) tonoplast intrinsic
protein [Phaseolus vulgaris]
Seq. No.
                    34843
                    LIB3029-010-Q1-B1-F8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4539010
BLAST score
                    122
E value
                    2.0e-15
Match length
                    124
% identity
                    42
NCBI Description
                    (AL049481) putative DNA-directed RNA polymerase
                    [Arabidopsis thaliana]
Seq. No.
                    34844
Seq. ID
                    LIB3029-010-Q1-B1-H6
Method
                    BLASTX
NCBI GI
                    g2232354
BLAST score
                    267
                    2.0e-23
E value
Match length
                    110
% identity
                    45
                    (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
NCBI Description
                    34845
Seq. No.
Seq. ID
                    LIB3029-011-Q1-B1-G3
Method
                    BLASTN
NCBI GI
                    q3399776
BLAST score
                    46
                    1.0e-16
E value
Match length
                    106
% identity
                    Glycine max symbiotic ammonium transporter (SAT1) mRNA,
NCBI Description
                    complete cds
                    34846
Seq. No.
                    LIB3029-012-Q1-B1-A5
Seq. ID
Method
                    BLASTN
NCBI GI
                    q256428
BLAST score
                    345
E value
                    0.0e+00
Match length
                    395
                    99
% identity
                    KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                    Forrest, mRNA, 1259 nt]
Seq. No.
                    34847
                    LIB3029-012-Q1-B1-C9
Seq. ID
Method
                    BLASTN
NCBI GI
                    g18634
BLAST score
                    80
                    2.0e-37
E value
Match length
                    132
                    90
% identity
```

NCBI Description Soybean Gyl gene for glycinin subunit G1

Seq. ID

```
Seq. No.
                   34848
Seq. ID
                   LIB3029-012-Q1-B1-D1
Method
                   BLASTX
NCBI GI
                   g99992
                   200
BLAST score
E value
                   1.0e-15
Match length
                   83
                   52
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                   alfalfa (clone B2) >gi 166418 (M82973) putative
                   endomembrane protein; putative [Medicago sativa]
Seq. No.
                   34849
Seq. ID
                   LIB3029-012-Q1-B1-D9
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   133
E value
                   1.0e-68
Match length
                   385
% identity
                   84
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
 ×*
Seq. No.
                   34850
                   LIB3029-012-Q1-B1-E12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g295117
BLAST score
                   236
E value
                   1.0e-130
Match length
                   349
                   97
% identity
NCBI Description
                  Soybean lipoxygenase-1 mRNA
Seq. No.
                   34851
Seq. ID
                   LIB3029-012-Q1-B1-F7
Method
                   BLASTX
NCBI GI
                   g4455232
BLAST score
                   478
E value
                   3.0e-48
Match length
                   131
% identity
                   66
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34852
Seq. ID
                   LIB3029-012-Q1-B1-G1
Method
                  BLASTN
NCBI GI
                   g21834
BLAST score
                   44
E value
                   2.0e-15
                  84
Match length
% identity
                  Wheat mRNA for cytosolic phosphoglycerate kinase (EC
NCBI Description
                   2.7.2.3)
Seq. No.
                   34853
```

LIB3029-012-Q1-B1-G2

E value

3.0e-13

```
BLASTX
Method
NCBI GI
                   g1931651
BLAST score
                   394
                   2.0e-38
E value
                   125
Match length
                   62
% identity
                   (U95973) membrane-associated salt-inducible protein isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   34854
                   LIB3029-012-Q1-B1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g229707
BLAST score
                   551
E value
                   8.0e-57
                   109
Match length
                   91
% identity
NCBI Description
                   Bean pod mottle virus
Seq. No.
                   34855
                   LIB3030-001-Q1-B1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262105
BLAST score
                   199
E value
                   8.0e-16
Match length
                   81
% identity
                   41
NCBI Description
                   (AC002343) unknown protein [Arabidopsis thaliana]
                   34856
Seq. No.
                   LIB3030-001-Q1-B1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160189
BLAST score
                   296
E value
                   8.0e-27
Match length
                   127
% identity
                   49
NCBI Description
                   (AC000132) Similar to A. thaliana receptor-like protein
                   kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   34857
Seq. ID
                   LIB3030-001-Q1-B1-H12
Method
                   BLASTX
NCBI GI
                   g3378650
BLAST score
                   159
E value
                   3.0e-17
Match length
                   83
% identity
                   61
                   (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                   34858
                   LIB3030-002-Q1-B1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3461829
BLAST score
                  179
```

Seq. No.

```
Match length
                   80
% identity
                   49
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34859
Seq. No.
                   LIB3030-002-Q1-B1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3947733
BLAST score
                   251
E value
                   1.0e-21
Match length
                   98
                   54
% identity
                   (AJ009719) NL25 [Solanum tuberosum]
NCBI Description
Seq. No.
                   34860
                   LIB3030-002-Q1-B1-C8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g914912
BLAST score
                   45
E value
                   2.0e-16
Match length
                   214
% identity
                   85
                  Brassica napus elongation factor EF-1A mRNA, partial cds
NCBI Description
Seq. No.
                   34861
                   LIB3030-002-Q1-B1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q529516
BLAST score
                   589
E value
                   3.0e-61
Match length
                   123
% identity
NCBI Description
                   (L29099) beta-fructosidase [Solanum tuberosum]
Sèq. No.
                   34862
Seq. ID
                   LIB3030-002-Q1-B1-D1
Method
                   BLASTN
                   g1066856
NCBI GI
BLAST score
                   73
E value
                   2.0e-33
Match length
                   117
% identity
                   91
NCBI Description
                   Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene,
                   5' end of cds
Seq. No.
                   34863
Seq. ID
                  LIB3030-002-Q1-B1-D7
Method
                  BLASTN
NCBI GI
                   g4263753
BLAST score
                   37
E value
                   2.0e-11
Match length
                   112
% identity
                   88
NCBI Description
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
```

NCBI GI

q18551

```
Seq. ID
                   LIB3030-003-Q1-B1-B5
Method
                   BLASTX
NCBI GI
                   g2388580
BLAST score
                   284
E value
                   1.0e-25
Match length
                   91
% identity
                   62
NCBI Description
                    (AC000098) Similar to Sequence 10 from patent 5477002
                    (gb_1253956). [Arabidopsis thaliana]
                   34865
Seq. No.
Seq. ID
                   LIB3030-003-Q1-B1-D3
Method
                   BLASTX
NCBI GI
                   q1707007
BLAST score
                   223
                   3.0e-18
E value
                   127
Match length
% identity
NCBI Description
                   (U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34866
Seq. ID
                   LIB3030-003-Q1-B1-D9
Method
                   BLASTX
NCBI GI
                   g2108252
BLAST score
                   320
E value
                   1.0e-29
Match length
                   127
% identity
                   40
                   (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                    (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.
                   34867
Seq. ID
                   LIB3030-003-Q1-B1-E10
Method
                   BLASTX
NCBI GI
                   g3721856
BLAST score
                   145
E value
                   4.0e-09
Match length
                   30
% identity
NCBI Description
                   (AB014057) beta-Amyrin Synthase [Panax ginseng]
Seq. No.
                   34868
Seq. ID
                   LIB3030-004-Q1-B1-B11
Method
                   BLASTX
NCBI GI
                   g4559351
BLAST score
                   141
E value
                   1.0e-08
Match length
                   40
% identity
NCBI Description
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   34869
Seq. ID
                   LIB3030-004-Q1-B1-D1
Method
                   BLASTN
```

% identity

```
BLAST score
                   338
E value
                   0.0e + 00
Match length
                   350
                   99
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   34870
Seq. No.
Seq. ID
                   LIB3030-004-Q1-B1-F4
Method
                   BLASTX
NCBI GI
                   g4335739
BLAST score
                   328
                   1.0e-30
E value
                   94
Match length
% identity
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   34871
Seq. No.
                   LIB3030-004-Q1-B1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982243
BLAST score
                   265
E value
                   4.0e-23
Match length
                   80
% identity
                   61
                   (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                   34872
Seq. No.
Seq. ID
                   LIB3030-004-Q1-B1-H4
Method
                   BLASTX
NCBI GI
                   g3702966
BLAST score
                   404
E value
                   1.0e-39
Match length
                   112
% identity
                   71
NCBI Description
                   (AF079486) rac GTP binding protein Arac8 [Arabidopsis
                   thaliana]
Seq. No.
                   34873
Seq. ID
                   LIB3030-005-Q1-B1-A3
Method
                   BLASTX
NCBI GI
                   g3819710
                   352
BLAST score
E value
                   2.0e-33
Match length
                  84
% identity
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                   thaliana]
                   34874
Seq. No.
                  LIB3030-005-Q1-B1-B10
Seq. ID
Method
                  BLASTX
                   g3080353
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
Match length
                  112
```

Seq. ID

```
NCBI Description
                   (AL022580) cytochrome P450 [Arabidopsis thaliana]
                   34875
Seq. No.
Seq. ID
                   LIB3030-005-Q1-B1-C1
Method
                   BLASTX
NCBI GI
                   g3252854
BLAST score
                   205
E value
                   1.0e-16
                  57
Match length
                   75
% identity
                   (AF020424) glutamate decarboxylase isozyme 2 [Nicotiana
NCBI Description
                   tabacum]
                   34876
Seq. No.
Seq. ID
                  LIB3030-005-Q1-B1-C7
Method
                   BLASTX
NCBI GI
                   g3702368
BLAST score
                   214
                   3.0e-17
E value
Match length
                   69
                   59
% identity
NCBI Description
                   (AJ001855) alpha subunit of F-actin capping protein
                   [Arabidopsis thaliana]
Seq. No.
                   34877
Seq. ID
                   LIB3030-005-Q1-B1-D5
Method
                   BLASTN
NCBI GI
                   g975703
BLAST score
                   40
E value
                   4.0e-13
Match length
                   119
                   50
% identity
NCBI Description
                   P.sativum GR gene
Seq. No.
                   34878
Seq. ID
                  LIB3030-005-Q1-B1-D6
Method
                   BLASTX
NCBI GI
                   g2073450
BLAST score
                   428
E value
                   3.0e-42
Match length
                   93
% identity
NCBI Description
                   (Y12859) Krm protein [Lotus japonicus]
Seq. No.
                   34879
Seq. ID
                  LIB3030-005-Q1-B1-D8
Method
                  BLASTX
NCBI GI
                   g4204695
BLAST score
                  179
                   4.0e-13
E value
Match length
                   93
% identity
                   (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                  At5P1 [Arabidopsis thaliana]
Seq. No.
                  34880
```

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BLAST score

E value

218

7.0e-18

```
Method
                  BLASTX
NCBI GI
                  g1703036
BLAST score
                  181
                  2.0e-13
E value
                  78
Match length
                  46
% identity
NCBI Description
                  5'-AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT (AMPK
                  BETA-1 CHAIN) (40 KD SUBUNIT) >gi_1335858 (U42411)
                  5'-AMP-activated protein kinase, beta subunit [Rattus
                  norvegicus]
                  34881
Seq. No.
Seq. ID
                  LIB3030-005-Q1-B1-H6
                  BLASTX
Method
NCBI GI
                  g2190259
BLAST score
                  423
                  8.0e-42
E value
              102
78
Match_length
% identity
NCBI Description (D86385) A-type cyclin [Catharanthus roseus]
Seq. No.
                  34882
Seq. ID
                  LIB3030-006-Q1-B1-B1
Method.
                  BLASTX
NCBI GI-
                  g2290532
BLAST score
                  402
E value
                  3.0e-39
Match length
                  121
                  65
% identity
NCBI Description
                  (U94748) AN11 [Petunia x hybrida]
Seq. No.
                  34883
Seq. ID
                  LIB3030-006-Q1-B1-B2
Method
                  BLASTX
NCBI GI
                  g2244985
BLAST score
                  295
E value
                  1.0e-26
Match length
                  96
% identity
NCBI Description
                  (Z97340) similarity to peroxidase [Arabidopsis thaliana]
Seq. No.
                  34884
                  LIB3030-006-Q1-B1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4371280
BLAST score
                  414
E value
                  1.0e-40
Match length
                  126
                  67
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34885
Seq. ID
                  LIB3030-006-Q1-B1-E3
                  BLASTX
Method
NCBI GI
                  g3242447
```

Seq. No.

```
Match length
                     54
                     69
  % identity
  NCBI Description
                     (AB003131) endonuclease [Zinnia elegans]
                     34886
  Seq. No.
  Seq. ID
                    LIB3030-007-Q1-B1-A11
  Method
                    BLASTX
  NCBI GI
                     g4220474
                     294
  BLAST score
                     1.0e-26
  E value
  Match length
                     102
                     54
  % identity
                     (AC006069) putative myosin heavy chain [Arabidopsis
  NCBI Description
                     thaliana]
                     34887
  Seq. No.
  Seq. ID
                    LIB3030-007-Q1-B1-A12
  Method
                     BLASTX
NCBI GI
                  : g4335857 ...
  BLAST score
                     344
  E value
                     2.0e-32
  Match length
                     126
                     50
  % identity
  NCBI Description
                     (AF049347) berberine bridge enzyme [Berberis stolonifera]
                     34888
  Seq. No.
  Seq. ID . .
                    LIB3030-007-Q1-B1-C7
  Method
                    BLASTX
  NCBI GI
                     g2827637
  BLAST score
                     211
  E value
                     6.0e-17
  Match length
                    111
  % identity
                     40
  NCBI Description
                     (AL021636) putative protein [Arabidopsis thaliana]
  Seq. No.
                    34889
  Seq. ID
                    LIB3030-007-Q1-B1-D5
  Method
                    BLASTX
  NCBI GI
                    g2465923
  BLAST score
                    272
  E value
                     5.0e-24
                    122
 Match length
  % identity
                    26
                     (AF024648) receptor-like serine/threonine kinase
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                    34890
                    LIB3030-007-Q1-B1-E3
  Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g18683
 BLAST score
                    75
 E value
                    5.0e-34
                    207
 Match length
                    74
  % identity
 NCBI Description
                    G.max N-20t gene
                    34891
```

```
LIB3030-007-Q1-B1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  242
                  2.0e-20
E value
Match length
                  125
                   49
% identity
                   (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  34892
Seq. No.
Seq. ID
                  LIB3030-007-Q1-B1-H11
Method
                  BLASTX
NCBI GI
                  q1041706
BLAST score
                  542
                  1.0e-55
E value
                  120
Match length
                  79
% identity
NCBI Description (U30480) expansin At-EXP6 [Arabidopsis thaliana]
Seq. No.
                  34893
Seq. ID
                  LIB3030-008-Q1-B1-A10
Method
                  BLASTX
NCBI GI
                  g2462744
BLAST score
                  176
£ value
                  8.0e-13
Match length
                  125
% identity
                  31
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34894
                  LIB3030-008-Q1-B1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415937
BLAST score
                  140
E value
                  1.0e-08
Match length
                  108
% identity
                  30
NCBI Description
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  34895
                  LIB3030-008-Q1-B1-G10
Seq. ID
Method
                  BLASTX
NCBI GI ·
                  g2244851
BLAST score
                  203
E value
                  5.0e-16
Match length
                  115
% identity
                  40
                  (Z97337) amine oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34896
Seq. ID
                  LIB3030-009-Q1-B1-A1
Method
                  BLASTN
NCBI GI
                  g3059094
BLAST score
                  166
E value
                  2.0e-88
```

E value

```
% identity
NCBI Description
                  Glycine max mRNA for magnesium chelatase subunit
Seq. No.
                  34897
Seq. ID
                  LIB3030-009-Q1-B1-A2
Method
                  BLASTX
NCBI GI
                  g4455192
BLAST score
                  185
E value
                  7.0e-14
Match length
                  109
% identity
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
                  34898
Seq. No.
Seq. ID
                  LIB3030-009-Q1-B1-B12
Method
                  BLASTX
NCBI GI
                  g115797
BLAST score
                  431
E value
                  1.0e-42
                  99
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                  (CAB-215) (LHCP) >gi 100026 pir S16592 chlorophyll
                  a/b-binding protein - garden pea >gi 20658 emb CAA40365
                  (X57082) chlorophyll a/b-binding protein [Pisum sativum]
Seq. No.
                  34899
Seq. ID
                  LIB3030-009-Q1-B1-B4
Method
                  BLASTX
NCBI GI
                  g544129
BLAST score
                  160
                  2.0e-11
E value
                  53
Match length
                  62
% identity
                  VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE
NCBI Description
                  EP-C1) >gi 20994 emb CAA44816 (X63102) endopeptidase
                  [Phaseolus vulgaris]
Seq. No.
                  34900
Seq. ID
                  LIB3030-009-Q1-B1-B5
Method
                  BLASTX
NCBI GI
                  g1168940
BLAST score
                  224
E value
                  2.0e-18
Match length
                  83
% identity
                  CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958
NCBI Description
                  chorismate mutase precursor - Arabidopsis thaliana
                  >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase
                  precursor [Arabidopsis thaliana]
                  34901
Seq. No.
                  LIB3030-009-Q1-B1-B6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g310575
BLAST score
                  286
                                                                       12.
```

1.0e-160

% identity

```
Match length
                   435
                   94
% identity
                   Glycine max nodulin-26 mRNA, complete cds
NCBI Description
Seq. No.
                   34902
Seq. ID
                   LIB3030-009-Q1-B1-C12
Method
                   BLASTX
NCBI GI
                   g2627181
BLAST score
                   476
                   6.0e-48
E value
                   117
Match length
                   74
% identity
                   (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
Seq. No.
                   34903
Seq. ID
                   LIB3030-009-Q1-B1-D12
Method
                   BLASTX
NCBI GI
                   g3850588
                   .527
BLAST score
                   8.0e-54
E value
Match length
                   141
% identity
                   49
                   (AC005278) Contains similarity to gb AB011110 KIAA0538
NCBI Description
                   protein from Homo sapiens brain and to phospholipid-binding
                   domain C2 PF 00168. ESTs gb AA585988 and gb T04384 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   34904
Seq. ID
                   LIB3030-009-Q1-B1-D3
Method
                   BLASTX
NCBI GI
                   g4049518
BLAST score
                   195
E value
                   3.0e-19
Match length
                   139
% identity
                   40
NCBI Description
                   (AL031852) conserved hypothetical protein.
                   [Schizosaccharomyces pombe]
                   34905
Seq. No.
Seq. ID
                   LIB3030-009-Q1-B1-D8
Method
                   BLASTX
NCBI GI
                   g4510339
BLAST score
                   583
E value
                   2.0e-60
                   147
Match length
% identity
NCBI Description
                   (AC006921) putative ABC transporter protein [Arabidopsis
                   thaliana]
                   34906
Seq. No.
Seq. ID
                   LIB3030-009-Q1-B1-F10
Method
                   BLASTX
NCBI GI
                   g2852449
BLAST score
                   470
E value
                   3.0e-47
Match length
                   119、
```

NCBI Description

```
NCBI Description
                   (D88207) protein kinase [Arabidopsis thaliana] >gi 2947061
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
                   34907
Seq. No.
Seq. ID
                   LIB3030-009-Q1-B1-F3
Method
                   BLASTX
NCBI GI
                   g280401
BLAST score
                   508
E value
                   1.0e-51
Match length
                   130
                   73
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - curled-leaved
NCBI Description
                   tobacco >gi_170206 (M27888) H+-translocating ATPase
                   [Nicotiana plumbaginifolia]
                   34908
Seq. No.
Seq. ID .
                   LIB3030-009-Q1-B1-H4
Method
                   BLASTX
NCBI GI -
                   g2578440
BLAST score
                   142
E value
                   4.0e-09
Match length
                   73
% identity
                   37
NCBI Description
                   (X67425) pectinesterase [Pisum sativum]
Seq. No.
                   34909
                   LIB3030-009-Q1-B1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4105782
BLAST score
                   156
E value
                   2.0e-10
Match length
                   41
% identity
                   80
NCBI Description
                   (AF049922) PGP169-12 [Petunia x hybrida]
Seq. No.
                   34910
Seq. ID
                   LIB3030-010-Q1-B1-A9
Method
                   BLASTX
NCBI GI
                   q2833329
BLAST score
                   443
E value
                   3.0e-44
                   99
Match length
% identity
                   36
                   ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE
NCBI Description
                   NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_1438860 (L11618) ADP/ATP carrier protein [Anopheles gambiae] >gi_1438862 (L11617)
                   ADP/ATP carrier protein [Anopheles gambiae]
Seq. No.
                   34911
                   LIB3030-010-Q1-B1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131199
BLAST score
                   158
E value
                   1.0e-10
Match length
                   110
% identity
                   40
```

PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR

```
- spinach >gi 21287 emb CAA34749 (X16858) psaH [Spinacia
                   oleracea]
Seq. No.
                   34912
Seq. ID
                  LIB3030-010-Q1-B1-D12
Method
                   BLASTX
NCBI GI
                   q4539303
BLAST score
                  184
                   1.0e-13
E value
Match length
                   94
                   37
% identity
                   (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
                   34913
Seq. No.
Seq. ID
                  LIB3030-010-Q1-B1-G5
Method
                  BLASTX
NCBI GI
                  g2281090
BLAST score
                  142
E value
                   4.0e-13
                   90
Match length
                   42
% identity
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34914
Seq. ID
                  LIB3030-010-Q1-B1-H3
Method
                  BLASTX
NCBI GI
                  g1888357
BLAST score
                  234
E value
                   9.0e-20
Match length
                  76
% identity
                   63
NCBI Description
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                   34915
Seq. No.
Seq. ID
                  LIB3030-011-Q1-B1-A11
Method
                  BLASTX
NCBI GI
                  g4337175
BLAST score
                  170
E value
                  3.0e-12
Match length
                  50
% identity
NCBI Description
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb AA720210 come from this gene. [Arabidopsis thaliana]
                  34916
Seq. No.
Seq. ID
                  LIB3030-011-Q1-B1-C11
Method
                  BLASTN
NCBI GI
                  g347454
BLAST score
                  33
                  5.0e-09
E value
Match length
                  101
```

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_81470_pir__S00453 photosystem I protein psaH precursor

```
% identity
NCBI Description
                  Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
                  end
                  34917
Seq. No.
Seq. ID
                  LIB3030-011-Q1-B1-E11
Method
                  BLASTX
NCBI GI
                  g4056506
BLAST score
                  565
                  2.0e-58
E value
Match length
                  136
% identity
                  74
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                  34918
Seq. No.
                  LIB3030-011-Q1-B1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170455
BLAST score
                  52
                  9.0e-21
E value
Match length
                  148
                  84
% identity
                  Tomato heat shock cognate protein 80 gene, 3' end
NCBI Description
Seq. No.
                  34919
                  LIB3030-012-Q1-B1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g128592
BLAST score
                  149
E value
                   6.0e-10
Match length
                  54
                  57
% identity
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                  >gi_82190_pir__S22495 pollen-specific protein precursor -
                  common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                  specific protein [Nicotiana tabacum]
                  34920
Seq. No.
Seq. ID
                  LIB3030-012-Q1-B1-C6
                  BLASTX
Method
NCBI GI
                  g2511693
BLAST score
                  166
                  4.0e-12
E value
Match length
                  58
% identity
NCBI Description
                  (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.
                  34921
Seq. ID
                  LIB3030-012-Q1-B1-D9
Method
                  BLASTN
NCBI GI
                  q1055367
BLAST score
                  191
E value
                  1.0e-103
                  319
Match length
                  90
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
```

subunit mRNA, complete cds

```
Seq. No.
                    34922
Seq. ID
                    LIB3030-012-Q1-B1-E8
Method
                    BLASTX
NCBI GI
                    g2832646
BLAST score
                    178
E value
                    5.0e-13
Match length
                    78
% identity
                    38
                    (AL021710) MuDR transposable element - like protein
NCBI Description
                    [Arabidopsis thaliana]
                    34923
Seq. No.
Seq. ID
                    LIB3030-012-Q1-B1-F10
Method
                    BLASTX
NCBI GI
                    g1705463
BLAST score
                    372
E value
                    8.0e-36
Match length
                    117
% identity
                    66
                    BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir_
NCBI Description
                    biotin sythase - Arabidopsis thaliana >gi_10453\overline{16} (\overline{U2}4147) biotin sythase [Arabidopsis thaliana] >gi_11403662 (U31806)
                    BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413)
                    biotin synthase [Arabidopsis thaliana] >gi 2288983
                    (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                    >gi 1589016 prf 2209438A biotin synthase [Arabidopsis
                    thaliana]
Seq. No.
                    34924
Seq. ID
                    LIB3030-012-Q1-B1-H10
Method
                    BLASTX
NCBI GI
                    g4006915
BLAST score
                    250
E value
                    2.0e-21
Match length
                    109
% identity
                    50
NCBI Description
                    (299708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    34925
Seq. ID
                    LIB3030-012-Q1-B1-H3
Method
                    BLASTX
NCBI GI
                    g3600039
BLAST score
                    487
E value
                    4.0e-49
Match length
                    143
% identity
                    61
NCBI Description
                    (AF080119) similar to Schizosaccharomyces pombe isp4
                    protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                    34926
Seq. ID
                    LIB3039-001-Q1-E1-E2
Method
                    BLASTN
NCBI GI
                    g168650
BLAST score
                    226
E value
                    1.0e-124
```

Method

BLASTN

```
% identity
NCBI Description
                  Zea mays ubiquitin fusion protein (UBF9) gene, complete cds
Seq. No.
Seq. ID
                  LIB3039-001-Q1-E1-F7
Method
                  BLASTX
NCBI GI
                  g1405561
BLAST score
                  276
E 'value
                  2.0e-24
Match length
                  56
% identity
NCBI Description
                  (X98540) FSGTP1 [Fagus sylvatica]
                  34928
Seq. No.
Seq. ID
                  LIB3039-001-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  293
E value
                  1.0e-29
Match length
                  116
% identity
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
                  34929
Seq. No.
Seq. ID
                  LIB3039-001-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                  g170091
BLAST score
                  64
E value
                  9.0e-28
Match length
                  180
% identity
                  84
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  34930
Seq. No.
Seq. ID
                  LIB3039-002-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  315
                  4.0e-29
E value
Match length
                  114
% identity
                  56
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  34931
Seq. No.
Seq. ID
                  LIB3039-002-Q1-E1-A11
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  122
E value
                  4.0e-62
Match length
                  350
% identity
                  84
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  34932
Seq. ID
                  LIB3039-002-Q1-E1-A9
```

% identity

```
g169974
 NCBI GI
 BLAST score
                    138
 E value
                    8.0e-72
                    178
 Match length
 % identity
                    94
 NCBI Description Glycine max vspA gene, complete cds
                    34933
 Seq. No.
                    LIB3039-002-Q1-E1-D11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3341443
 BLAST score
                    175
                    1.0e-12
 E value
                    74
 Match length
 % identity
 NCBI Description
                    (AJ223074) acid phosphatase [Glycine max]
                    34934
 Seq. No.
                    LIB3039-002-Q1-E1-E10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g126151
 BLAST score
                    167
 E value
                    5.0e-12 ···
 Match length
                    61
 % identity
                    56
                    LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi 282898 pir S27365
 NCBI Description
                    lectin precursor - soybean >gi_170006 (K00821) lectin
                    prepeptide [Glycine max]
                    34935
 Seq. No.
 Seq. ID
                    LIB3039-002-Q1-E1-E6
                    BLASTX
 Method
 NCBI GI
                    g3341443
 BLAST score
                    339
 E value
                    8.0e-32
 Match length
                    127
                    54
 % identity
 NCBI Description (AJ223074) acid phosphatase [Glycine max]
                    34936
 Seq. No.
 Seq. ID
                    LIB3039-002-Q1-E1-G5
 Method
                    BLASTX
 NCBI GI
                    g3341443
 BLAST score
                    250
 E value
                    3.0e-29
 Match length
                    126
 % identity
                    55
NCBI Description (AJ223074) acid phosphatase [Glycine max]
 Seq. No.
                    34937
                    LIB3039-002-Q1-E1-H6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2795803
 BLAST score
                    187
 E value
                    5.0e-14
 Match length
                    78
```

```
NCBI Description
                  (AC003674) putative beta-1,3-endoglucanase [Arabidopsis
                  thaliana] >gi 3355491 (AC004218) putative
                  beta-1,3-endoglucanase [Arabidopsis thaliana]
Seq. No.
                  34938
Seq. ID
                  LIB3039-002-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                  g296408
BLAST score
                  127
E value
                  3.0e-65
Match length
                  215
% identity
                  90
NCBI Description G.max ADR12 mRNA
                  34939
Seq. No.
Seq. ID
                  LIB3039-002-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g2244839
BLAST score
                  368
E value
                  2.0e-35
                  117
Match length '
                  62
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  34940
Seq. No.
Seq. ID
                  LIB3039-003-Q1-E1-A2
Method
                  BLASTN
NCBI GI
                  g3452136
BLAST score
                  187
                  1.0e-101
E value
                  239
Match length
                  95
% identity
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                  partial
Seq. No.
                  34941
Seq. ID
                  LIB3039-003-Q1-E1-B12
Method
                  BLASTN
                                                          NCBI GI
                  q169974
BLAST score
                  106
E value
                  1.0e-52
Match length
                  268
                  91
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  34942
                  LIB3039-003-Q1-E1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2058280
BLAST score
                  253
E value
                  3.0e-23
Match length
                  88
% identity
NCBI Description
                  (X97381) atran3 [Arabidopsis thaliana]
                  34943
Seq. No.
Seq. ID
                  LIB3039-003-Q1-E1-C12
```

```
Method
                   BLASTN
NCBI GI
                  g170089
BLAST score
                   246
                   1.0e-136
E value
Match length
                   330
% identity
                   94
NCBI Description
                  G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                   34944
                   LIB3039-003-Q1-E1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   117
E value
                   3.0e-59
Match length
                   213
% identity
                   89
NCBI Description
                  Glycine max vspA gene, complete cds
                   34945
Seq. No.
                                                   6.4
Seq. ID
                  LIB3039-003-Q1-E1-D2
Method
                   BLASTN
NCBI GI
                   g18764
BLAST score
                   35
E value
                   1.0e-10
Match length
                  71
                   87
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
Seq. No.
                   34946
Seq. ID
                  LIB3039-003-Q1-E1-E6
Method
                   BLASTN
NCBI GI
                   g18761
BLAST score
                   40
E value
                   4.0e-13
Match length
                   116
                   85
% identity
NCBI Description
                  Soybean stem mRNA for 31 kD glycoprotein ,
                   34947
Seq. No.
Seq. ID
                  LIB3039-004-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  g2961372
BLAST score
                  169
E value
                   5.0e-17
Match length
                  76
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                  34948
Seq. No.
Seq. ID
                  LIB3039-004-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  228
E value
                  4.0e-19
```

Seq. No.

```
% identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  34949
Seq. No.
Seq. ID
                  LIB3039-004-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  g2052379
BLAST score
                  142
                  5.0e-09
E value
Match length
                  69
% identity
NCBI Description
                  (U66343) calreticulin [Arabidopsis thaliana]
                  34950
Seq. No.
Seq. ID
                  LIB3039-004-Q1-E1-C3
                  BLASTX
Method
NCBI GI
                  g232031
                  191
BLAST score
E value
                  1.0e-14
                  97
Match length
% identity
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224
NCBI Description
                  translation elongation factor eEF-1 beta chain - rice
                  >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                  34951
Seq. No.
Seq. ID
                  LIB3039-004-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g3687251
                  420
BLAST score
                  3.0e-41
E value
Match length
                  118
% identity
                  69
NCBI Description
                  (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  34952
Seq. ID
                  LIB3039-005-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g3341443
                  305
BLAST score
                  7.0e-28
E value
                  121
Match length
                  51
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                  34953
Seq. ID
                  LIB3039-005-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  173
                  1.0e-92
E value
                  253
Match length
                  92
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
```

```
LIB3039-005-Q1-E1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1495767
                   37
BLAST score
E value
                   1.0e-11
Match length
                   77
% identity
                   87
NCBI Description
                   P.sativum mRNA for 110 kD chloroplast inner envelope
                   protein IEP110
                   34955
Seq. No.
                   LIB3039-005-Q1-E1-B8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18551
BLAST score
                   392
                   0.0e+00
E value
Match length
                   396
                   100
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   34956
Seq. No.
                   LIB3039-005-Q1-E1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   159
                   3.0e-11
E value
Match length
                   52
% identity
                   62
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   34957
Seq. ID
                   LIB3039-005-Q1-E1-C5
Method
                   BLASTX
NCBI GI
                   g3236238
BLAST score
                   449
E value
                   1.0e-44
Match length
                   97
% identity
                   (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                   34958
                   LIB3039-005-Q1-E1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18644
BLAST score
                   240
                   1.0e-132
E value
Match length
                   312
                   94
% identity
                   Soybean mRNA for HMG-1 like protein
NCBI Description
                   34959
Seq. No.
Seq. ID
                   LIB3039-005-Q1-E1-F8
```

BLASTN

Method

```
g170091
NCBI GI
BLAST score
                   322
E value
                   0.0e + 00
Match length
                   374
% identity
                   .97
NCBI Description `
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   34960
Seq. ID
                   LIB3039-005-Q1-E1-G9
Method
                   BLASTN
NCBI GI
                   g414831
BLAST score
                   131
E value
                   2.0e-67
Match length
                   239
% identity
                   97
NCBI Description
                  Glycine max (Rablp) mRNA, complete cds
Seq. No.
                   34961
Seq. ID
                   LIB3039-005-Q1-E1-H9
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   260
E value
                   1:0e-144
Match length
                   384
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
                   34962
Seq. No.
Seq. ID
                   LIB3039-006-Q1-E1-A9
Method
                   BLASTN
NCBI GI
                   g1173641
BLAST score
                   70
E value
                   2.0e-31
Match length
                   106
                   92
% identity
                  Glycine max lipoxygenase (lox7) mRNA, complete cds
NCBI Description
                   34963
Seq. No.
Seq. ID
                  LIB3039-006-Q1-E1-B3
Method
                   BLASTN
NCBI GI
                   g170053
BLAST score
                   41
E value
                   5.0e-14
Match length
                   65
% identity
                   92
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                   34964
Seq. No.
Seq. ID
                  LIB3039-006-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  198
                   9.0e-19
E value
Match length
                  75
% identity
                   63
NCBI Description 60S RIBOSOMAL PROTEIN L32
```

Method

BLASTN

```
34965
Seq. No.
Seq. ID
                   LIB3039-006-Q1-E1-D3
Method
                   BLASTN
NCBI GI
                   g510875
BLAST score
                   40
E value
                   3.0e-13
Match length
                   99
% identity
NCBI Description
                  P.vulgaris PvME1 gene
                   34966
Seq. No.
Seq. ID
                   LIB3039-006-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g1076510
BLAST score
                   169
E value
                   2.0e-12
Match length
                   48
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                   >gi 829119 emb CAA52414 (X74403) cyclophilin [Phaseolus
                  vulgaris]
                   34967
Seq. No.
                  LIB3039-006-Q1-E1-E5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   156
E value
                   1.0e-82
Match length
                   236
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   34968
Seq. No.
Seq. ID
                  LIB3039-006-Q1-E1-H2
Method
                  BLASTN
NCBI GI
                  g1370199
BLAST score
                   49
E value
                  1.0e-18
                  77
Match length
% identity
                   91
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1
                  34969
Seq. No.
                  LIB3039-007-Q1-E1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135264
BLAST score
                  241
                  2.0e-20
E value
                  75
Match length
% identity
                  (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  34970
                  LIB3039-007-Q1-E1-C1
Seq. ID
```

```
NCBI GI
                  q170091
BLAST score
                  287
                  1.0e-160
E value
Match length
                  295
                  99
% identity
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  34971
Seq. No.
Seq. ID
                  LIB3039-007-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  q82080
                  239
BLAST score
                  3.0e-20
E value
                  89
Match length
                  57
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  34972
Seq. ID
                  LIB3039-007-Q1-E1-C7
Method
                  BLASTX
                                 4.0
NCBI GI
                  g4510379
                  252
BLAST score
                  9.0e-22
E value
                  80
Match length
                  57
% identity
NCBI Description
                   (AC007017) hypothetical protein [Arabidopsis thaliana]
                  34973
Seq. No.
                  LIB3039-007-Q1-E1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  191
E value
                  1.0e-14
                  92
Match length
                   47
% identity
NCBI Description
                   (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  34974
Seq. ID
                  LIB3039-007-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  178
E value
                  1.0e-95
Match length
                  313
                  90
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                  34975
Seq. No.
Seq. ID
                  LIB3039-007-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  g1053059
BLAST score
                  165
                  1.0e-11
E value
```

Seq. ID

```
% identity
NCBI Description
                   (U38423) histone H3 [Triticum aestivum]
                   34976
Seq. No.
Seq. ID
                   LIB3039-007-Q1-E1-H6
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   321
                   0.0e + 00
E value
Match length
                   389
                   96
% identity
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   34977
Seq. No.
Seq. ID
                   LIB3039-007-Q1-E1-H8
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   91
                                                                         A. Car
E value
                   8.0e-44
                   203
Match length
                   86
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                   34978
Seq. No.
Seq. ID
                   LIB3039-008-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g3402687
BLAST score
                   181
                   2.0e-13
E value
                   53
Match length
                   62
% identity
NCBI Description
                   (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                   34979
Seq. ID
                   LIB3039-008-Q1-E1-D5
Method
                   BLASTX
NCBI GI
                   q576775
BLAST score
                   236
E value
                   5.0e-20
Match length
                   80
% identity
                   (U16992) ubiquitin-carboxy extension protein fusion
NCBI Description
                   [Filobasidiella neoformans]
Seq. No.
                   34980
Seq. ID
                   LIB3039-008-Q1-E1-E10
                   BLASTX
Method
NCBI GI
                   g4454026
BLAST score
                   116
                   1.0e-11
E value
Match length
                   74
% identity
                   (AL035394) phosphatase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
```

LIB3039-008-Q1-E1-E7

% identity

```
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   145
                   6.0e-76
E value
                   281
Match length
                   88
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                   34982
Seq. No.
Seq. ID
                   LIB3039-008-Q1-E1-G3
Method
                   BLASTN
NCBI GI
                   g303900
BLAST score
                   233
                   1.0e-128
E value
Match length
                   389
                   35
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   34983
Seq. No.
                   LIB3039-008-Q1-E1-G7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2598656
BLAST score
                   151
E value
                   2.0e-79
                   278
Match length
                   89
% identity
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
                   34984
Seq. No.
                   LIB3039-008-Q1-E1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   291
E value
                   1.0e-163
Match length
                   367
% identity
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   34985
                   LIB3039-009-Q1-E1-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   99
E value
                   1.0e-48
Match length
                  147
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
                   34986
Seq. No.
Seq. ID
                  LIB3039-009-Q1-E1-B2
                  BLASTX `
Method
                   g3894158
NCBI GI
                  269
BLAST score
E value
                   1.0e-23
Match length
                  115
```

```
(AC005312) similar to phloem-specific lectin (Arabidopsis
NCBI Description
                   thaliana]
                   34987
Seq. No.
Seq. ID
                   LIB3039-009-Q1-E1-D9
Method
                   BLASTN
NCBI GI
                   g18551
                   322
BLAST score
E value
                   0.0e + 00
Match length
                   382
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   34988
Seq. No.
Seq. ID
                   LIB3039-009-Q1-E1-E11
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   262
                   1.0e-145
E value
                   382
Match length
                   92
% identity
NCBI Description Glycine max vspA gene, complete cds
                   34989
Seq. No.
                   LIB3039-009-Q1-E1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g134145
BLAST score
                   156
E value
                   2.0e-10
Match length
                   101
                   25
% identity
NCBI Description
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
                   PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean
                   >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975
                   (M76981) vegetative storage protein [Glycine max]
                   >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
                   [Glycine max]
                   34990
Seq. No.
Seq. ID
                   LIB3039-009-Q1-E1-F6
Method
                   BLASTX
NCBI GI
                   g3341443
BLAST score
                   261
                   7.0e-23
E value
                   81
Match length
% identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   34991
Seq. ID
                   LIB3039-009-Q1-E1-G4
                   BLASTN
Method
NCBI GI
                   q435678
BLAST score
                   37
E value
                   1.0e-11
```

E value

```
% identity
NCBI Description
                  L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
                   S25
Seq. No.
                   34992
Seq. ID
                  LIB3039-009-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   q548774
BLAST score
                   166
                   9.0e-12
E value
Match length
                   60
                   62
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                   34993
Seq. ID
                  LIB3039-010-Q1-E1-A10
Methód
                  BLASTN
NCBI GI
                  g1262439
BLAST score
                   341
E value
                   0.0e + 00
Match length
                   357
                   99
% identity
NCBI Description
                  Glycine max lipoxygenase (vlxC) mRNA, complete cds
                   34994
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                   g421867
BLAST score
                   277
E value
                   8.0e-25
                   89
Match length
% identity
                  ubiquitin / ribosomal protein CEP52 - turnip >gi_347064
NCBI Description
                   (L21898) ubiquitin/ribosomal protein [Brassica rapa]
                  >gi_395079 emb CAA80863 (Z24738) ubiquitin/ribosomal
                  protein [Brassica rapa]
                   34995
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g120666
BLAST score
                  200
                   4.0e-25
E value
Match length
                  99
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66012_pir__DESKG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - garden snapdragon
                  34996
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  g170091
BLAST score
                  202
```

1.0e-110

NCBI GI

g169974

```
302
Match length
% identity
                  92
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                  complete cds ·
Seq. No.
                  34997
Seq. ID
                  LIB3039-010-Q1-E1-D11
Method
                  BLASTX
NCBI GI
                  q3341443
BLAST score
                  190
E value
                  2.0e-14
Match length
                  113
% identity
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  34998
                 ·LIB3039-010-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730241
                  191
BLAST score
                  1.0e-14
E value
Match length
                  84
% identity
                  46
NCBI Description
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN
                  GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL
                  TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115)
                  (HA0643) >gi_473947_dbj_BAA06126_ (D29643) similar to Canis
                  oligosaccharyltransferase 48 kDa subunit (M98392). [Homo
                  sapiens]
Seq. No.
                  34999
Seq. ID
                  LIB3039-010-Q1-E1-F1
Method
                  BLASTX
                  g1710530
NCBI GI
BLAST score
                  376
E value
                  3.0e-36
Match length
                  108
% identity
                  62
NCBI Description
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487_emb_CAA63025 (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
Seq. No.
                  35000
Seq. ID
                  LIB3039-010-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q480390
BLAST score
                  234
E value
                  1.0e-19
Match length
                  83
% identity
                  55
NCBI Description lectin BMA - Bowringia mildbraedii
Seq. No.
                  35001
Seq. ID
                  LIB3039-010-Q1-E1-F5
Method
                  BLASTN
```

```
BLAST score
E value
                   1.0e-177
Match length
                   379
                   96
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35002
                  LIB3039-010-Q1-E1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  143
E value
                   3.0e-09
Match length
                   69
                   45
% identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  35003
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g541943
                  179
BLAST score
                  3.0e-15
E value
Match length
                  56
                  79
% identity
NCBI Description
                  metallothionein - soybean >gi 228682 prf 1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  35004
Seq. ID
                  LIB3039-010-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g2431771
BLAST score
                  156
E value
                  1.0e-10
Match length
                  51
% identity
                   61
                   (U62753) acidic ribosomal protein P2b [Zea mays]
NCBI Description
                  35005
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-H1
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  235
E value
                  1.0e-129
                  303
Match length
% identity
                  94
NCBI Description
                  Glycine max vspA gene, complete cds
                  35006
Seq. No.
Seq. ID
                  LIB3039-010-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  q169974
                  145
BLAST score
                  8.0e-76
E value
                  277
Match length
                  91
% identity
NCBI Description Glycine max vspA gene, complete cds
```

```
Seq. No.
                   35007
Seq. ID
                  LIB3039-011-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                   g2129721
BLAST score
                   178
E value
                   8.0e-18
Match length
                   104
% identity
                   56
NCBI Description
                  ribosomal protein S15 - Arabidopsis thaliana
                  >gi 1107485 emb CAA63028 (X91962) 40S ribosomal protein
                  S15 [Arabidopsis thaliana]
Seq. No.
                   35008
Seq. ID
                  LIB3039-011-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                   g3876716
BLAST score
                  255
E value
                   4.0e-22
Match length
                  80
% identity
                   51
NCBI Description
                   (Z46242) similar to Zinc finger, C3HC4 type (RING finger)
                   [Caenorhabditis elegans]
Seq. No.
                  35009
Seq. ID
                  LIB3039-011-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  173
E value
                   1.0e-92
Match length
                  348
% identity
                  88
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35010
Seq. ID
                  LIB3039-011-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q3914431
BLAST score
                  141
E value
                  5.0e-16
Match length
                  77
                  58
% identity
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                  >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                  subunit [Spinacia oleracea]
Seq. No.
                  35011
Seq. ID
                  LIB3039-011-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g3914136
BLAST score
                  258
E value
                  2.0e-22
Match length
                  100
                  52
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
```

[Cicer arietinum]

```
35012
Seq. No.
Seq. ID
                   LIB3039-011-Q1-E1-E6
Method
                   BLASTX
NCBI GI
                   g2961372
BLAST score
                   140
                   9.0e-09
E value
Match length
                   97
% identity
NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                   thaliana] >gi 3036817 emb CAA18507 (AL022373) ribosomal
                   protein L2 [Arabidopsis thaliana]
Seq. No.
                   35013
Seq. ID
                   LIB3039-011-Q1-E1-E9
Method
                   BLASTN
NCBI GI
                   q170091
BLAST score
                   289
E value
                   1.0e-162
Match length
                   369
% identity
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description -
                   complete cds
                   35014
Seq. No.
Seq. ID
                   LIB3039-011-Q1-E1-F7
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   245
                   1.0e-135
E value
Match length
                   357
% identity
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   35015
Seq. No.
                  LIB3039-012-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g169974
BLAST score
                   54
                   6.0e-22
E value
Match length
                   158
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                   35016
Seq. No.
Seq. ID
                  LIB3039-012-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                   g1076510
BLAST score
                   186
E value
                   3.0e-14
Match length
                   58
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
                  >gi 829119 emb CAA52414 (X74403) cyclophilin [Phaseolus
```

vulgaris]

Match length

```
Seq. No.
                    35017
 Seq. ID
                    LIB3039-012-Q1-E1-C8
 Method
                    BLASTN
 NCBI GI
                    g169974
 BLAST score
                    159
                    2.0e-84 ·
 E value
                    259
 Match length
                    90
 % identity
                    Glycine max vspA gene, complete cds
 NCBI Description
 Seq. No.
                    35018
                    LIB3039-012-Q1-E1-D4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3341443
 BLAST score
                    224
 E value
                    3.0e-20
 Match length
                    94
                    59
 % identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                    35019
 Seq. No.
 Seq. ID
                    LIB3039-012-Q1-E1-D5
 Method
                    BLASTX
 NCBI GI
                    g4006867
 BLAST score
                    178 ·
                    3.0e-13
 E value
 Match length
                    67
 % identity
                   (299707) putative protein [Arabidopsis thaliana]
 NCBI Description
                    35020
 Seq. No.
 Seq. ID
                    LIB3039-012-Q1-E1-E1
 Method
                    BLASTX
 NCBI GI
                    g2961300
 BLAST score
                    210
 E value
                    6.0e-17
 Match length
                    84
 % identity
                    52
 NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
                    35021
 Seq. No.
 Seq. ID
                    LIB3039-012-Q1-E1-E12
 Method
                    BLASTX
 NCBI GI
                    g3341443
 BLAST score
                    216
 E value
                    2.0e-17
 Match length
                    88
 % identity
 NCBI Description (AJ223074) acid phosphatase [Glycine max]
                    35022
 Seq. No.
                    LIB3039-012-Q1-E1-E2
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g456713
 BLAST score
                    105
                    4.0e-52
 E value
```

Seq. No.

```
% identity
NCBI Description
                  Glycine max gene for ubiquitin, complete cds
Seq. No.
                  LIB3039-012-Q1-E1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q170091
BLAST score
                   193
E value
                   1.0e-104
Match length
                   356
% identity
                   97
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
Seq. No.
                   35024
Seq. ID
                  LIB3039-012-Q1-E1-F11
Method
                  BLASTN
NCBI GI
                   g410285
BLAST score
                  100
                   6.0e-49
E value
Match length
                   211
% identity
                   87
NCBI Description
                  Pisum sativum rho (ras-related) GTP-binding protein mRNA,
                  complete cds
Seq. No.
                   35025
Seq. ID
                  LIB3039-012-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  g1336081
BLAST score
                  73
E value
                   7.0e-33
Match length
                   325
% identity
                   82
NCBI Description
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
                  mRNA, complete cds
                  35026
Seq. No.
Seq. ID
                  LIB3039-012-Q1-E1-H2
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  231
E value
                   1.0e-127
Match length
                  355
% identity
                   91
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35027
                  LIB3039-013-01-E1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538965
BLAST score
                  180
E value
                  3.0e-13
Match length
                  87
% identity
                  45
NCBI Description
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
```

BLAST score

```
LIB3039-013-Q1-E1-B9
Seq. ID
                  BLASTN
Method
                   g170087
NCBI GI
BLAST score
                   32
E value
                   1.0e-08
Match length
                   60
% identity
                   88
                  G.max vegetative storage protein mRNA (VSP25 gene)
NCBI Description
Seq. No.
                   35029
                  LIB3039-013-Q1-E1-D12
Seq. ID
Method
                  BLASTX
                  g136057
NCBI GI
BLAST score
                  277
E value
                   2.0e-37
Match length
                   85
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >qi 99499 pir A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                  35030
Seq. No.
Seq. ID
                  LIB3039-013-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q2961300
BLAST score
                  142
E value
                  7.0e-09
Match length
                  59
% identity
NCBI Description
                   (AJ225027) ribosomal protein L24 [Cicer arietinum]
Seq. No.
                  35031
Seq. ID
                  LIB3039-014-01-E1-B5
Method
                  BLASTX
NCBI GI
                  q3341443
BLAST score
                  302
E value
                  1.0e-27
Match length
                  116
% identity
NCBI Description
                   (AJ223074) acid phosphatase [Glycine max]
Seq. No.
                  35032
Seq. ID
                  LIB3039-014-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  199
E value
                  1.0e-108
Match length
                  319
% identity
                  91
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35033
Seq. ID
                  LIB3039-014-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  q169974
```

```
E value
                   4.0e-83
Match length
                   208
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                   35034
                   LIB3039-014-Q1-E1-F8
Seq. ID
Method
                   BLASTX
                   q4127352
NCBI GI
BLAST score
                   321
E value
                   9.0e-30
Match length
                   122
% identity
                   (AJ010451) glutathione transferase [Alopecurus myosuroides]
NCBI Description
                   35035
Seq. No.
Seq. ID
                  LIB3039-014-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g3292849
BLAST score
                   317
                   3.0e-29
E value
                   85
Match length
% identity
                   72
                   (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   35036
Seq. No.
                  LIB3039-015-Q1-E1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2558962
BLAST score
                   169
E value
                   4.0e-12
                  75
Match length
                   49
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                   35037
Seq. No.
Seq. ID
                  LIB3039-015-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                   g488573
BLAST score
                  242
E value
                   1.0e-20
Match length
                  81
% identity
NCBI Description (U09463) histone H3.2 [Medicago sativa]
                  35038
Seq. No.
Seq. ID
                  LIB3039-015-Q1-E1-C5
Method
                  BLASTX
NCBI GI
                  g134145
BLAST score
                  144
                  2.0e-09
E value
Match length
                  44
% identity
                   64
                  STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                  PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean
```

>gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975

(M76981) vegetative storage protein [Glycine max]
>gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein
[Glycine max]

Seq. No. 35039

Seq. ID LIB3039-015-Q1-E1-F7

Method BLASTN
NCBI GI g169974
BLAST score 212
E value 1.0e-116
Match length 316
% identity 92

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35040

Seq. ID LIB3039-015-Q1-E1-G7

Method BLASTN
NCBI GI g169974
BLAST score 146
E value 2.0e-76
Match length 290
% identity 88

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35041

Seq. ID LIB3039-015-Q1-E1-H2

Method BLASTX
NCBI GI g3283026
BLAST score 180
E value 3.0e-13
Match length 113
% identity 34

NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

Seq. No. 35042

Seq. ID LIB3039-015-Q1-E1-H9

Method BLASTN
NCBI GI g18551
BLAST score 375
E value 0.0e+00
Match length 383
% identity 99

NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 35043

Seq. ID LIB3039-016-Q1-E1-A3

Method BLASTN
NCBI GI g18644
BLAST score 272
E value 1.0e-151
Match length 316
% identity 97

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 35044

Seq. ID

Method

NCBI GI



```
LIB3039-016-Q1-E1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  189
E value
                  1.0e-102
                  380
Match length
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35045
                  LIB3039-016-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152583
BLAST score
                  197
E value
                  3.0e-15
Match length
                  119
% identity
                   (AC002986) Contains similarity to inhibitor of apoptosis
NCBI Description
                  protein gb U45881 from D. melanogaster. [Arabidopsis .
                  thaliana
Seq. No.
                  35046
Seq. ID
                  LIB3039-017-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  g541950
BLAST score
                  136
E value
                  1.0e-08
Match length
                  51
% identity
NCBI Description
                  SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
                  [Glycine max]
Seq. No.
                  35047
Seq. ID
                  LIB3039-017-01-E1-D3
Method
                  BLASTX
NCBI GI
                  g2281449
BLAST score
                  183
E value
                  1.0e-13
Match length
                  55
% identity
                  78
NCBI Description
                   (U90214) leucine zipper transcription factor TGA2.1
                   [Nicotiana tabacum]
Seq. No.
                  35048
Seq. ID
                  LIB3039-017-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  a169974
BLAST score
                  222
E value
                  1.0e-122
Match length
                  321
% identity
                  93
NCBI Description
                  Glycine max vspA gene, complete cds
Seq. No.
                  35049
```

5299

LIB3039-017-Q1-E1-E12

g- ...

BLASTX

q3482925

% identity

```
180
BLAST score
E value
                   2.0e-13.
Match length
                   69
% identity
                   54
NCBI Description
                   (AC003970) Highly similar to cinnamyl alcohol
                   dehydrogenase, gi 1143445 [Arabidopsis thaliana]
                   35050
Seq. No.
Seq. ID
                   LIB3039-017-Q1-E1-H10
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   329
E value
                   0.0e + 00
Match length
                   361
% identity
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   35051
Seq. No.
                   LIB3039-017-Q1-E1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3341443
BLAST score
                   235
E value
                   1.0e-19
Match length
                   98
                   52
% identity
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
                   35052
Seq. No.
Seq. ID
                   LIB3039-018-Q1-E1-A4
Method
                   BLASTN
NCBI GI
                   g558922
BLAST score
                   67
E value
                   3.0e-29
Match length
                   179
                   92
% identity
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                   complete cds
                   35053
Seq. No.
Seq. ID
                   LIB3039-018-Q1-E1-B10
Method
                   BLASTX
NCBI GI
                   g3341443
BLAST score
                   324
E value
                   4.0e-30
Match length
                   113
% identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   35054
Seq. ID
                   LIB3039-018-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   g4262140
BLAST score
                  170
E value
                   4.0e-12
Match length
                   68
```